QUANTITATIVE CHEMICAL ANALYSIS



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Quantitative Chemical Analysis

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Detailed Licensing

Detailed Licensing

Licensing

*A detailed breakdown of this resource's licensing can be found in **Back Matter/Detailed Licensing**.*

CHAPTER OVERVIEW

1: INTRODUCTION TO ANALYTICAL CHEMISTRY

Chemistry is the study of matter, including its composition, its structure, its physical properties, and its reactivity. Although there are many ways to study chemistry, traditionally we divide it into five areas: organic chemistry, inorganic chemistry, biochemistry, physical chemistry, and analytical chemistry. This division is historical and, perhaps, arbitrary, as suggested by current interest in interdisciplinary areas, such as bioanalytical chemistry and organometallic chemistry. Nevertheless, these five areas remain the simplest division that spans the discipline of chemistry.

Each of these traditional areas of chemistry brings a unique perspective to how a chemist makes sense of the diverse array of elements, ions, and molecules (both small and large) that make up our physical environment. An undergraduate chemistry course, therefore, is much more than a collection of facts; it is, instead, the means by which we learn to see the chemical world from a different perspective. In keeping with this spirit, this chapter introduces you to the field of analytical chemistry and highlights the unique perspectives that analytical chemists bring to the study of chemistry.

- 1.1: What is Analytical Chemistry
- 1.2: The Analytical Perspective
- 1.3: Common Analytical Problems
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Thumbnail: Several graduated cylinders of various thickness and heights with white side markings in front of a large beaker. They are all filled about halfway with red or blue chemical compounds. The blue ink is showing signs of Brownian motion when dissolving into water. (CC BY-SA 3.0; Horia Varlan via Wikipedia).

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1.1: WHAT IS ANALYTICAL CHEMISTRY

"ANALYTICAL CHEMISTRY IS WHAT ANALYTICAL CHEMISTS DO."

This quote is attributed to C. N. Reilly (1925-1981) on receipt of the 1965 Fisher Award in Analytical Chemistry. Reilly, who was a professor of chemistry at the University of North Carolina at Chapel Hill, was one of the most influential analytical chemists of the last half of the twentieth century.

For another view of what constitutes analytical chemistry, see the article "Quo Vadis, Analytical Chemistry?", the full reference for which is Valcárcel, M. *Anal. Bioanal. Chem.* **2016**, *408*, 13-21.

Let's begin with a deceptively simple question: What is analytical chemistry? Like all areas of chemistry, analytical chemistry is so broad in scope and so much in flux that it is difficult to find a simple definition more revealing than that quoted above. In this chapter we will try to expand upon this simple definition by saying a little about what analytical chemistry is, as well as a little about what analytical chemistry is not.

Analytical chemistry often is described as the area of chemistry responsible for characterizing the composition of matter, both qualitatively (Is there lead in this paint chip?) and quantitatively (How much lead is in this paint chip?). As we shall see, this description is misleading.

Most chemists routinely make qualitative and quantitative measurements. For this reason, some scientists suggest that analytical chemistry is not a separate branch of chemistry, but simply the application of chemical knowledge [Ravey, M. *Spectroscopy*, **1990**, *5(7)*, 11]. In fact, you probably have performed many such quantitative and qualitative analyses in other chemistry courses.

> You might, for example, have determined the concentration of acetic acid in vinegar using an acid–base titration, or used a qualitative analysis scheme to identify which of several metal ions are in an aqueous sample.

Defining analytical chemistry as the application of chemical knowledge ignores the unique perspective that an analytical chemist bring to the study of chemistry. The craft of analytical chemistry is found not in performing a routine analysis on a routine sample—a task we appropriately call chemical analysis—but in improving established analytical methods, in extending these analytical methods to new types of samples, and in developing new analytical methods to measure chemical phenomena [de Haseth, J. *Spectroscopy*, **1990**, *5(7)*, 11].

Here is one example of the distinction between analytical chemistry and chemical analysis. A mining engineer evaluates an ore by comparing the cost of removing the ore from the earth with the value of its contents, which they estimate by analyzing a sample of the ore. The challenge of developing and validating a quantitative analytical method is the analytical chemist's responsibility; the routine, daily application of the analytical method is the job of the chemical analyst.

THE SEVEN STAGES OF AN ANALYTICAL METHOD

1. Conception of analytical method (birth).
2. Successful demonstration that the analytical method works.
3. Establishment of the analytical method's capabilities.
4. Widespread acceptance of the analytical method.
5. Continued development of the analytical method leads to significant improvements.
6. New cycle through steps 3–5.
7. Analytical method can no longer compete with newer analytical methods (death).

Steps 1–3 and 5 are the province of analytical chemistry; step 4 is the realm of chemical analysis.

The seven stages of an analytical method listed here are modified from Fassel, V. A. *Fresenius' Z. Anal. Chem.* **1986**, *324*, 511–518 and Hieftje, G. M. *J. Chem. Educ.* **2000**, *77*, 577–583.

Another difference between analytical chemistry and chemical analysis is that an analytical chemist works to improve and to extend established analytical methods. For example, several factors complicate the quantitative analysis of nickel in ores, including nickel's unequal distribution within the ore, the ore's complex matrix of silicates and oxides, and the presence of other metals that may interfere with the analysis. Figure 1.1.1 outlines one standard analytical method in use during the late nineteenth century [Fresenius. C. R. *A System of Instruction in Quantitative Chemical Analysis*; John Wiley and Sons: New York, 1881]. The need for many reactions, digestions, and filtrations makes this analytical method both time-consuming and difficult to perform accurately.

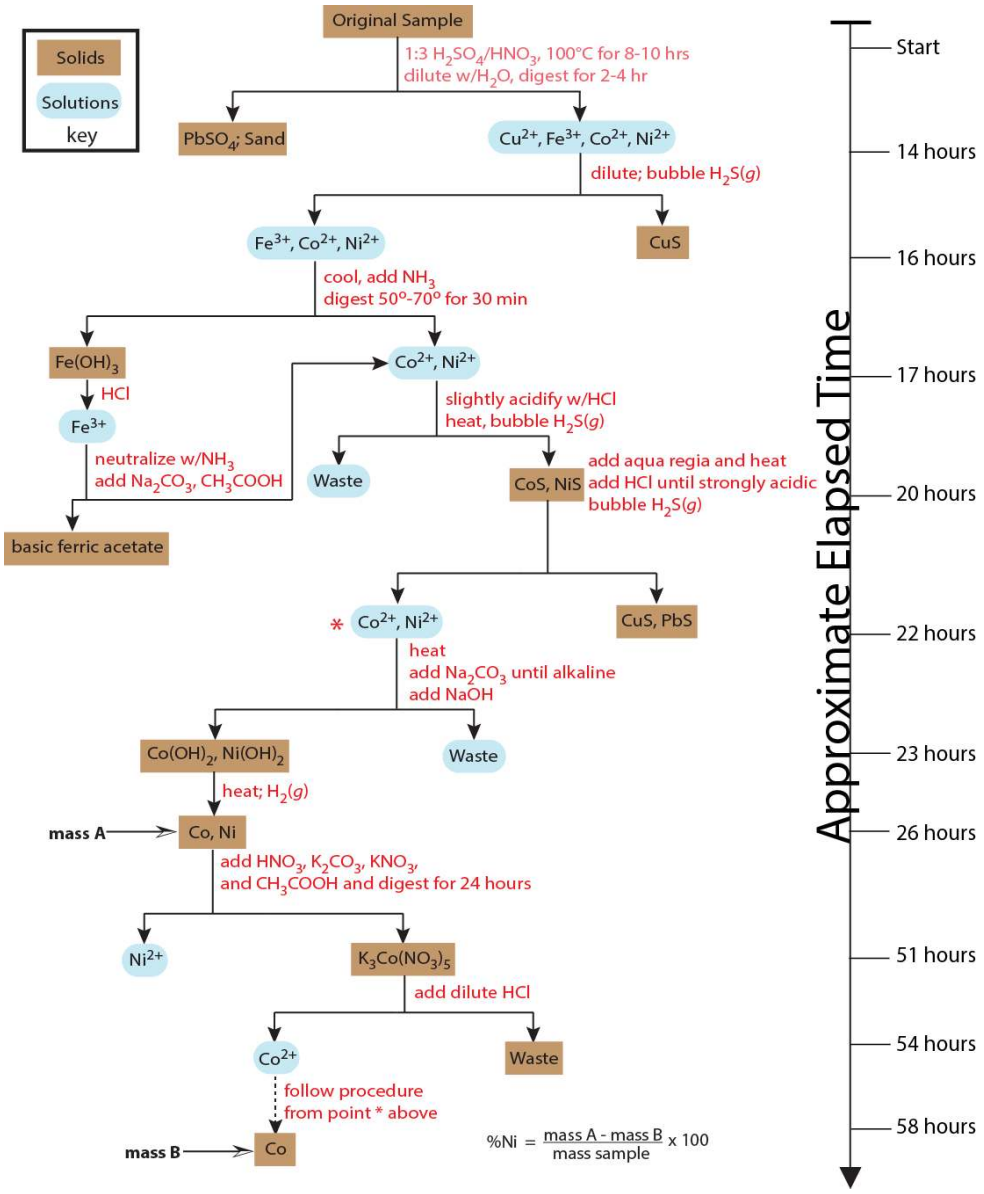


Figure 1.1.1 : Fresenius' analytical scheme for the gravimetric analysis of Ni in ores. After each step, the solid and the solution are separated by gravity filtration. Note that the mass of nickel is not determined directly. Instead, Co and Ni first are isolated and weighed together (**mass A**), and then Co is isolated and weighed separately (**mass B**). The timeline shows that it takes approximately 58 hours to analyze one sample. This scheme is an example of a gravimetric analysis, which is explored further in Chapter 8.

The discovery, in 1905, that dimethylglyoxime (dmg) selectively precipitates Ni^{2+} and Pd^{2+} led to an improved analytical method for the quantitative analysis of nickel [Kolthoff, I. M.; Sandell, E. B. *Textbook of Quantitative Inorganic Analysis*, 3rd Ed., The Macmillan Company: New York, 1952]. The resulting analysis, which is outlined in Figure 1.1.2 , requires fewer manipulations and less time. By the 1970s, flame atomic absorption spectrometry replaced gravimetry as the standard method for analyzing nickel in ores, resulting in an even more rapid analysis [Van Loon, J. C. *Analytical Atomic Absorption Spectroscopy*, Academic Press: New York, 1980]. Today, the standard analytical method utilizes an inductively coupled plasma optical emission spectrometer.

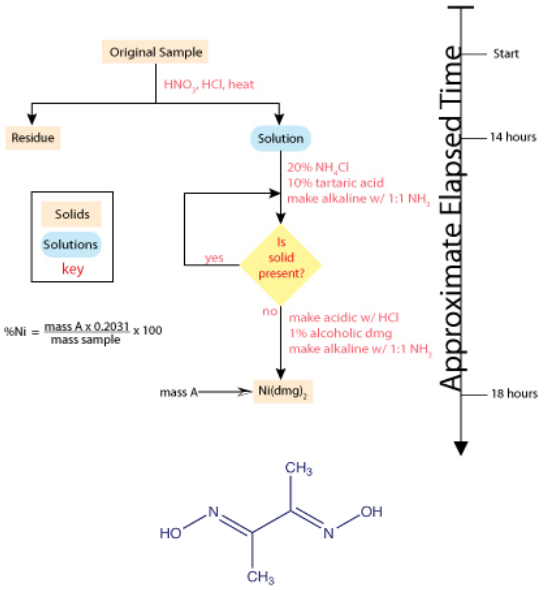


Figure 1.1.2 : Gravimetric analysis for Ni in ores by precipitating $Ni(dmg)_2$. The timeline shows that it takes approximately 18 hours to analyze a single sample, substantially less than 58 hours for the method in Figure 1.1.1 . The factor of 0.2301 in the equation for %Ni accounts for the difference in the formula weights of Ni and $Ni(dmg)_2$; see Chapter 8 for further details. The structure of dmg is shown below the method's flow chart.

Perhaps a more appropriate description of analytical chemistry is “the science of inventing and applying the concepts, principles, and...strategies for measuring the characteristics of chemical systems” [Murray, R. W. *Anal. Chem.* **1991**, *63*, 271A]. Analytical chemists often work at the extreme edges of analysis, extending and improving the ability of all chemists to make meaningful measurements on smaller samples, on more complex samples, on shorter time scales, and on species present at lower concentrations. Throughout its history, analytical chemistry has provided many of the tools and methods necessary for research in other traditional areas of chemistry, as well as fostering multidisciplinary research in, to name a few, medicinal chemistry, clinical chemistry, toxicology, forensic chemistry, materials science, geochemistry, and environmental chemistry.

> To an analytical chemist, the process of making a useful measurement is critical; if the measurement is not of central importance to the work, then it is not analytical chemistry.

You will come across numerous examples of analytical methods in this textbook, most of which are routine examples of chemical analysis. It is important to remember, however, that nonroutine problems prompted analytical chemists to develop these methods.

> An editorial in *Analytical Chemistry* entitled “Some Words about Categories of Manuscripts” highlights nicely what makes a research endeavor relevant to modern analytical chemistry. The full citation is Murray, R. W. *Anal. Chem.* **2008**, *80*, 4775; for a more recent editorial, see “The Scope of *Analytical Chemistry*” by Sweedler, J. V. et. al. *Anal. Chem.* **2015**, *87*, 6425.

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1.2: THE ANALYTICAL PERSPECTIVE

Having noted that each area of chemistry brings a unique perspective to the study of chemistry, let's ask a second deceptively simple question: What is the analytical perspective? Many analytical chemists describe this perspective as an analytical approach to solving problems.

> For different viewpoints on the analytical approach see (a) Beilby, A. L. *J. Chem. Educ.* **1970**, *47*, 237-238; (b) Lucchesi, C. A. *Am. Lab.* **1980**, October, 112-119; (c) Atkinson, G. F. *J. Chem. Educ.* **1982**, *59*, 201-202; (d) Pardue, H. L.; Woo, J. *J. Chem. Educ.* **1984**, *61*, 409-412; (e) Guarnieri, M. *J. Chem. Educ.* **1988**, *65*, 201-203, (f) Strobel, H. A. *Am. Lab.* **1990**, October, 17-24.

Although there likely are as many descriptions of the analytical approach as there are analytical chemists, it is convenient to define it as the five-step process shown in Figure 1.2.1 .

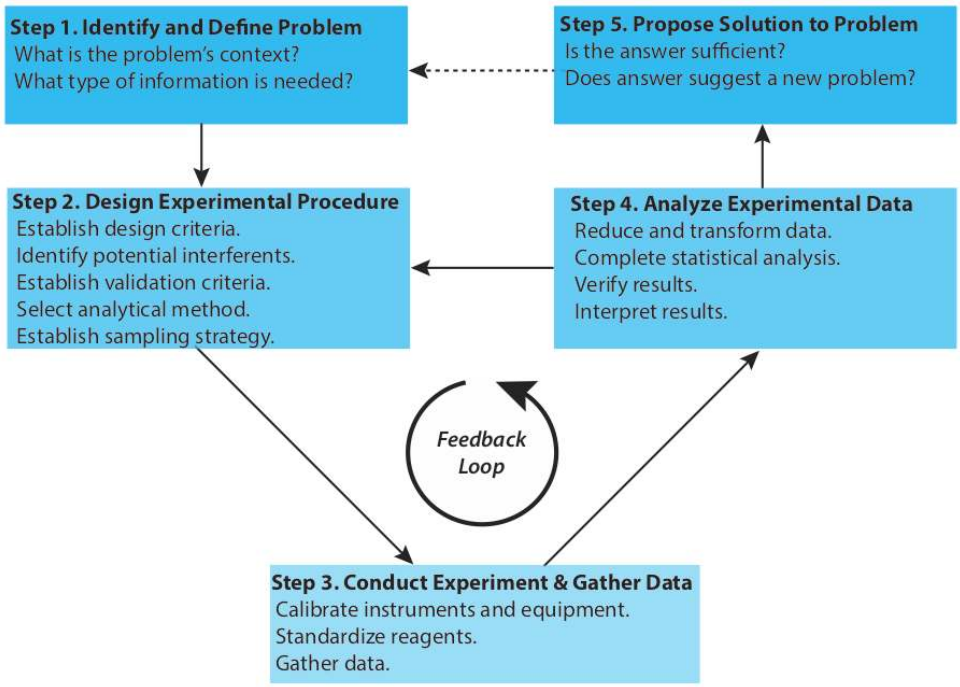


Figure 1.2.1 : Flow diagram showing one view of the analytical approach to solving problems (modified after Atkinson, G. F. *J. Chem. Educ.* **1982**, *59*, 201-202).

Three general features of this approach deserve our attention. First, in steps 1 and 5 analytical chemists have the opportunity to collaborate with individuals outside the realm of analytical chemistry. In fact, many problems on which analytical chemists work originate in other fields. Second, the heart of the analytical approach is a feedback loop (steps 2, 3, and 4) in which the result of one step requires that we reevaluate the other steps. Finally, the solution to one problem often suggests a new problem.

Analytical chemistry begins with a problem, examples of which include evaluating the amount of dust and soil ingested by children as an indicator of environmental exposure to particulate based pollutants, resolving contradictory evidence regarding the toxicity of perfluoro polymers during combustion, and developing rapid and sensitive detectors for chemical and biological weapons. At this point the analytical approach involves a collaboration between the analytical chemist and the individual or agency working on the problem. Together they determine what information is needed and clarify how the problem relates to broader research goals or policy issues, both essential to the design of an appropriate experimental procedure.

> These examples are taken from a series of articles, entitled the "Analytical Approach," which for many years was a regular feature of the journal *Analytical Chemistry*.

To design the experimental procedure the analytical chemist considers criteria, such as the required accuracy, precision, sensitivity, and detection limit, the urgency with which results are needed, the cost of a single analysis, the number of samples to analyze, and the amount of sample available for analysis. Finding an appropriate balance between these criteria frequently is complicated by their interdependence. For example, improving precision may require a larger amount of sample than is available. Consideration also is given to how to collect, store,

and prepare samples, and to whether chemical or physical interferences will affect the analysis. Finally a good experimental procedure may yield useless information if there is no method for validating the results.

The most visible part of the analytical approach occurs in the laboratory. As part of the validation process, appropriate chemical and physical standards are used to calibrate equipment and to standardize reagents.

The data collected during the experiment are then analyzed. Frequently the data first is reduced or transformed to a more readily analyzable form and then a statistical treatment of the data is used to evaluate accuracy and precision, and to validate the procedure. Results are compared to the original design criteria and the experimental design is reconsidered, additional trials are run, or a solution to the problem is proposed. When a solution is proposed, the results are subject to an external evaluation that may result in a new problem and the beginning of a new cycle.

> Chapter 3 introduces you to the language of analytical chemistry. You will find terms such accuracy, precision, and sensitivity defined there. Chapter 4 introduces the statistical analysis of data. Calibration and standardization methods, including a discussion of linear regression, are covered in Chapter 5. See Chapter 7 for a discussion of how to collect, store, and prepare samples for analysis. See Chapter 14 for a discussion about how to validate an analytical method.

As noted earlier some scientists question whether the analytical approach is unique to analytical chemistry. Here, again, it helps to distinguish between a chemical analysis and analytical chemistry. For an analytically-oriented scientist, such as a physical organic chemist or a public health officer, the primary emphasis is how the analysis supports larger research goals that involve fundamental studies of chemical or physical processes, or that improve access to medical care. The essence of analytical chemistry, however, is in developing new tools for solving problems, and in defining the type and quality of information available to other scientists.

? EXERCISE 1.2.1

As an exercise, let's adapt our model of the analytical approach to the development of a simple, inexpensive, portable device for completing bioassays in the field. Before continuing, locate and read the article

"Simple Telemedicine for Developing Regions: Camera Phones and Paper-Based Microfluidic Devices for Real-Time, Off-Site Diagnosis"

by Andres W. Martinez, Scott T. Phillips, Emanuel Carriho, Samuel W. Thomas III, Hayat Sindi, and George M. Whitesides. You will find it on pages 3699-3707 in Volume 80 of the journal *Analytical Chemistry*, which was published in 2008. As you read the article, pay particular attention to how it emulates the analytical approach and consider the following questions:

1. What is the analytical problem and why is it important?
2. What criteria did the authors consider in designing their experiments? What is the basic experimental procedure?
3. What interferences were considered and how did they overcome them? How did the authors calibrate the assay?
4. How did the authors validate their experimental method?
5. Is there evidence that steps 2, 3, and 4 in Figure 1.2.1 are repeated?
6. Was there a successful conclusion to the analytical problem?

Don't let the technical details in the paper overwhelm you; if you skim over these you will find the paper both well-written and accessible.

Answer

What is the analytical problem and why is it important?

A medical diagnoses often relies on the results of a clinical analysis. When you visit a doctor, they may draw a sample of your blood and send it to the lab for analysis. In some cases the result of the analysis is available in 10-15 minutes. What is possible in a developed country, such as the United States, may not be feasible in a country with less access to expensive lab equipment and with fewer trained personnel available to run the tests and to interpret the results. The problem addressed in this paper, therefore, is the development of a reliable device for rapidly performing a clinical assay under less than ideal circumstances.

What criteria did the authors consider in designing their experiments?

In considering a solution to this problem, the authors identify seven important criteria for the analytical method: (1) it must be inexpensive; (2) it must operate without the need for much electricity, so that it can be used in remote locations; (3) it must be adaptable to many types of assays; (4) its must not require a highly skilled technician; (5) it must be quantitative; (6) it must be accurate; and (7) it must produce results rapidly.

What is the basic experimental procedure?

The authors describe how they developed a paper-based microfluidic device that allows anyone to run an analysis simply by dipping the device into a sample (synthetic urine, in this case). The sample moves by capillary action into test zones containing reagents that react with specific species (glucose and protein, for this prototype device). The reagents react to produce a color whose intensity is proportional to the species' concentration. A digital photograph of the microfluidic device is taken using a cell phone camera and sent to an off-site physician who uses image editing software to analyze the photograph and to interpret the assay's result.

What interferences were considered and how did they overcome them?

In developing this analytical method the authors considered several chemical or physical interferences. One concern was the possibility of non-specific interactions between the paper and the glucose or protein, which might lead to non-uniform image in the test zones. A careful analysis of the distribution of glucose and protein in the test zones showed that this was not a problem. A second concern was the possibility that particulate materials in the sample might interfere with the analyses. Paper is a natural filter for particulate materials and the authors found that samples containing dust, sawdust, and pollen do not interfere with the analysis for glucose. Pollen, however, is an interferent for the protein analysis, presumably because it, too, contains protein.

How did the author's calibrate the assay?

To calibrate the device the authors analyzed a series of standard solutions that contained known concentrations of glucose and protein. Because an image's intensity depends upon the available light, a standard sample is run with the test samples, which allows a single calibration curve to be used for samples collected under different lighting conditions.

How did the author's validate their experimental method?

The test device contains two test zones for each analyte, which allows for duplicate analyses and provides one level of experimental validation. To further validate the device, the authors completed 12 analyses at each of three known concentrations of glucose and protein, obtaining acceptable accuracy and precision in all cases.

Is there any evidence of repeating steps 2, 3, and 4 in Figure 1.2.1?

Developing this analytical method required several cycles through steps 2, 3, and 4 of the analytical approach. Examples of this feedback loop include optimizing the shape of the test zones and evaluating the importance of sample size.

Was there a successful conclusion to the analytical problem?

Yes. The authors were successful in meeting their goals by developing and testing an inexpensive, portable, and easy-to-use device for running clinical samples in developing countries.

This exercise provides you with an opportunity to think about the analytical approach in the context of a real analytical problem. Practice exercises such as this provide you with a variety of challenges ranging from simple review problems to more open-ended exercises. You will find answers to practice exercises at the end of each chapter.

Use this link to access the article's abstract from the journal's web site. If your institution has an on-line subscription you also will be able to download a PDF version of the article.

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1.3: COMMON ANALYTICAL PROBLEMS

Many problems in analytical chemistry begin with the need to identify what is present in a sample. This is the scope of a ***qualitative analysis***, examples of which include identifying the products of a chemical reaction, screening an athlete's urine for a performance-enhancing drug, or determining the spatial distribution of Pb on the surface of an airborne particulate. An early challenge for analytical chemists was developing simple chemical tests to identify inorganic ions and organic functional groups. The classical laboratory courses in inorganic and organic qualitative analysis, still taught at some schools, are based on this work.

> See, for example, the following laboratory textbooks: (a) Sorum, C. H.; Lagowski, J. J. *Introduction to Semimicro Qualitative Analysis*, 5th Ed.; Prentice-Hall: Englewood, NJ, 1977; (b) Shriner, R. L.; Fuson, R. C.; Curtin, D. Y. *The Systematic Identification of Organic Compounds*, 5th Ed.; John Wiley and Sons: New York, 1964.

Modern methods for qualitative analysis rely on instrumental techniques, such as infrared (IR) spectroscopy, nuclear magnetic resonance (NMR) spectroscopy, and mass spectrometry (MS). Because these qualitative applications are covered adequately elsewhere in the undergraduate curriculum, typically in organic chemistry, they receive no further consideration in this text.

Perhaps the most common analytical problem is a ***quantitative analysis***, examples of which include the elemental analysis of a newly synthesized compound, measuring the concentration of glucose in blood, or determining the difference between the bulk and the surface concentrations of Cr in steel. Much of the analytical work in clinical, pharmaceutical, environmental, and industrial labs involves developing new quantitative methods to detect trace amounts of chemical species in complex samples. Most of the examples in this text are of quantitative analyses.

Another important area of analytical chemistry, which receives some attention in this text, are methods for characterizing physical and chemical properties. The determination of chemical structure, of equilibrium constants, of particle size, and of surface structure are examples of a ***characterization analysis***.

The purpose of a qualitative, a quantitative, or a characterization analysis is to solve a problem associated with a particular sample. The purpose of a ***fundamental analysis***, on the other hand, is to improve our understanding of the theory that supports an analytical method and to understand better an analytical method's limitations.

> A good resource for current examples of qualitative, quantitative, characterization, and fundamental analyses is *Analytical Chemistry's* annual review issue that highlights fundamental and applied research in analytical chemistry. Examples of review articles in the 2015 issue include "Analytical Chemistry in Archaeological Research," "Recent Developments in Paper-Based Microfluidic Devices," and "Vibrational Spectroscopy: Recent Developments to Revolutionize Forensic Science."

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1.4: PROBLEMS

1. For each of the following problems indicate whether its solution requires a qualitative analysis, a quantitative analysis, a characterization analysis, and/or a fundamental analysis. More than one type of analysis may be appropriate for some problems.
   a. The residents in a neighborhood near a hazardous-waste disposal site are concerned that it is leaking contaminants into their groundwater.
   b. An art museum is concerned that a recently acquired oil painting is a forgery.
   c. Airport security needs a more reliable method for detecting the presence of explosive materials in luggage.
   d. The structure of a newly discovered virus needs to be determined.
   e. A new visual indicator is needed for an acid–base titration.
   f. A new law requires a method for evaluating whether automobiles are emitting too much carbon monoxide.
2. Read the article "When Machine Tastes Coffee: Instrumental Approach to Predict the Sensory Profile of Espresso Coffee," which discusses work completed at the Nestlé Research Center in Lausanne, Switzerland. You will find the article on pages 1574-1581 in Volume 80 of *Analytical Chemistry*, published in 2008. Prepare an essay that summarizes the nature of the problem and how it was solved. Do not worry about the nitty-gritty details of the mathematical model developed by the authors, which relies on a combination of an analysis of variance (ANOVA), a topic we will consider in Chapter 14, and a principle component regression (PCR), at topic that we will not consider in this text. Instead, focus on the results of the model by examining the visualizations in Figure 3 and Figure 4 of the paper. As a guide, refer to Figure 1.2.1 in this chapter for a model of the analytical approach to solving problems. Use this link to access the article's abstract from the journal's web site. If your institution has an on-line subscription you also will be able to download a PDF version of the article.

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1.5: ADDITIONAL RESOURCES

The role of analytical chemistry within the broader discipline of chemistry has been discussed by many prominent analytical chemists; several notable examples are listed here.

- Baiulescu, G. E.; Patroescu, C; Chalmers, R. A. *Education and Teaching in Analytical Chemistry*, Ellis Horwood: Chichester, 1982.
- de Haseth, J. "What is Analytical Chemistry?," *Spectroscopy* **1990**, *5*, 19–21.
- Heiftje, G. M. "The Two Sides of Analytical Chemistry," *Anal. Chem.* **1985**, *57*, 256A–267A.
- Heiftje, G. M. "But is it analytical chemistry?," *Am. Lab.* **1993**, October, 53–61.
- Kissinger, P. T. "Analytical Chemistry—What is It? Why Teach It?," *Trends Anal. Chem.* **1992**, *11*, 57–57.
- Laitinen, H. A.; Ewing, G. (eds.) *A History of Analytical Chemistry*, The Division of Analytical Chemistry of the American Chemical Society: Washington, D. C., 1972.
- Laitinen, H. A. "Analytical Chemistry in a Changing World," *Anal. Chem.* **1980**, *52*, 605A–609A.
- Laitinen, H. A. "History of Analytical Chemistry in the U. S. A.," *Talanta*, **1989**, *36*, 1–9.
- McLafferty, F. W. "Analytical Chemistry: Historic and Modern," *Acc. Chem. Res.* **1990**, *23*, 63–64.
- Mottola, H. A. "The Interdisciplinary and Multidisciplinary Nature of Contemporary Analytical Chemistry and its Core Components," *Anal. Chim. Acta* **1991**, *242*, 1–3.
- Noble, D. "From Wet Chemistry to Instrumental Analysis: A Perspective on Analytical Sciences," *Anal. Chem.* **1994**, *66*, 251A–263A.
- Tyson, J. *Analysis: What Analytical Chemists Do*, Royal Society of Chemistry: Cambridge, England 1988.

For additional discussion of clinical assays based on paper-based microfluidic devices, see the following papers.

- Ellerbee, A. K.; Phillips, S. T.; Siegel, A. C.; Mirica, K. A.; Martinez, A. W.; Striehl, P.; Jain, N.; Prentiss, M.; Whitesides, G. M. "Quantifying Colorimetric Assays in Paper-Based Microfluidic Devices by Measuring the Transmission of Light Through Paper," *Anal. Chem.* **2009**, *81*, 8447–8452.
- Martinez, A. W.; Phillips, S. T.; Whitesides, G. M. "Diagnostics for the Developing World: Microfluidic Paper-Based Analytical Devices," *Anal. Chem.* **2010**, *82*, 3–10.

This textbook provides one introduction to the discipline of analytical chemistry. There are other textbooks for introductory courses in analytical chemistry and you may find it useful to consult them when you encounter a difficult concept; often a fresh perspective will help crystallize your understanding. The textbooks listed here are excellent resources.

- Enke, C. *The Art and Science of Chemical Analysis*, Wiley: New York.
- Christian, G. D.; Dasgupta, P, K.; Schug; K. A. *Analytical Chemistry*, Wiley: New York.
- Harris, D. *Quantitative Chemical Analysis*, W. H. Freeman and Company: New York.
- Kellner, R.; Mermet, J.-M.; Otto, M.; Valcárcel, M.; Widmer, H. M. *Analytical Chemistry*, Wiley- VCH: Weinheim, Germany.
- Rubinson, J. F.; Rubinson, K. A. *Contemporary Chemical Analysis*, Prentice Hall: Upper Saddle River, NJ.
- Skoog, D. A.; West, D. M.; Holler, F. J. *Fundamentals of Analytical Chemistry*, Saunders: Philadelphia.

To explore the practice of modern analytical chemistry there is no better resource than the primary literature. The following journals publish broadly in the area of analytical chemistry.

- Analytical and Bioanalytical Chemistry
- Analytical Chemistry
- Analytical Chimica Acta
- Analyst
- Talanta

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1.6: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

Analytical chemists work to improve the ability of chemists and other scientists to make meaningful measurements. The need to work with smaller samples, with more complex materials, with processes occurring on shorter time scales, and with species present at lower concentrations challenges analytical chemists to improve existing analytical methods and to develop new ones.

Typical problems on which analytical chemists work include qualitative analyses (What is present?), quantitative analyses (How much is present?), characterization analyses (What are the sample's chemical and physical properties?), and fundamental analyses (How does this method work and how can it be improved?).

KEY TERMS

- characterization analysis
- fundamental analysis
- qualitative analysis
- quantitative analysis

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CHAPTER OVERVIEW

2: BASIC TOOLS OF ANALYTICAL CHEMISTRY

In the chapters that follow we will explore many aspects of analytical chemistry. In the process we will consider important questions, such as “How do we extract useful results from experimental data?”, “How do we ensure our results are accurate?”, “How do we obtain a representative sample?”, and “How do we select an appropriate analytical technique?” Before we consider these and other questions, we first must review some basic tools of importance to analytical chemists.

2.1: Measurements in Analytical Chemistry
2.2: Concentration
2.3: Stoichiometric Calculations
2.4: Basic Equipment
2.5: Preparing Solutions
2.6: Spreadsheets and Computational Software
2.7: The Laboratory Notebook
2.8: Problems
2.9: Additional Resources
2.10: Chapter Summary and Key Terms

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2.1: MEASUREMENTS IN ANALYTICAL CHEMISTRY

Analytical chemistry is a quantitative science. Whether determining the concentration of a species, evaluating an equilibrium constant, measuring a reaction rate, or drawing a correlation between a compound's structure and its reactivity, analytical chemists engage in "measuring important chemical things" [Murray, R. W. *Anal. Chem.* **2007**, *79*, 1765]. In this section we review briefly the basic units of measurement and the proper use of significant figures.

UNITS OF MEASUREMENT

A measurement usually consists of a unit and a number that expresses the quantity of that unit. We can express the same physical measurement with different units, which creates confusion if we are not careful to specify the unit. For example, the mass of a sample that weighs 1.5 g is equivalent to 0.0033 lb or to 0.053 oz. To ensure consistency, and to avoid problems, scientists use the common set of fundamental base units listed in Table 2.1.1 . These units are called SI units after the Système International d'Unités.

> It is important for scientists to agree upon a common set of units. In 1999, for example, NASA lost a Mars Orbiter spacecraft because one engineering team used English units in their calculations and another engineering team used metric units. As a result, the spacecraft came too close to the planet's surface, causing its propulsion system to overheat and fail.
>
> Some measurements, such as absorbance, do not have units. Because the meaning of a unitless number often is unclear, some authors include an artificial unit. It is not unusual to see the abbreviation AU—short for absorbance unit—following an absorbance value, which helps clarify that the measurement is an absorbance value.

Table 2.1.1 : Fundamental Base SI Units

Measurement	Unit	Symbol	Definition (1 unit is...)
mass	kilogram	kg	...the mass of the international prototype, a Pt-Ir object housed at the Bureau International de Poids and Measures at Sèvres, France. (Note: The mass of the international prototype changes at a rate of approximately 1 µg per year due to reversible surface contamination. The reference mass, therefore, is determined immediately after its cleaning using a specified procedure. Current plans call for retiring the international prototype and defining the kilogram in terms of Planck's constant; see this link for more details.)
distance	meter	m	...the distance light travels in $(299\ 792\ 458)^{-1}$ seconds.
temperature	kelvin	K	...equal to $(273.16)^{-1}$, where 273.16 K is the triple point of water (where its solid, liquid, and gaseous forms are in equilibrium. and where 0 is the lowest possible temperature).
time	second	s	...the time it takes for 9 192 631 770 periods of radiation corresponding to a specific transition of the ^{133}Cs atom.
current	ampere	A	...the current producing a force of 2×10^{-7} N/m between two straight parallel conductors of infinite length separated by one meter (in a vacuum).
amount of substance	mole	mol	...the amount of a substance containing as many particles as there are atoms in exactly 0.012 kilogram of ^{12}C.
light	candela	cd	...the luminous intensity of a source with a monochromatic frequency of 540×10^{12} hertz and a radiant power of $(683)^{-1}$ watts per steradian.

> There is some disagreement on the use of "amount of substance" to describe the measurement for which the mole is the base SI unit; see "What's in a Name? Amount of Substance, Chemical Amount, and Stoichiometric Amount," the full reference for which is Giunta, C. J. *J. Chem. Educ.* **2016**, *93*, 583–586.

We define other measurements using these fundamental SI units. For example, we measure the quantity of heat produced during a chemical reaction in joules, (J), where 1 J is equivalent to 1 m kg/s . Table 2.1.2 provides a list of some important derived SI units, as well as a few common non-SI units.

Table 2.1.2 : Derived SI Units and Non-SI Units of Importance to Analytical Chemistry

Measurement	Unit	Symbol	Equivalent SI Units
length	angstrom (non-SI)	Å	$1\ Å = 1 \times 10^{-10}$ m
volume	liter (non-SI)	L	$1\ L = 10^{-3}\ m^3$
force	newton (SI)	N	$1\ N = 1\ m{\cdot}kg/s^2$
pressure	pascal (SI) atmosphere (non-SI)	Pa atm	$1\ Pa = 1\ N/m^3 = 1\ kg/(m{\cdot}s^2)$ 1 atm = 101 325 Pa
energy, work, heat	joule (SI) calorie (non-SI) electron volt (non-SI)	J cal eV	$1\ J = 1\ N{\cdot}m = 1\ m^2{\cdot}kg/s^2$ 1 cal = 4.184 J $1\ eV = 1.602\ 177\ 33 \times 10^{-19}$ J
power	watt (SI)	W	$1\ W = 1\ J/s = 1\ m^2{\cdot}kg/s^3$
charge	coulomb (SI)	C	$1\ C = 1\ A{\cdot}s$
potential	volt (SI)	V	$1\ V = 1\ W/A = 1\ m^2{\cdot}kg/(s^3{\cdot}A)$
frequency	hertz (SI)	Hz	$1\ Hz = s^{-1}$
temperature	Celcius (non-SI)	°C	°C = K – 273.15

Chemists frequently work with measurements that are very large or very small. A mole contains 602 213 670 000 000 000 000 000 particles and some analytical techniques can detect as little as 0.000 000 000 000 001 g of a compound. For simplicity, we express these measurements using scientific notation; thus, a mole contains $6.022\ 136\ 7 \times 10^{23}$ particles, and the detected mass is 1×10^{-15} g. Sometimes we wish to express a measurement without the exponential term, replacing it with a prefix (Table 2.1.3). A mass of 1×10^{-15} g, for example, is the same as 1 fg, or femtogram.

> Writing a lengthy number with spaces instead of commas may strike you as unusual. For a number with more than four digits on either side of the decimal point, however, the recommendation from the International Union of Pure and Applied Chemistry is to use a thin space instead of a comma.

Table 2.1.3 : Common Prefixes for Exponential Notation

Prefix	Symbol	Factor	Prefix	Symbol	Factor	Prefix	Symbol	Factor
yotta	Y	10^{24}	kilo	k	10^{3}	micro	μ	10^{-6}
zetta	Z	10^{21}	hecto	h	10^{2}	nano	n	10^{-9}
eta	E	10^{18}	deka	da	10^{1}	pico	p	10^{-12}
peta	P	10^{15}	—	—	10^{0}	femto	f	10^{-15}
tera	T	10^{12}	deci	d	10^{-1}	atto	a	10^{-18}
giga	G	10^{9}	centi	c	10^{-2}	zepto	z	10^{-21}
mega	M	10^{6}	milli	m	10^{-3}	yocto	y	10^{-24}

UNCERTAINTY IN MEASUREMENTS

A measurement provides information about both its magnitude and its uncertainty. Consider, for example, the three photos in Figure 2.1.1 , taken at intervals of approximately 1 sec after placing a sample on the balance. Assuming the balance is properly calibrated, we are certain that the sample's mass is more than 0.5729 g and less than 0.5731 g. We are uncertain, however, about the sample's mass in the last decimal place since the final two decimal places fluctuate between 29, 30, and 31. The best we can do is to report the sample's mass as 0.5730 g ± 0.0001 g, indicating both its magnitude and its absolute uncertainty.



Figure 2.1.1 : When weighing a sample on a balance, the measurement fluctuates in the final decimal place. We record this sample's mass as 0.5730 g ± 0.0001 g.

SIGNIFICANT FIGURES

A measurement's significant figures convey information about a measurement's magnitude and uncertainty. The number of significant figures in a measurement is the number of digits known exactly plus one digit whose value is uncertain. The mass shown in Figure 2.1.1 , for example, has four significant figures, three which we know exactly and one, the last, which is uncertain.

Suppose we weigh a second sample, using the same balance, and obtain a mass of 0.0990 g. Does this measurement have 3, 4, or 5 significant figures? The zero in the last decimal place is the one uncertain digit and is significant. The other two zeros, however, simply indicates the decimal point's location. Writing the measurement in scientific notation, 9.90×10^{-2}, clarifies that there are three significant figures in 0.0990.

> In the measurement **0.0**99**0** g, the zero in **green** is a significant digit and the zeros in **red** are not significant digits.

EXAMPLE 2.1.1

How many significant figures are in each of the following measurements? Convert each measurement to its equivalent scientific notation or decimal form.

a. 0.0120 mol HCl
b. 605.3 mg $CaCO_3$
c. 1.043×10^{-4} mol Ag^+
d. 9.3×10^{4} mg NaOH

Solution

(a) Three significant figures; 1.20×10^{-2} mol HCl.

(b) Four significant figures; 6.053×10^{2} mg $CaCO_3$.

(c) Four significant figures; 0.000 104 3 mol Ag^+.

(d) Two significant figures; 93 000 mg NaOH.

There are two special cases when determining the number of significant figures in a measurement. For a measurement given as a logarithm, such as pH, the number of significant figures is equal to the number of digits to the right of the decimal point. Digits to the left of the decimal point are not significant figures since they indicate only the power of 10. A pH of 2.45, therefore, contains two significant figures.

> The log of 2.8×10^{2} is 2.45. The log of 2.8 is 0.45 and the log of 10^2 is 2. The 2 in 2.45, therefore, only indicates the power of 10 and is not a significant digit.

An exact number, such as a stoichiometric coefficient, has an infinite number of significant figures. A mole of $CaCl_2$, for example, contains exactly two moles of chloride ions and one mole of calcium ions. Another example of an exact number is the relationship between some units. There are, for example, exactly 1000 mL in 1 L. Both the 1 and the 1000 have an infinite number of significant figures.

Using the correct number of significant figures is important because it tells other scientists about the uncertainty of your measurements. Suppose you weigh a sample on a balance that measures mass to the nearest ±0.1 mg. Reporting the sample's mass as 1.762 g instead of 1.7623 g is incorrect because it does not convey properly the measurement's uncertainty. Reporting the sample's mass as 1.76231 g also is incorrect because it falsely suggests an uncertainty of ±0.01 mg.

SIGNIFICANT FIGURES IN CALCULATIONS

Significant figures are also important because they guide us when reporting the result of an analysis. When we calculate a result, the answer cannot be more certain than the least certain measurement in the analysis. Rounding an answer to the correct number of significant figures is important.

For addition and subtraction, we round the answer to the last decimal place in common for each measurement in the calculation. The exact sum of 135.621, 97.33, and 21.2163 is 254.1673. Since the last decimal place common to all three numbers is the hundredth's place

$$\begin{array}{r} 135.621 \\ 97.33 \\ 21.2163 \\ \hline 254.1673 \end{array}$$

we round the result to 254.17.

The last common decimal place shared by 135.621, 97.33, and 21.2163 is shown in **red**.

When working with scientific notation, first convert each measurement to a common exponent before determining the number of significant figures. For example, the sum of 6.17×10^7, 4.3×10^5, and 3.23×10^4 is 6.22×10^7.

$$\begin{array}{ll} 6.17 & \times 10^7 \\ 0.043 & \times 10^7 \\ \underline{0.00323} & \times 10^7 \\ 6.21623 & \times 10^7 \end{array}$$

The last common decimal place shared by 6.17×10^7, 4.3×10^5 and 3.23×10^4 is shown in **red**.

For multiplication and division, we round the answer to the same number of significant figures as the measurement with the fewest number of significant figures. For example, when we divide the product of 22.91 and 0.152 by 16.302, we report the answer as 0.214 (three significant figures) because 0.152 has the fewest number of significant figures.

$$\frac{22.91 \times 0.152}{16.302} = 0.2136 = 0.214$$

There is no need to convert measurements in scientific notation to a common exponent when multiplying or dividing.

It is important to recognize that the rules presented here for working with significant figures are generalizations. What actually is conserved is uncertainty, not the number of significant figures. For example, the following calculation

$$101/99 = 1.02$$

is correct even though it violates the general rules outlined earlier. Since the relative uncertainty in each measurement is approximately 1% (101 ± 1 and 99 ± 1), the relative uncertainty in the final answer also is approximately 1%. Reporting the answer as 1.0 (two significant figures), as required by the general rules, implies a relative uncertainty of 10%, which is too large. The correct answer, with three significant figures, yields the expected relative uncertainty. Chapter 4 presents a more thorough treatment of uncertainty and its importance in reporting the result of an analysis.

Finally, to avoid "round-off" errors, it is a good idea to retain at least one extra significant figure throughout any calculation. Better yet, invest in a good scientific calculator that allows you to perform lengthy calculations without the need to record intermediate values. When your calculation is complete, round the answer to the correct number of significant figures using the following simple rules.

1. Retain the least significant figure if it and the digits that follow are less than halfway to the next higher digit. For example, rounding 12.442 to the nearest tenth gives 12.4 since 0.442 is less than half way between 0.400 and 0.500.
2. Increase the least significant figure by 1 if it and the digits that follow are more than halfway to the next higher digit. For example, rounding 12.476 to the nearest tenth gives 12.5 since 0.476 is more than halfway between 0.400 and 0.500.
3. If the least significant figure and the digits that follow are exactly halfway to the next higher digit, then round the least significant figure to the nearest even number. For example, rounding 12.450 to the nearest tenth gives 12.4, while rounding 12.550 to the nearest tenth gives 12.6. Rounding in this manner ensures that we round up as often as we round down.

? EXERCISE 2.1.1

For a problem that involves both addition and/or subtraction, and multiplication and/or division, be sure to account for significant figures at each step of the calculation. With this in mind, report the result of this calculation to the correct number of significant figures.

$$\frac{0.250 \times (9.93 \times 10^{-3}) - 0.100 \times (1.927 \times 10^{-2})}{9.93 \times 10^{-3} + 1.927 \times 10^{-2}} =$$

Answer

The correct answer to this exercise is 1.9×10^{-2}. To see why this is correct, let's work through the problem in a series of steps. Here is the original problem

$$\frac{0.250 \times (9.93 \times 10^{-3}) - 0.100 \times (1.927 \times 10^{-2})}{9.93 \times 10^{-3} + 1.927 \times 10^{-2}} =$$

Following the correct order of operations we first complete the two multiplications in the numerator. In each case the answer has three significant figures, although we retain an extra digit, highlight in **red**, to avoid round-off errors.

$$\frac{2.482 \times 10^{-3} - 1.927 \times 10^{-3}}{9.93 \times 10^{-3} + 1.927 \times 10^{-2}} =$$

Completing the subtraction in the numerator leaves us with two significant figures since the last significant digit for each value is in the hundredths place.

$$\frac{0.555 \times 10^{-3}}{9.93 \times 10^{-3} + 1.927 \times 10^{-2}} =$$

The two values in the denominator have different exponents. Because we are adding together these values, we first rewrite them using a common exponent.

$$\frac{0.555 \times 10^{-3}}{0.993 \times 10^{-2} + 1.927 \times 10^{-2}} =$$

The sum in the denominator has four significant figures since each of the addends has three decimal places.

$$\frac{0.555 \times 10^{-3}}{2.920 \times 10^{-2}} =$$

Finally, we complete the division, which leaves us with a result having two significant figures.

$$\frac{0.555 \times 10^{-3}}{2.920 \times 10^{-2}} = 1.9 \times 10^{-2}$$

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2.2: CONCENTRATION

Concentration is a general measurement unit that reports the amount of solute present in a known amount of solution or solvent

$$\text{concentration} = \frac{\text{amount of solute}}{\text{amount of solution}} \tag{2.2.1}$$

Although we associate the terms "solute" and "solution" with liquid samples, we can extend their use to gas-phase and solid-phase samples as well. Table 2.2.1 lists the most common units of concentration.

Table 2.2.1 : Common Units for Reporting Concentration

Name	Units	Symbol
molarity	$\frac{\text{moles solute}}{\text{liters solution}}$	M
formality	$\frac{\text{moles solute}}{\text{liters solution}}$	F
normality	$\frac{\text{equivalents solute}}{\text{liters solution}}$	N
molality	$\frac{\text{moles solute}}{\text{kilograms solvent}}$	m
weight percent	$\frac{\text{grams solute}}{\text{100 grams solution}}$	% w/w
volume percent	$\frac{\text{mL solute}}{\text{100 mL solution}}$	% v/v
weight-to-volume percent	$\frac{\text{grams solute}}{\text{100 mL solution}}$	% w/v
parts per million	$\frac{\text{grams solute}}{10^6 \text{ grams solution}}$	ppm
parts per billion	$\frac{\text{grams solute}}{10^9 \text{ grams solution}}$	ppb

An alternative expression for weight percent is

$$\frac{\text{grams solute}}{\text{grams solution}} \times 100$$

You can use similar alternative expressions for volume percent and for weight-to-volume percent.

MOLARITY AND FORMALITY

Both molarity and formality express concentration as moles of solute per liter of solution; however, there is a subtle difference between them. ***Molarity*** is the concentration of a particular chemical species. ***Formality***, on the other hand, is a substance's total concentration without regard to its specific chemical form. There is no difference between a compound's molarity and formality if it dissolves without dissociating into ions. The formal concentration of a solution of glucose, for example, is the same as its molarity.

For a compound that ionizes in solution, such as $CaCl_2$, molarity and formality are different. When we dissolve 0.1 moles of $CaCl_2$ in 1 L of water, the solution contains 0.1 moles of Ca^{2+} and 0.2 moles of Cl^-. The molarity of $CaCl_2$, therefore, is zero since there is no undissociated $CaCl_2$ in solution; instead, the solution is 0.1 M in Ca^{2+} and 0.2 M in Cl^-. The formality of $CaCl_2$, however, is 0.1 F since it represents the total amount of $CaCl_2$ in solution. This more rigorous definition of molarity, for better or worse, largely is ignored in the current literature, as it is in this textbook. When we state that a solution is 0.1 M $CaCl_2$ we understand it to consist of Ca^{2+} and Cl^- ions. We will reserve the unit of formality to situations where it provides a clearer description of solution chemistry.

Molarity is used so frequently that we use a symbolic notation to simplify its expression in equations and in writing. Square brackets around a species indicate that we are referring to that species' molarity. Thus, $[Ca^{2+}]$ is read as "the molarity of calcium ions."

For a solute that dissolves without undergoing ionization, molarity and formality have the same value. A solution that is 0.0259 M in glucose, for example, is 0.0259 F in glucose as well.

NORMALITY

Normality is a concentration unit that no longer is in common use; however, because you may encounter normality in older handbooks of analytical methods, it is helpful to understand its meaning. ***Normality*** defines concentration in terms of an equivalent, which is the amount of one chemical species that reacts stoichiometrically with another chemical species. Note that this definition makes an equivalent, and thus

normality, a function of the chemical reaction in which the species participates. Although a solution of H_2SO_4 has a fixed molarity, its normality depends on how it reacts. You will find a more detailed treatment of normality in Appendix 1.

> One handbook that still uses normality is *Standard Methods for the Examination of Water and Wastewater*, a joint publication of the American Public Health Association, the American Water Works Association, and the Water Environment Federation. This handbook is one of the primary resources for the environmental analysis of water and wastewater.

MOLALITY

Molality is used in thermodynamic calculations where a temperature independent unit of concentration is needed. Molarity is based on the volume of solution that contains the solute. Since density is a temperature dependent property, a solution's volume, and thus its molar concentration, changes with temperature. By using the solvent's mass in place of the solution's volume, the resulting concentration becomes independent of temperature.

WEIGHT, VOLUME, AND WEIGHT-TO-VOLUME PERCENT

Weight percent (% w/w), ***volume percent*** (% v/v) and ***weight-to-volume percent*** (% w/v) express concentration as the units of solute present in 100 units of solution. A solution that is 1.5% w/v NH_4NO_3, for example, contains 1.5 gram of NH_4NO_3 in 100 mL of solution.

PARTS PER MILLION AND PARTS PER BILLION

Parts per million (ppm) and ***parts per billion*** (ppb) are ratios that give the grams of solute in, respectively, one million or one billion grams of sample. For example, a sample of steel that is 450 ppm in Mn contains 450 µg of Mn for every gram of steel. If we approximate the density of an aqueous solution as 1.00 g/mL, then we can express solution concentrations in ppm or ppb using the following relationships.

$$\text{ppm} = \frac{\mu\text{g}}{\text{g}} = \frac{\text{mg}}{\text{L}} = \frac{\mu\text{g}}{\text{mL}} \quad \text{ppb} = \frac{\text{ng}}{\text{g}} = \frac{\mu\text{g}}{\text{L}} = \frac{\text{ng}}{\text{mL}}$$

For gases a part per million usually is expressed as a volume ratio; for example, a helium concentration of 6.3 ppm means that one liter of air contains 6.3 µL of He.

> You should be careful when using parts per million and parts per billion to express the concentration of an aqueous solute. The difference between a solute's concentration in mg/L and ng/g, for example, is significant if the solution's density is not 1.00 g/mL. For this reason many organizations advise against using the abbreviation ppm and ppb (see section 7.10.3 at www.nist.gov). If in doubt, include the exact units, such as 0.53 µg Pb^{2+}/L for the concentration of lead in a sample of seawater.

CONVERTING BETWEEN CONCENTRATION UNITS

The most common ways to express concentration in analytical chemistry are molarity, weight percent, volume percent, weight-to-volume percent, parts per million and parts per billion. The general definition of concentration in Equation 2.2.1 makes it is easy to convert between concentration units.

✔ EXAMPLE 2.2.1

A concentrated solution of ammonia is 28.0% w/w NH_3 and has a density of 0.899 g/mL. What is the molar concentration of NH_3 in this solution?

Solution

$$\frac{28.0\text{ g NH}_3}{100\text{ g soln}} \times \frac{0.899\text{ g soln}}{\text{ml soln}} \times \frac{1\text{ mol NH}_3}{17.03\text{ g NH}_3} \times \frac{1000\text{mL}}{\text{L}} = 14.8\text{ M}$$

✔ EXAMPLE 2.2.2

The maximum permissible concentration of chloride ion in a municipal drinking water supply is 2.50×10^2 ppm Cl^-. When the supply of water exceeds this limit it often has a distinctive salty taste. What is the equivalent molar concentration of Cl^-?

Solution

$$\frac{2.50 \times 10^2\text{ mg Cl}^-}{\text{L}} \times \frac{1\text{ g}}{1000\text{ mg}} \times \frac{1\text{ mol Cl}^-}{35.453\text{ gCl}^-} = 7.05 \times 10^{-3}\text{ M}$$

EXERCISE 2.2.1

Which solution—0.50 M NaCl or 0.25 M $SrCl_2$—has the larger concentration when expressed in mg/mL?

Answer

The concentrations of the two solutions are

$$\frac{0.50 \text{ mol NaCl}}{\text{L}} \times \frac{58.44 \text{ g NaCl}}{\text{mol NaCl}} \times \frac{10^6 \ \mu\text{g}}{\text{g}} \times \frac{1\text{L}}{1000 \text{ mL}} = 2.9 \times 10^4 \ \mu\text{g/mL NaCl}$$

$$\frac{0.25 \text{ mol } SrCl_2}{\text{L}} \times \frac{158.5 \text{ g } SrCl_2}{\text{mol } SrCl_2} \times \frac{10^6 \ \mu\text{g}}{\text{g}} \times \frac{1\text{L}}{1000 \text{ mL}} = 4.0 \times 10^4 \ \mu\text{g/ml } SrCl_2$$

The solution of $SrCl_2$ has the larger concentration when it is expressed in µg/mL instead of in mol/L.

P-FUNCTIONS

Sometimes it is inconvenient to use the concentration units in Table 2.2.1 . For example, during a chemical reaction a species' concentration may change by many orders of magnitude. If we want to display the reaction's progress graphically we might wish to plot the reactant's concentration as a function of the volume of a reagent added to the reaction. Such is the case in Figure 2.2.1 for the titration of HCl with NaOH. The *y*-axis on the left-side of the figure displays the $[H^+]$ as a function of the volume of NaOH. The initial $[H^+]$ is 0.10 M and its concentration after adding 80 mL of NaOH is 4.3×10^{-13} M. We easily can follow the change in $[H^+]$ for the addition of the first 50 mL of NaOH; however, for the remaining volumes of NaOH the change in $[H^+]$ is too small to see.

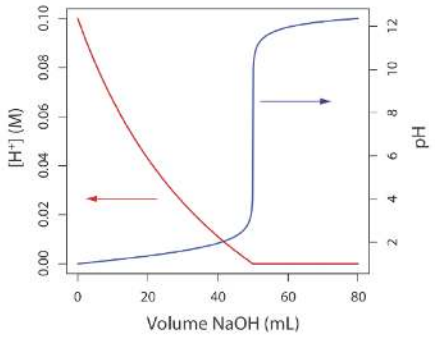


Figure 2.2.1 : Two curves showing the progress of a titration of 50.0 mL of 0.10 M HCl with 0.10 M NaOH. The $[H^+]$ is shown on the left *y*-axis and the pH on the right *y*-axis.

When working with concentrations that span many orders of magnitude, it often is more convenient to express concentration using a p-function. The p-function of *X* is written as p*X* and is defined as

$$\text{p}X = -\log(X)$$

The pH of a solution that is 0.10 M H^+ for example, is

$$\text{pH} = -\log[H^+] = -\log(0.10) = 1.00$$

and the pH of 4.3×10^{-13} M H^+ is

$$\text{pH} = -\log[H^+] = -\log(4.3 \times 10^{-13}) = 12.37$$

Figure 2.2.1 shows that plotting pH as a function of the volume of NaOH provides more useful information about how the concentration of H^+ changes during the titration.

A more appropriate equation for pH is $\text{pH} = -\log(a_{H^+})$ where a_{H^+} is the activity of the hydrogen ion. See Chapter 6.9 for more details. For now the approximate equation $\text{pH} = -\log[H^+]$ is sufficient.

EXAMPLE 2.2.3

What is pNa for a solution of 1.76×10^{-3} M Na_3PO_4?

Solution

Since each mole of Na_3PO_4 contains three moles of Na^+, the concentration of Na^+ is

$$[Na^+] = (1.76 \times 10^{-3}\ M) \times \frac{3\ mol\ Na^+}{mol\ Na_3PO_4} = 5.28 \times 10^{-3}\ M$$

and pNa is

$$pNa = -\log[Na^+] = -\log(5.28 \times 10^{-3}) = 2.277$$

Remember that a pNa of 2.777 has three, not four, significant figures; the 2 that appears in the one's place indicates the power of 10 when we write $[Na^+]$ as 0.528×10^{-2} M.

EXAMPLE 2.2.4

What is the $[H^+]$ in a solution that has a pH of 5.16?

Solution

The concentration of H^+ is

$$pH = -\log[H^+] = 5.16$$

$$\log[H^+] = -5.16$$

$$[H^+] = 10^{-5.16} = 6.9 \times 10^{-6}\ M$$

Recall that if $\log(X) = a$, then $X = 10^a$.

EXERCISE 2.2.2

What are the values for pNa and pSO_4 if we dissolve 1.5 g Na_2SO_4 in a total solution volume of 500.0 mL?

Answer

The concentrations of Na^+ and SO_4^{2-} are

$$\frac{1.5\ g\ Na_2SO_4}{0.500L} \times \frac{1\ mol\ Na_2SO_4}{142.0\ g\ Na_2SO_4} \times \frac{2\ mol\ Na^+}{mol\ molNa_2SO_4} = 4.23 \times 10^{-2}\ M\ Na^+$$

$$\frac{1.5\ g\ Na_2SO_4}{0.500L} \times \frac{1\ mol\ Na_2SO_4}{142.0\ g\ Na_2SO_4} \times \frac{1\ mol\ SO_4^{2-}}{mol\ molNa_2SO_4} = 2.11 \times 10^{-2}\ M\ SO_4^{2-}$$

The pNa and pSO_4 values are

$$pNa = -\log(4.23 \times 10^{-2}\ M\ Na^+) = 1.37$$

$$pSO_4 = -\log(2.11 \times 10^{-2}\ M\ SO_4^{2-}) = 1.68$$

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2.3: STOICHIOMETRIC CALCULATIONS

A balanced reaction, which defines the stoichiometric relationship between the moles of reactants and the moles of products, provides the basis for many analytical calculations. Consider, for example, an analysis for oxalic acid, $H_2C_2O_4$, in which Fe^{3+} oxidizes oxalic acid to CO_2

$$2Fe^{3+}(aq) + H_2C_2O_4(aq) + 2H_2O(l) \longrightarrow 2Fe^{2+}(aq) + 2CO_2(g) + 2H_3O^+(aq)$$

The balanced reaction shows us that one mole of oxalic acid reacts with two moles of Fe^{3+}. As shown in the following example, we can use this balanced reaction to determine the amount of $H_2C_2O_4$ in a sample of rhubarb if we know the moles of Fe^{3+} needed to react completely with oxalic acid.

In sufficient amounts, oxalic acid, the structure for which is shown to the right, is toxic. At lower physiological concentrations it leads to
the formation of kidney stones. The leaves of the rhubarb plant contain relatively high concentrations of oxalic acid. The stalk, which many individuals enjoy eating, contains much smaller concentrations of oxalic acid.



In the examples that follow, note that we retain an extra significant figure throughout the calculation, rounding to the correct number of significant figures at the end. We will follow this convention in any calculation that involves more than one step. If we forget that we are retaining an extra significant figure, we might report the final answer with one too many significant figures. Here we mark the extra digit in **red** for emphasis. Be sure you pick a system for keeping track of significant figures.

EXAMPLE 2.3.1

The amount of oxalic acid in a sample of rhubarb was determined by reacting with Fe^{3+}. After extracting a 10.62 g of rhubarb with a solvent, oxidation of the oxalic acid required 36.44 mL of 0.0130 M Fe^{3+}. What is the weight percent of oxalic acid in the sample of rhubarb?

Solution

We begin by calculating the moles of Fe^{3+} used in the reaction

$$\frac{0.0130 \text{ mol } Fe^{3+}}{\text{L}} \times 0.03644 \text{ M} = 4.737 \times 10^{-4} \text{ mol } Fe^{3+}$$

The moles of oxalic acid reacting with the Fe^{3+}, therefore, is

$$4.737 \times 10^{-4} \text{ mol } Fe^{3+} \times \frac{1 \text{ mol } H_2C_2O_4}{2 \text{ mol } Fe^{3+}} = 2.368 \times 10^{-4} \text{ mol } H_2C_2O_4$$

Converting the moles of oxalic acid to grams of oxalic acid

$$2.368 \times 10^{-4} \text{ mol } H_2C_2O_4 \times \frac{90.03 \text{ g } H_2C_2O_4}{\text{mol } H_2C_2O_4} = 2.132 \times 10^{-2} \text{ g } H_2C_2O_4$$

and calculating the weight percent gives the concentration of oxalic acid in the sample of rhubarb as

$$\frac{2.132 \times 10^{-2} \text{ g } H_2C_2O_4}{10.62 \text{ g rhubarb}} \times 100 = 0.201\% \text{ w/w } H_2C_2O_4$$

EXERCISE 2.3.1

You can dissolve a precipitate of AgBr by reacting it with $Na_2S_2O_3$, as shown here.

$$AgBr(s) + 2Na_2S_2O_3(aq) \longrightarrow Ag(S_2O_3)_2^{3-}(aq) + Br^-(aq) + 4Na^+(aq)$$

How many mL of 0.0138 M $Na_2S_2O_3$ do you need to dissolve 0.250 g of AgBr?

Answer

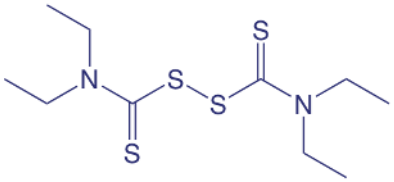
First, we find the moles of AgBr

$$0.250 \text{ g AgBr} \times \frac{1 \text{ mol AgBr}}{187.8 \text{ g AgBr}} = 1.331 \times 10^{-3} \text{ mol AgBr}$$

and then the moles and volume of $Na_2S_2O_3$

$$1.331 \times 10^{-3} \text{ mol AgBr} \times \frac{2 \text{ mol } Na_2S_2O_3}{\text{mol AgBr}} = 2.662 \times 10^{-3} \text{ mol } Na_2S_2O_3$$

$$2.662 \times 10^{-3} \text{ mol } Na_2S_2O_3 \times \frac{1 \text{ L}}{0.0138 \text{ mol } Na_2S_2O_3} \times \frac{1000 \text{ mL}}{\text{L}} = 193 \text{ mL}$$



The analyte in Example 2.3.1 , oxalic acid, is in a chemically useful form because there is a reagent, Fe^{3+}, that reacts with it quantitatively. In many analytical methods, we first must convert the analyte into a more accessible form before we can complete the analysis. For example, one method for the quantitative analysis of disulfiram, $C_{10}H_{20}N_2S_4$—the active ingredient in the drug Antabuse, and whose structure is shown to the right —requires that we first convert the sulfur to SO_2 by combustion, and then oxidize the SO_2 to H_2SO_4 by bubbling it through a solution of H_2O_2. When the conversion is complete, the amount of H_2SO_4 is determined by titrating with NaOH.

To convert the moles of NaOH used in the titration to the moles of disulfiram in the sample, we need to know the stoichiometry of each reaction. Writing a balanced reaction for H_2SO_4 and NaOH is straightforward

$$H_2SO_4(aq) + 2NaOH(aq) \longrightarrow 2H_2O(l) + Na_2SO_4(aq)$$

but the balanced reactions for the oxidations of $C_{10}H_{20}N_2S_4$ to SO_2, and of SO_2 to H_2SO_4 are not as immediately obvious. Although we can balance these redox reactions, it is often easier to deduce the overall stoichiometry by using a little chemical logic.

EXAMPLE 2.3.2

An analysis for disulfiram, $C_{10}H_{20}N_2S_4$, in Antabuse is carried out by oxidizing the sulfur to H_2SO_4 and titrating the H_2SO_4 with NaOH. If a 0.4613-g sample of Antabuse requires 34.85 mL of 0.02500 M NaOH to titrate the H_2SO_4, what is the %w/w disulfiram in the sample?

Solution

Calculating the moles of H_2SO_4 is easy—first, we calculate the moles of NaOH used in the titration

$$(0.02500 \text{ M}) \times (0.03485 \text{ L}) = 8.7125 \times 10^{-4} \text{ mol NaOH}$$

and then we use the titration reaction's stoichiometry to calculate the corresponding moles of H_2SO_4.

$$8.7125 \times 10^{-4} \text{ mol NaOH} \times \frac{1 \text{ mol } H_2SO_4}{2 \text{ mol NaOH}} = 4.3562 \times 10^{-4} \text{ mol } H_2SO_4$$

Here is where we use a little chemical logic. Instead of balancing the reactions for the combustion of $C_{10}H_{20}N_2S_4$ to SO_2 and for the subsequent oxidation of SO_2 to H_2SO_4, we recognize that a conservation of mass requires that all the sulfur in $C_{10}H_{20}N_2S_4$ ends up in the H_2SO_4; thus

$$4.3562 \times 10^{-4} \text{ mol } H_2SO_4 \times \frac{1 \text{ mol S}}{\text{mol } H_2SO_4} \times \frac{1 \text{ mol } C_{10}H_{20}N_2S_4}{4 \text{ mol S}} = 1.0890 \times 10^{-4} \text{ mol } C_{10}H_{20}N_2S_4$$

$$1.0890 \times 10^{-4} \text{ mol } C_{10}H_{20}N_2S_4 \times \frac{296.54 \text{ g } C_{10}H_{20}N_2S_4}{\text{mol } C_{10}H_{20}N_2S_4} = 0.032293 \text{ g } C_{10}H_{20}N_2S_4$$

$$\frac{0.032293 \text{ g } C_{10}H_{20}N_2S_4}{0.4613 \text{ g sample}} \times 100 = 7.000\% \text{ w/w } C_{10}H_{20}N_2S_4$$

A conservation of mass is the essence of stoichiometry!

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2.4: BASIC EQUIPMENT

The array of equipment available for making analytical measurements and working with analytical samples is impressive, ranging from the simple and inexpensive, to the complex and expensive. With three exceptions—the measurement of mass, the measurement of volume, and the drying of materials—we will postpone the discussion of equipment to later chapters where its application to specific analytical methods is relevant.

EQUIPMENT FOR MEASURING MASS

An object's mass is measured using a digital electronic analytical balance (Figure 2.4.1). An electromagnet levitates the sample pan above a permanent cylindrical magnet. When we place an object on the sample pan, it displaces the sample pan downward by a force equal to the product of the sample's mass and its acceleration due to gravity. The balance detects this downward movement and generates a counterbalancing force by increasing the current to the electromagnet. The current needed to return the balance to its original position is proportional to the object's mass. A typical electronic balance has a capacity of 100–200 g, and can measure mass to the nearest ±0.01 mg to ±1 mg.



Figure 2.4.1 : The photo shows a typical digital electronic balance capable of determining mass to the nearest ±0.1 mg. The sticker inside the balance's wind shield is its annual calibration certification. For a review of other types of electronic balances, see Schoonover, R. M. *Anal. Chem.* **1982**, *54*, 973A-980A.

Although we tend to use interchangeably, the terms "weight" and "mass," there is an important distinction between them. Mass is the absolute amount of matter in an object, measured in grams. Weight, *W*, is a measure of gravitational acceleration, *g*, acting on that mass, *m*:

$$W = m \times g$$

An object has a fixed mass but its weight depends upon the acceleration due to gravity, which varies subtly from location-to-location.

A balance measures an object's weight, not its mass. Because weight and mass are proportional to each other, we can calibrate a balance using a standard weight whose mass is traceable to the standard prototype for the kilogram. A properly calibrated balance gives an accurate value for an object's mass; see Appendix 9 for more details on calibrating a balance.

If the sample is not moisture sensitive, a clean and dry container is placed on the balance. The container's mass is called the ***tare*** and most balances allow you to set the container's tare to a mass of zero. The sample is transferred to the container, the new mass is measured and the sample's mass determined by subtracting the tare. A sample that absorbs moisture from the air is treated differently. The sample is placed in a covered weighing bottle and their combined mass is determined. A portion of the sample is removed and the weighing bottle and the remaining sample are reweighed. The difference between the two masses gives the sample's mass.

Several important precautions help to minimize errors when we determine an object's mass. To minimize the effect of vibrations, the balance is placed on a stable surface and in a level position. Because the sensitivity of an analytical balance is sufficient to measure the mass of a fingerprint, materials often are handled using tongs or laboratory tissues. Volatile liquid samples must be weighed in a covered container to avoid the loss of sample by evaporation. To minimize fluctuations in mass due to air currents, the balance pan often is housed within a wind shield, as seen in Figure 2.4.1 . A sample that is cooler or warmer than the surrounding air will create a convective air current that affects the measurement of its mass. For this reason, bring your samples to room temperature before determining their mass. Finally, samples dried in an oven are stored in a desiccator to prevent them from reabsorbing moisture from the atmosphere.

EQUIPMENT FOR MEASURING VOLUME

Analytical chemists use a variety of glassware to measure volume, including graduated cylinders, volumetric pipets, and volumetric flasks. The choice of what type of glassware to use depends on how accurately and how precisely we need to measure the volume and whether we are interested in containing or delivering the sample.

A ***graduated cylinder*** is the simplest device for delivering a known volume of a liquid reagent (Figure 2.4.2). The graduated scale allows you to deliver any volume up to the cylinder's maximum. Typical accuracy is ±1% of the maximum volume. A 100-mL graduated cylinder, for example, is accurate to ±1 mL.



Figure 2.4.2 : An example of a 250-mL graduated cylinder.

A ***volumetric pipet*** provides a more accurate method for delivering a known volume of solution. Several different styles of pipets are available, two of which are shown in Figure 2.4.3 . Transfer pipets provide the most accurate means for delivering a known volume of solution. A transfer pipet delivering less than 100 mL generally is accurate to the hundredth of a mL. Larger transfer pipets are accurate to a tenth of a mL. For example, the 10-mL transfer pipet in Figure 2.4.3 will deliver 10.00 mL with an accuracy of ±0.02 mL.

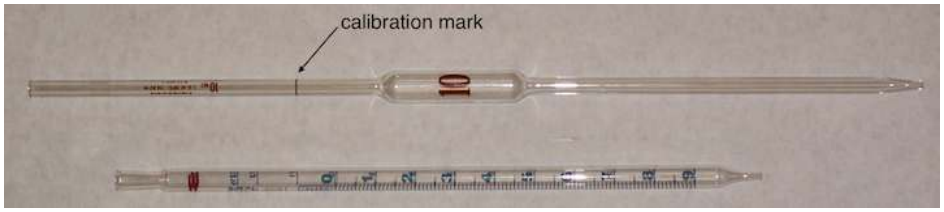


Figure 2.4.3 : Two examples of 10-mL volumetric pipets. The pipet on the top is a transfer pipet and the pipet on the bottom is a Mohr measuring pipet. The transfer pipet delivers a single volume of 10.00 mL when filled to its calibration mark. The Mohr pipet has a mark every 0.1 mL, allowing for the delivery of variable volumes. It also has additional graduations at 11 mL, 12 mL, and 12.5 mL.

> Scientists at the Brookhaven National Laboratory used a germanium nanowire to make a pipet that delivers a 35 zeptoliter (10^{-21} L) drop of a liquid gold-germanium alloy. You can read about this work in the April 21, 2007 issue of *Science News*.

To fill a transfer pipet, use a rubber suction bulb to pull the solution up past the calibration mark (*Never use your mouth to suck a solution into a pipet!*). After replacing the bulb with your finger, adjust the solution's level to the calibration mark and dry the outside of the pipet with a laboratory tissue. Allow the pipet's contents to drain into the receiving container with the pipet's tip touching the inner wall of the container. A small portion of the liquid remains in the pipet's tip and is not be blown out. With some measuring pipets any solution remaining in the tip must be blown out.

Delivering microliter volumes of liquids is not possible using transfer or measuring pipets. Digital micropipets (Figure 2.4.4), which come in a variety of volume ranges, provide for the routine measurement of microliter volumes.



Figure 2.4.4 : A set of two digital micropipets. The pipet on the top delivers volumes between 0.5 mL and 10 µL and the pipet on the bottom delivers volumes between 10 mL and 100 µL.

Graduated cylinders and pipets deliver a known volume of solution. A ***volumetric flask***, on the other hand, contains a specific volume of solution (Figure 2.4.5). When filled to its calibration mark, a volumetric flask that contains less than 100 mL generally is accurate to the hundredth of a mL, whereas larger volumetric flasks are accurate to the tenth of a mL. For example, a 10-mL volumetric flask contains 10.00 mL ± 0.02 mL and a 250-mL volumetric flask contains 250.0 mL ± 0.12 mL.



Figure 2.4.5 : A collection of volumetric flasks with volumes of 10 mL, 50 mL, 100, mL, 250 mL, and 500 mL.

Because a volumetric flask contains a solution, it is used to prepare a solution with an accurately known concentration. Transfer the reagent to the volumetric flask and add enough solvent to bring the reagent into solution. Continue adding solvent in several portions, mixing thoroughly after each addition, and then adjust the volume to the flask's calibration mark using a dropper. Finally, complete the mixing process by inverting and shaking the flask at least 10 times.

If you look closely at a volumetric pipet or a volumetric flask you will see markings similar to those shown in Figure 2.4.6 . The text of the markings, which reads

$$10 \text{ mL T. D. at } 20\ ^{o}\text{C} \pm 0.02 \text{ mL}$$

indicates that the pipet is calibrated to deliver (T. D.) 10 mL of solution with an uncertainty of ±0.02 mL at a temperature of 20 ^{o}C. The temperature is important because glass expands and contracts with changes in temperatures; thus, the pipet's accuracy is less than ±0.02 mL at a higher or a lower temperature. For a more accurate result, you can calibrate your volumetric glassware at the temperature you are working by weighing the amount of water contained or delivered and calculating the volume using its temperature dependent density.



Figure 2.4.6 : Close-up of the 10-mL transfer pipet from Figure 2.4.3 .

> A volumetric flask has similar markings, but uses the abbreviation T. C. for "to contain" in place of T. D.

You should take three additional precautions when you work with pipets and volumetric flasks. First, the volume delivered by a pipet or contained by a volumetric flask assumes that the glassware is clean. Dirt and grease on the inner surface prevent liquids from draining evenly, leaving droplets of liquid on the container's walls. For a pipet this means the delivered volume is less than the calibrated volume, while drops of liquid above the calibration mark mean that a volumetric flask contains more than its calibrated volume. Commercially available cleaning solutions are available for cleaning pipets and volumetric flasks.

Second, when filling a pipet or volumetric flask the liquid's level must be set exactly at the calibration mark. The liquid's top surface is curved into a meniscus, the bottom of which should align with the glassware's calibration mark (Figure 2.4.7). When adjusting the meniscus, keep your eye in line with the calibration mark to avoid parallax errors. If your eye level is above the calibration mark you will overfill the pipet or the volumetric flask and you will underfill them if your eye level is below the calibration mark.



Figure 2.4.7 : Proper position of the solution's meniscus relative to the volumetric flask's calibration mark.

Finally, before using a pipet or volumetric flask rinse it with several small portions of the solution whose volume you are measuring. This ensures the removal of any residual liquid remaining in the pipet or volumetric flask.

EQUIPMENT FOR DRYING SAMPLES

Many materials need to be dried prior to their analysis to remove residual moisture. Depending on the material, heating to a temperature between 110 ^{o}C and 140 ^{o}C usually is sufficient. Other materials need much higher temperatures to initiate thermal decomposition.

Conventional drying ovens provide maximum temperatures of 160 ^{o}C to 325 ^{o}C, depending on the model. Some ovens include the ability to circulate heated air, which allows for a more efficient removal of moisture and shorter drying times. Other ovens provide a tight seal for the door, which allows the oven to be evacuated. In some situations a microwave oven can replace a conventional laboratory oven. Higher temperatures, up to as much as 1700 ^{o}C, require a muffle furnace (Figure 2.4.8).



Figure 2.4.8 : Example of a muffle furnace.

After drying or decomposing a sample, it is cooled to room temperature in a desiccator to prevent the readsorption of moisture. A ***desiccator*** (Figure 2.4.9) is a closed container that isolates the sample from the atmosphere. A drying agent, called a ***desiccant***, is placed in the bottom of the container. Typical desiccants include calcium chloride and silica gel. A perforated plate sits above the desiccant, providing a shelf for storing samples. Some desiccators include a stopcock that allows them to be evacuated.



Figure 2.4.9 : Example of a desiccator. The solid in the bottom of the desiccator is the desiccant, which in this case is silica gel.

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2.5: PREPARING SOLUTIONS

Preparing a solution of known concentration is perhaps the most common activity in any analytical lab. The method for measuring out the solute and the solvent depend on the desired concentration and how exact the solution's concentration needs to be known. Pipets and volumetric flasks are used when we need to know a solution's exact concentration; graduated cylinders, beakers, and/or reagent bottles suffice when a concentrations need only be approximate. Two methods for preparing solutions are described in this section.

PREPARING STOCK SOLUTIONS

A ***stock solution*** is prepared by weighing out an appropriate portion of a pure solid or by measuring out an appropriate volume of a pure liquid, placing it in a suitable flask, and diluting to a known volume. Exactly how one measure's the reagent depends on the desired concentration unit. For example, to prepare a solution with a known molarity you weigh out an appropriate mass of the reagent, dissolve it in a portion of solvent, and bring it to the desired volume. To prepare a solution where the solute's concentration is a volume percent, you measure out an appropriate volume of solute and add sufficient solvent to obtain the desired total volume.

✔ EXAMPLE 2.5.1

Describe how to prepare the following three solutions: (a) 500 mL of approximately 0.20 M NaOH using solid NaOH; (b) 1 L of 150.0 ppm Cu^{2+} using Cu metal; and (c) 2 L of 4% v/v acetic acid using concentrated glacial acetic acid (99.8% w/w acetic acid).

Solution

(a) Because the desired concentration is known to two significant figures, we do not need to measure precisely the mass of NaOH or the volume of solution. The desired mass of NaOH is

$$\frac{0.20\text{ mol NaOH}}{\text{L}} \times \frac{40.0\text{ g NaOH}}{\text{mol NaOH}} \times 0.50\text{ L} = 4.0\text{ g NaOH}$$

To prepare the solution, place 4.0 grams of NaOH, weighed to the nearest tenth of a gram, in a bottle or beaker and add approximately 500 mL of water.

(b) Since the desired concentration of Cu^{2+} is given to four significant figures, we must measure precisely the mass of Cu metal and the final solution volume. The desired mass of Cu metal is

$$\frac{150.0\text{ mg Cu}}{\text{L}} \times 1.000\text{ M} \times \frac{1\text{ g}}{1000\text{ mg}} = 0.1500\text{ g Cu}$$

To prepare the solution, measure out exactly 0.1500 g of Cu into a small beaker and dissolve it using a small portion of concentrated HNO_3. To ensure a complete transfer of Cu^{2+} from the beaker to the volumetric flask—what we call a ***quantitative transfer***—rinse the beaker several times with small portions of water, adding each rinse to the volumetric flask. Finally, add additional water to the volumetric flask's calibration mark.

(c) The concentration of this solution is only approximate so it is not necessary to measure exactly the volumes, nor is it necessary to account for the fact that glacial acetic acid is slightly less than 100% w/w acetic acid (it is approximately 99.8% w/w). The necessary volume of glacial acetic acid is

$$\frac{4\text{ mL }CH_3COOH}{100\text{ mL}} \times 2000\text{ mL} = 80\text{ mL }CH_3COOH$$

To prepare the solution, use a graduated cylinder to transfer 80 mL of glacial acetic acid to a container that holds approximately 2 L and add sufficient water to bring the solution to the desired volume.

? EXERCISE 2.5.1

Provide instructions for preparing 500 mL of 0.1250 M $KBrO_3$.

Answer

Preparing 500 mL of 0.1250 M $KBrO_3$ requires

$$0.5000\text{ L} \times \frac{0.1250\text{ mol }KBrO_3}{\text{L}} \times \frac{167.00\text{ g }KBrO_3}{\text{mol }KBrO_3} = 10.44\text{ g }KBrO_3$$

Because the concentration has four significant figures, we must prepare the solution using volumetric glassware. Place a 10.44 g sample of $KBrO_3$ in a 500-mL volumetric flask and fill part way with water. Swirl to dissolve the $KBrO_3$ and then dilute with water

to the flask's calibration mark.

PREPARING SOLUTIONS BY DILUTION

Solutions are often prepared by diluting a more concentrated stock solution. A known volume of the stock solution is transferred to a new container and brought to a new volume. Since the total amount of solute is the same before and after dilution, we know that

$$C_o \times V_o = C_d \times V_d \tag{2.5.1}$$

where C_o is the stock solution's concentration, V_o is the volume of stock solution being diluted, C_d is the dilute solution's concentration, and V_d is the volume of the dilute solution. Again, the type of glassware used to measure V_o and V_d depends on how precisely we need to know the solution's concentration.

Note that Equation 2.5.1 applies only to those concentration units that are expressed in terms of the solution's volume, including molarity, formality, normality, volume percent, and weight-to-volume percent. It also applies to weight percent, parts per million, and parts per billion if the solution's density is 1.00 g/mL. We cannot use Equation 2.5.1 if we express concentration in terms of molality as this is based on the mass of solvent, not the volume of solution. See Rodríquez-López, M.; Carrasquillo, A. *J. Chem. Educ.* **2005**, *82*, 1327-1328 for further discussion.

EXAMPLE 2.5.2

A laboratory procedure calls for 250 mL of an approximately 0.10 M solution of NH_3. Describe how you would prepare this solution using a stock solution of concentrated NH_3 (14.8 M).

Solution

Substituting known values into Equation 2.5.1

$$14.8\ \text{M} \times V_o = 0.10\ \text{M} \times 250\ \text{mL}$$

and solving for V_o gives 1.7 mL. Since we are making a solution that is approximately 0.10 M NH_3, we can use a graduated cylinder to measure the 1.7 mL of concentrated NH_3, transfer the NH_3 to a beaker, and add sufficient water to give a total volume of approximately 250 mL.

Although usually we express molarity as mol/L, we can express the volumes in mL if we do so both for both V_o and V_d.

EXERCISE 2.5.2

To prepare a standard solution of Zn^{2+} you dissolve a 1.004 g sample of Zn wire in a minimal amount of HCl and dilute to volume in a 500-mL volumetric flask. If you dilute 2.000 mL of this stock solution to 250.0 mL, what is the concentration of Zn^{2+}, in μg/mL, in your standard solution?

Answer

The first solution is a stock solution, which we then dilute to prepare the standard solution. The concentration of Zn^{2+} in the stock solution is

$$\frac{1.004\ \text{g Zn}^{2+}}{500.0\ \text{mL}} \times \frac{10^6\ \mu\text{g}}{\text{g}} = 2008\ \mu\text{g Zn}^{2+}/\text{mL}$$

To find the concentration of the standard solution we use Equation 2.5.1

$$\frac{2008\ \mu\text{g Zn}^{2+}}{\text{mL}} \times 2.000\ \text{mL} = C_d \times 250.0\ \text{mL}$$

where C_d is the standard solution's concentration. Solving gives a concentration of 16.06 μg Zn^{2+}/mL.

As shown in the following example, we can use Equation 2.5.1 to calculate a solution's original concentration using its known concentration after dilution.

EXAMPLE 2.5.3

A sample of an ore was analyzed for Cu^{2+} as follows. A 1.25 gram sample of the ore was dissolved in acid and diluted to volume in a 250-mL volumetric flask. A 20 mL portion of the resulting solution was transferred by pipet to a 50-mL volumetric flask and diluted to volume. An analysis of this solution gives the concentration of Cu^{2+} as 4.62 μg/mL. What is the weight percent of Cu in the original ore?

Solution

Substituting known values (with significant figures appropriate for pipets and volumetric flasks) into Equation 2.5.1

$$(C_{\text{Cu}})_o \times 20.00\ \text{mL} = 4.62\ \mu\text{g/mL Cu}^{2+} \times 50.00\ \text{mL}$$

and solving for $(C_{\text{Cu}})_o$ gives the original concentration as 11.55 μg/mL Cu^{2+}. To calculate the grams of Cu^{2+} we multiply this concentration by the total volume

$$\frac{11.55 \mu\text{g Cu}^{2+}}{\text{mL}} \times 250.0\ \text{mL} \times \frac{1\ \text{g}}{10^6\ \mu\text{g}} = 2.888 \times 10^{-3}\ \text{g Cu}^{2+}$$

The weight percent Cu is

$$\frac{2.888 \times 10^{-3}\ \text{g Cu}^{2+}}{1.25\ \text{g sample}} \times 100 = 0.231\%\ \text{w/w Cu}^{2+}$$

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2.6: SPREADSHEETS AND COMPUTATIONAL SOFTWARE

Analytical chemistry is a quantitative discipline. Whether you are completing a statistical analysis, trying to optimize experimental conditions, or exploring how a change in pH affects a compound's solubility, the ability to work with complex mathematical equations is essential. Spreadsheets, such as Microsoft Excel are an important tool for analyzing your data and for preparing graphs of your results. Scattered throughout this textbook you will find instructions for using spreadsheets.

> If you do not have access to Microsoft Excel or another commercial spreadsheet package, you might considering using Calc, a freely available open-source spreadsheet that is part of the OpenOffice.org software package at www.openoffice.org, or Google Sheets.

Although spreadsheets are useful, they are not always well suited for working with scientific data. If you plan to pursue a career in chemistry, you may wish to familiarize yourself with a more sophisticated computational software package, such as the freely available open-source program that goes by the name R, or commercial programs such as Mathematica or Matlab. You will find instructions for using R scattered throughout this textbook.

> You can download the current version of R from www.r-project.org. Click on the link for Download: CRAN and find a local mirror site. Click on the link for the mirror site and then use the link for Linux, MacOS X, or Windows under the heading "Download and Install R."

Despite the power of spreadsheets and computational programs, *don't forget that the most important software is behind your eyes and between your ears*. The ability to think intuitively about chemistry is a critically important skill. In many cases you will find that it is possible to determine if an analytical method is feasible or to approximate the optimum conditions for an analytical method without resorting to complex calculations. Why spend time developing a complex spreadsheet or writing software code when a "back-of-the-envelope" estimate will do the trick? Once you know the general solution to your problem, you can use a spreadsheet or a computational program to work out the specifics. Throughout this textbook we will introduce tools to help develop your ability to think intuitively.

> For an interesting take on the importance of intuitive thinking, see *Are You Smart Enough to Work at Google?* by William Poundstone (Little, Brown and Company, New York, 2012).

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2.7: THE LABORATORY NOTEBOOK

Finally, we can not end a chapter on the basic tools of analytical chemistry without mentioning the laboratory notebook. A laboratory notebook is your most important tool when working in the lab. If kept properly, you should be able to look back at your laboratory notebook several years from now and reconstruct the experiments on which you worked.

Your instructor will provide you with detailed instructions on how he or she wants you to maintain your notebook. Of course, you should expect to bring your notebook to the lab. Everything you do, measure, or observe while working in the lab should be recorded in your notebook as it takes place. Preparing data tables to organize your data will help ensure that you record the data you need, and that you can find the data when it is time to calculate and analyze your results. Writing a narrative to accompany your data will help you remember what you did, why you did it, and why you thought it was significant. Reserve space for your calculations, for analyzing your data, and for interpreting your results. Take your notebook with you when you do research in the library.

Maintaining a laboratory notebook may seem like a great deal of effort, but if you do it well you will have a permanent record of your work. Scientists working in academic, industrial and governmental research labs rely on their notebooks to provide a written record of their work. Questions about research carried out at some time in the past can be answered by finding the appropriate pages in the laboratory notebook. A laboratory notebook is also a legal document that helps establish patent rights and proof of discovery.

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2.8: PROBLEMS

1. Indicate how many significant figures are in each of the following numbers.
   a. 903 b. 0.903 c. 1.0903
   d. 0.0903 e. 0.09030 f. 9.03×10^2
2. Round each of the following to three significant figures.
   a. 0.89377 b. 0.89328 c. 0.89350
   d. 0.8997 e. 0.08907
3. Round each to the stated number of significant figures.
   a. the atomic weight of carbon to 4 significant figures b. the atomic weight of oxygen to 3 significant figures
   c. Avogadro's number to 4 significant figures d. Faraday's constant to 3 significant figures
4. Report results for the following calculations to the correct number of significant figures.
   a. 4.591 + 0.2309 + 67.1 = b. 313 – 273.15 = c. 712×8.6 =
   d. 1.43/0.026 = e. (8.314 × 298)/96 485 = f. $\log(6.53 \times 10^{-5})$ =
   g. $10^{-7.14}$ = h. $(6.51 \times 10^{-5}) \times (8.14 \times 10^{-9})$
5. A 12.1374 g sample of an ore containing Ni and Co is carried through Fresenius' analytical scheme, as shown in Figure 1.1.1. At point A the combined mass of Ni and Co is 0.2306 g, while at point B the mass of Co is 0.0813 g. Report the weight percent Ni in the ore to the correct number of significant figures.
6. Figure 1.1.2 shows an analytical method for the analysis of Ni in ores based on the precipitation of Ni^{2+} using dimethylglyoxime. The formula for the precipitate is $Ni(C_4H_7N_2O_2)_2$. Calculate the precipitate's formula weight to the correct number of significant figures.
7. An analyst wishes to add 256 mg of Cl^- to a reaction mixture. How many mL of 0.217 M $BaCl_2$ is this?
8. The concentration of lead in an industrial waste stream is 0.28 ppm. What is its molar concentration?
9. Commercially available concentrated hydrochloric acid is 37.0% w/w HCl. Its density is 1.18 g/mL. Using this information calculate (a) the molarity of concentrated HCl, and (b) the mass and volume, in mL, of a solution that contains 0.315 moles of HCl.
10. The density of concentrated ammonia, which is 28.0% w/w NH_3, is 0.899 g/mL. What volume of this reagent should you dilute to 1.0×10^3 mL to make a solution that is 0.036 M in NH_3?
11. A 250.0 mL aqueous solution contains 45.1 µg of a pesticide. Express the pesticide's concentration in weight-to-volume percent, in parts per million, and in parts per billion.
12. A city's water supply is fluoridated by adding NaF. The desired concentration of F^- is 1.6 ppm. How many mg of NaF should you add per gallon of treated water if the water supply already is 0.2 ppm in F^-?
13. What is the pH of a solution for which the concentration of H^+ is 6.92×10^{-6} M ? What is the $[H^+]$ in a solution whose pH is 8.923?
14. When using a graduated cylinder, the absolute accuracy with which you can deliver a given volume is ±1% of the cylinder's maximum volume. What are the absolute and the relative uncertainties if you deliver 15 mL of a reagent using a 25 mL graduated cylinder? Repeat for a 50 mL graduated cylinder.
15. Calculate the molarity of a potassium dichromate solution prepared by placing 9.67 grams of $K_2Cr_2O_7$ in a 100-mL volumetric flask, dissolving, and diluting to the calibration mark.
16. For each of the following explain how you would prepare 1.0 L of a solution that is 0.10 M in K^+. Repeat for concentrations of 1.0×10^2 ppm K^+ and 1.0% w/v K^+.
    a. KCl b. K_2SO_4 c. $K_3Fe(CN)_6$
17. A series of dilute NaCl solutions are prepared starting with an initial stock solution of 0.100 M NaCl. Solution A is prepared by pipeting 10 mL of the stock solution into a 250-mL volumetric flask and diluting to volume. Solution B is prepared by pipeting 25 mL of solution A into a 100-mL volumetric flask and diluting to volume. Solution C is prepared by pipeting 20 mL of solution B into a 500-mL volumetric flask and diluting to volume. What is the molar concentration of NaCl in solutions A, B and C?
18. Calculate the molar concentration of NaCl, to the correct number of significant figures, if 1.917 g of NaCl is placed in a beaker and dissolved in 50 mL of water measured with a graduated cylinder. If this solution is quantitatively transferred to a 250-mL volumetric flask and diluted to volume, what is its concentration to the correct number of significant figures?
19. What is the molar concentration of NO_3^- in a solution prepared by mixing 50.0 mL of 0.050 M KNO_3 with 40.0 mL of 0.075 M $NaNO_3$? What is pNO_3 for the mixture?
20. What is the molar concentration of Cl^- in a solution prepared by mixing 25.0 mL of 0.025 M NaCl with 35.0 mL of 0.050 M $BaCl_2$? What is pCl for the mixture?
21. To determine the concentration of ethanol in cognac a 5.00 mL sample of the cognac is diluted to 0.500 L. Analysis of the diluted cognac gives an ethanol concentration of 0.0844 M. What is the molar concentration of ethanol in the undiluted cognac?

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2.9: ADDITIONAL RESOURCES

The following two web sites contain useful information about the SI system of units.

- http://www.bipm.org/en/home/ – The home page for the Bureau International des Poids and Measures.
- http://physics.nist.gov/cuu/Units/index.html – The National Institute of Standards and Technology's introduction to SI units.

For a chemist's perspective on the SI units for mass and amount, consult the following papers.

- Davis, R. S. "What is a Kilogram in the Revised International System of Units (SI)?", *J. Chem. Educ.* **2015**, *92*, 1604–1609.
- Freeman, R. D. "SI for Chemists: Persistent Problems, Solid Solutions," *J. Chem. Educ.* **2003**, *80*, 16–20.
- Gorin, G. "Mole, Mole per Liter, and Molar: A Primer on SI and Related Units for Chemistry Students," *J. Chem. Educ.* **2003**, *80*, 103–104.

Discussions regarding possible changes in the SI base units are reviewed in these articles.

- Chao, L. S.; Schlamminger, S.; Newell, D. B.; Pratt, J. R.; Seifert, F.; Zhang, X.; Sineriz, M. L.; Haddad, D. "A LEGO Watt Balance: An Apparatus to Determine a Mass Based on the New SI," arXiv:1412.1699 [physics.ins-det].
- Fraundorf, P. "A Multiple of 12 for Avogadro," arXiv:1201.5537 [physics.gen-ph].
- Kemsley, J. "Rethinking the Mole and Kilogram," *C&E News*, August 25, 2014, p. 25.

The following are useful resources for maintaining a laboratory notebook and for preparing laboratory reports.

- Coghill, A. M.; Garson, L. M. (eds) *The ACS Style Guide: Effective Communication of Scientific Information*, 3rd Edition, American Chemical Society: Washington, D. C.; 2006.
- Kanare, H. M. *Writing the Laboratory Notebook*, American Chemical Society: Washington, D. C.; 1985.

The following texts provide instructions for using spreadsheets in analytical chemistry.

- de Levie, R. *How to Use Excel® in Analytical Chemistry and in General Scientific Data Analysis*, Cambridge University Press: Cambridge, UK, 2001.
- Diamond, D.; Hanratty, V. C. A., *Spreadsheet Applications in Chemistry*, Wiley-Interscience: New York, 1997.
- Feiser, H. *Concepts and Calculations in Analytical Chemistry: A Spreadsheet Approach*, CRC Press: Boca Raton, FL, 1992.

The following classic textbook emphasizes the application of intuitive thinking to the solving of problems.

- Harte, J. *Consider a Spherical Cow: A Course in Environmental Problem Solving*, University Science Books: Sausalito, CA, 1988.

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2.10: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

There are a few basic numerical and experimental tools with which you must be familiar. Fundamental measurements in analytical chemistry, such as mass, use base SI units, such as the kilogram. Other units, such as energy, are defined in terms of these base units. When reporting a measurement, we must be careful to include only those digits that are significant, and to maintain the uncertainty implied by these significant figures when trans- forming measurements into results.

The relative amount of a constituent in a sample is expressed as a concentration. There are many ways to express concentration, the most common of which are molarity, weight percent, volume percent, weight-to-volume percent, parts per million and parts per billion. Concentrations also can be expressed using p-functions.

Stoichiometric relationships and calculations are important in many quantitative analyses. The stoichiometry between the reactants and the products of a chemical reaction are given by the coefficients of a balanced chemical reaction.

Balances, volumetric flasks, pipets, and ovens are standard pieces of equipment that you will use routinely in the analytical lab. You should be familiar with the proper way to use this equipment. You also should be familiar with how to prepare a stock solution of known concentration, and how to prepare a dilute solution from a stock solution.

KEY TERMS

analytical balance
concentration
desiccant
desiccator
dilution
formality
graduated cylinder
meniscus
molality
molarity
normality
parts per million
parts per billion
p-function
quantitative transfer
scientific notation
significant figures
SI units
stock solution
tare
volume percent
volumetric flask
volumetric pipet
weight percent
weight-to-volume percent

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CHAPTER OVERVIEW

3: THE VOCABULARY OF ANALYTICAL CHEMISTRY

If you browse through an issue of the journal *Analytical Chemistry*, you will discover that the authors and readers share a common vocabulary of analytical terms. You probably are familiar with some of these terms, such as accuracy and precision, but other terms, such as analyte and matrix, are perhaps less familiar to you. In order to participate in any community, one must first understand its vocabulary; the goal of this chapter, therefore, is to introduce some important analytical terms. Becoming comfortable with these terms will make the chapters that follow easier to read and to understand.

3.1: Analysis, Determination, and Measurement
3.2: Techniques, Methods, Procedures, and Protocols
3.3: Classifying Analytical Techniques
3.4: Selecting an Analytical Method
3.5: Developing the Procedure
3.6: Protocols
3.7: The Importance of Analytical Methodology
3.8: Problems
3.9: Additional Resources
3.10: Chapter Summary and Key Terms

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3.1: ANALYSIS, DETERMINATION, AND MEASUREMENT

The first important distinction we will make is among the terms analysis, determination, and measurement. An analysis provides chemical or physical information about a sample. The component in the sample of interest to us is called the ***analyte***, and the remainder of the sample is the matrix. In an analysis we determine the identity, the concentration, or the properties of an analyte. To make this determination we measure one or more of the analyte's chemical or physical properties.

An example will help clarify the difference between an ***analysis***, a ***determination*** and a ***measurement***. In 1974 the federal government enacted the Safe Drinking Water Act to ensure the safety of the nation's public drinking water supplies. To comply with this act, municipalities monitor their drinking water supply for potentially harmful substances, such as fecal coliform bacteria. Municipal water departments collect and analyze samples from their water supply. To determine the concentration of fecal coliform bacteria an analyst passes a portion of water through a membrane filter, places the filter in a dish that contains a nutrient broth, and incubates the sample for 22–24 hrs at 44.5 ºC ± 0.2 ºC. At the end of the incubation period the analyst counts the number of bacterial colonies in the dish and reports the result as the number of colonies per 100 mL (Figure 3.1.1). Thus, a municipal water department analyzes samples of water to determine the concentration of fecal coliform bacteria by measuring the number of bacterial colonies that form during a carefully defined incubation period

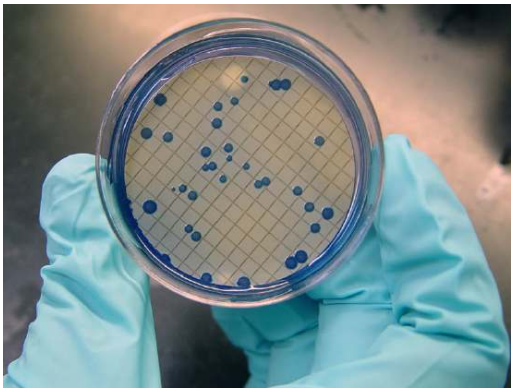


Figure 3.1.1 : Colonies of fecal coliform bacteria from a water supply. Source: Susan Boyer. Photo courtesy of ARS–USDA (www.ars.usda.gov).

A fecal coliform count provides a general measure of the presence of pathogenic organisms in a water supply. For drinking water, the current maximum contaminant level (MCL) for total coliforms, including fecal coliforms is less than 1 colony/100 mL. Municipal water departments must regularly test the water supply and must take action if more than 5% of the samples in any month test positive for coliform bacteria.

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3.2: TECHNIQUES, METHODS, PROCEDURES, AND PROTOCOLS

Suppose you are asked to develop an analytical method to determine the concentration of lead in drinking water. How would you approach this problem? To provide a structure for answering this question, it is helpful to consider four levels of analytical methodology: techniques, methods, procedures, and protocols [Taylor, J. K. *Anal. Chem.* **1983**, *55*, 600A–608A].

A ***technique*** is any chemical or physical principle that we can use to study an analyte. There are many techniques for that we can use to determine the concentration of lead in drinking water [Fitch, A.; Wang, Y.; Mellican, S.; Macha, S. *Anal. Chem.* **1996**, *68*, 727A–731A]. In graphite furnace atomic absorption spectroscopy (GFAAS), for example, we first convert aqueous lead ions into free atoms—a process we call atomization. We then measure the amount of light absorbed by the free atoms. Thus, GFAAS uses both a chemical principle (atomization) and a physical principle (absorption of light).

> See Chapter 10 for a discussion of graphite furnace atomic absorption spectroscopy.

A ***method*** is the application of a technique for a specific analyte in a specific matrix. As shown in Figure 3.2.1 , the GFAAS method for determining the concentration of lead in water is different from that for lead in soil or blood.

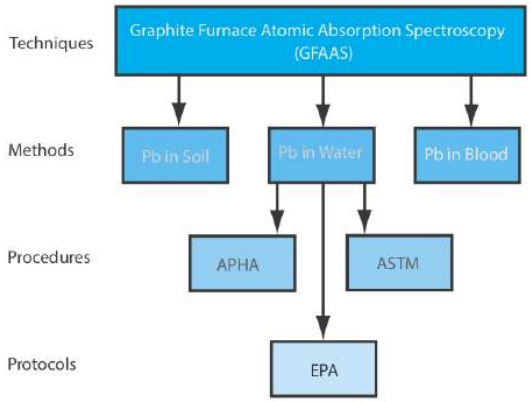


Figure 3.2.1 : Chart showing the hierarchical relationship between a technique, methods that use the technique, and procedures and protocols for a method. The abbreviations are APHA: American Public Health Association, ASTM: American Society for Testing Materials, EPA: Environmental Protection Agency.

A ***procedure*** is a set of written directions that tell us how to apply a method to a particular sample, including information on how to collect the sample, how to handle interferents, and how to validate results. A method may have several procedures as each analyst or agency adapts it to a specific need. As shown in Figure 3.2.1 , the American Public Health Agency and the American Society for Testing Materials publish separate procedures for determining the concentration of lead in water.

Finally, a ***protocol*** is a set of stringent guidelines that specify a procedure that an analyst must follow if an agency is to accept the results. Protocols are common when the result of an analysis supports or defines public policy. When determining the concentration of lead in water under the Safe Drinking Water Act, for example, the analyst must use a protocol specified by the Environmental Protection Agency.

There is an obvious order to these four levels of analytical methodology. Ideally, a protocol uses a previously validated procedure. Before developing and validating a procedure, a method of analysis must be selected. This requires, in turn, an initial screening of available techniques to determine those that have the potential for monitoring the analyte.

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3.3: CLASSIFYING ANALYTICAL TECHNIQUES

The analysis of a sample generates a chemical or physical signal that is proportional to the amount of analyte in the sample. This signal may be anything we can measure, such as volume or absorbance. It is convenient to divide analytical techniques into two general classes based on whether the signal is proportional to the mass or moles of analyte, or is proportional to the analyte's concentration

Consider the two graduated cylinders in Figure 3.3.1 , each of which contains a solution of 0.010 M $Cu(NO_3)_2$. Cylinder 1 contains 10 mL, or 1.0×10^{-4} moles of Cu^{2+}, and cylinder 2 contains 20 mL, or 2.0×10^{-4} moles of Cu^{2+}. If a technique responds to the absolute amount of analyte in the sample, then the signal due to the analyte S_A

$$S_A = k_A n_A \tag{3.3.1}$$

where n_A is the moles or grams of analyte in the sample, and k_A is a proportionality constant. Because cylinder 2 contains twice as many moles of Cu^{2+} as cylinder 1, analyzing the contents of cylinder 2 gives a signal twice as large as that for cylinder 1.



Figure 3.3.1 : Two graduated cylinders, each containing 0.10 M $Cu(NO_3)_2$. Although the cylinders contain the same concentration of Cu^{2+}, the cylinder on the left contains 1.0×10^{-4} mol Cu^{2+} and the cylinder on the right contains 2.0×10^{-4} mol Cu^{2+}.

A second class of analytical techniques are those that respond to the analyte's concentration, C_A

$$S_A = k_A C_A \tag{3.3.2}$$

Since the solutions in both cylinders have the same concentration of Cu^{2+}, their analysis yields identical signals.

A technique that responds to the absolute amount of analyte is a ***total analysis*** technique. Mass and volume are the most common signals for a total analysis technique, and the corresponding techniques are gravimetry (Chapter 8) and titrimetry (Chapter 9). With a few exceptions, the signal for a total analysis technique is the result of one or more chemical reactions, the stoichiometry of which determines the value of k_A in Equation 3.3.1 .

> Historically, most early analytical methods used a total analysis technique. For this reason, total analysis techniques are often called "classical" techniques.

Spectroscopy (Chapter 10) and electrochemistry (Chapter 11), in which an optical or an electrical signal is proportional to the relative amount of analyte in a sample, are examples of concentration techniques. The relationship between the signal and the analyte's concentration is a theoretical function that depends on experimental conditions and the instrumentation used to measure the signal. For this reason the value of k_A in Equation 3.3.2 is determined experimentally.

> Since most concentration techniques rely on measuring an optical or electrical signal, they also are known as "instrumental" techniques.

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3.4: SELECTING AN ANALYTICAL METHOD

A method is the application of a technique to a specific analyte in a specific matrix. We can develop an analytical method to determine the concentration of lead in drinking water using any of the techniques mentioned in the previous section. A gravimetric method, for example, might precipiate the lead as $PbSO_4$ or as $PbCrO_4$, and use the precipitate's mass as the analytical signal. Lead forms several soluble complexes, which we can use to design a complexation titrimetric method. As shown in Figure 3.2.1, we can use graphite furnace atomic absorption spectroscopy to determine the concentration of lead in drinking water. Finally, lead's multiple oxidation states (Pb^0, Pb^{2+}, Pb^{4+}) makes feasible a variety of electrochemical methods.

Ultimately, the requirements of the analysis determine the best method. In choosing among the available methods, we give consideration to some or all the following design criteria: accuracy, precision, sensitivity, selectivity, robustness, ruggedness, scale of operation, analysis time, availability of equipment, and cost.

ACCURACY

Accuracy is how closely the result of an experiment agrees with the "true" or expected result. We can express accuracy as an absolute error, e

$$e = \text{obtained result} - \text{expected result}$$

or as a percentage relative error, $\%e_r$

$$\%e_r = \frac{\text{obtained result} - \text{expected result}}{\text{expected result}} \times 100$$

A method's accuracy depends on many things, including the signal's source, the value of k_A in Equation 3.3.1 or Equation 3.3.2, and the ease of handling samples without loss or contamination. A total analysis technique, such as gravimetry and titrimetry, often produce more accurate results than does a concentration technique because we can measure mass and volume with high accuracy, and because the value of k_A is known exactly through stoichiometry.

> Because it is unlikely that we know the true result, we use an expected or accepted result to evaluate accuracy. For example, we might use a standard reference material, which has an accepted value, to establish an analytical method's accuracy. You will find a more detailed treatment of accuracy in Chapter 4, including a discussion of sources of errors.

PRECISION

When a sample is analyzed several times, the individual results vary from trial-to-trial. ***Precision*** is a measure of this variability. The closer the agreement between individual analyses, the more precise the results. For example, the results shown in the upper half of Figure 3.4.1 for the concentration of K^+ in a sample of serum are more precise than those in the lower half of Figure 3.4.1 . It is important to understand that precision does not imply accuracy. That the data in the upper half of Figure 3.4.1 are more precise does not mean that the first set of results is more accurate. In fact, neither set of results may be accurate.

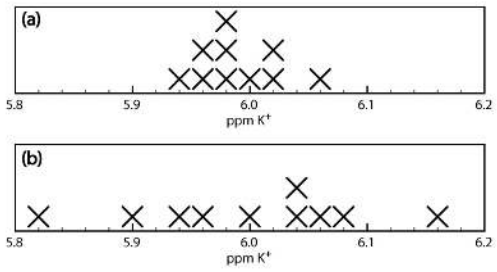


Figure 3.4.1 : Two determinations of the concentration of K^+ in serum, showing the effect of precision on the distribution of individual results. The data in (a) are less scattered and, therefore, more precise than the data in (b).

A method's precision depends on several factors, including the uncertainty in measuring the signal and the ease of handling samples reproducibly. In most cases we can measure the signal for a total analysis technique with a higher precision than is the case for a concentration method.

Confusing accuracy and precision is a common mistake. See Ryder, J.; Clark, A. *U. Chem. Ed.* **2002**, *6*, 1–3, and Tomlinson, J.; Dyson, P. J.; Garratt, J. *U. Chem. Ed.* **2001**, *5*, 16–23 for discussions of this and other common misconceptions about the meaning of error. You will find a more detailed treatment of precision in Chapter 4, including a discussion of sources of errors.

SENSITIVITY

The ability to demonstrate that two samples have different amounts of analyte is an essential part of many analyses. A method's ***sensitivity*** is a measure of its ability to establish that such a difference is significant. Sensitivity is often confused with a method's ***detection limit***, which is the smallest amount of analyte we can determine with confidence.

Confidence, as we will see in Chapter 4, is a statistical concept that builds on the idea of a population of results. For this reason, we will postpone our discussion of detection limits to Chapter 4. For now, the definition of a detection limit given here is sufficient.

Sensitivity is equivalent to the proportionality constant, k_A, in Equation 3.3.1 and Equation 3.3.2 [IUPAC Compendium of Chemical Terminology, Electronic version]. If ΔS_A is the smallest difference we can measure between two signals, then the smallest detectable difference in the absolute amount or the relative amount of analyte is

$$\Delta n_A = \frac{\Delta S_A}{k_A} \quad \text{or} \quad \Delta C_A = \frac{\Delta S_A}{k_A}$$

Suppose, for example, that our analytical signal is a measurement of mass using a balance whose smallest detectable increment is ±0.0001 g. If our method's sensitivity is 0.200, then our method can conceivably detect a difference in mass of as little as

$$\Delta n_A = \frac{\pm 0.0001 \text{ g}}{0.200} = \pm 0.0005 \text{ g}$$

For two methods with the same ΔS_A, the method with the greater sensitivity—that is, the method with the larger k_A—is better able to discriminate between smaller amounts of analyte.

SPECIFICITY AND SELECTIVITY

An analytical method is specific if its signal depends only on the analyte [Persson, B-A; Vessman, J. *Trends Anal. Chem.* **1998**, *17*, 117–119; Persson, B-A; Vessman, J. *Trends Anal. Chem.* **2001**, *20*, 526–532]. Although ***specificity*** is the ideal, few analytical methods are free from interferences. When an ***interferent*** contributes to the signal, we expand Equation 3.3.1 and Equation 3.3.2 to include its contribution to the sample's signal, S_{samp}

$$S_{samp} = S_A + S_I = k_A n_A + k_I n_I \tag{3.4.1}$$

$$S_{samp} = S_A + S_I = k_A C_A + k_I C_I \tag{3.4.2}$$

where S_I is the interferent's contribution to the signal, k_I is the interferent's sensitivity, and n_I and C_I are the moles (or grams) and the concentration of interferent in the sample, respectively.

Selectivity is a measure of a method's freedom from interferences [Valcárcel, M.; Gomez-Hens, A.; Rubio, S. *Trends Anal. Chem.* **2001**, *20*, 386–393]. A method's selectivity for an interferent relative to the analyte is defined by a ***selectivity coefficient***, $K_{A,I}$

$$K_{A,I} = \frac{k_I}{k_A} \tag{3.4.3}$$

which may be positive or negative depending on the signs of k_I and k_A. The selectivity coefficient is greater than +1 or less than –1 when the method is more selective for the interferent than for the analyte.

Although k_A and k_I usually are positive, they can be negative. For example, some analytical methods work by measuring the concentration of a species that remains after is reacts with the analyte. As the analyte's concentration increases, the concentration of the species that produces the signal decreases, and the signal becomes smaller. If the signal in the absence of analyte is assigned a value of zero, then the subsequent signals are negative.

Determining the selectivity coefficient's value is easy if we already know the values for k_A and k_I. As shown by Example 3.4.1 , we also can determine $K_{A,I}$ by measuring S_{samp} in the presence of and in the absence of the interferent.

EXAMPLE 3.4.1

A method for the analysis of Ca^{2+} in water suffers from an interference in the presence of Zn^{2+}. When the concentration of Ca^{2+} is 100 times greater than that of Zn^{2+}, an analysis for Ca^{2+} has a relative error of +0.5%. What is the selectivity coefficient for this method?

Solution

Since only relative concentrations are reported, we can arbitrarily assign absolute concentrations. To make the calculations easy, we will let C_{Ca} = 100 (arbitrary units) and C_{Zn} = 1. A relative error of +0.5% means the signal in the presence of Zn^{2+} is 0.5% greater than the signal in the absence of Zn^{2+}. Again, we can assign values to make the calculation easier. If the signal for Cu^{2+} in the absence of Zn^{2+} is 100 (arbitrary units), then the signal in the presence of Zn^{2+} is 100.5.

The value of k_{Ca} is determined using Equation 3.3.2

$$k_{Ca} = \frac{S_{Ca}}{C_{Ca}} = \frac{100}{100} = 1$$

In the presence of Zn^{2+} the signal is given by Equation 3.4.2; thus

$$S_{samp} = 100.5 = k_{Ca}C_{Ca} + k_{Zn}C_{Zn} = (1 \times 100) + k_{Zn} \times 1$$

Solving for k_{Zn} gives its value as 0.5. The selectivity coefficient is

$$K_{Ca,Zn} = \frac{k_{Zn}}{k_{Ca}} = \frac{0.5}{1} = 0.5$$

If you are unsure why, in the above example, the signal in the presence of zinc is 100.5, note that the percentage relative error for this problem is given by

$$\frac{\text{obtained result} - 100}{100} \times 100 = +0.5\%$$

Solving gives an obtained result of 100.5.

EXERCISE 3.4.1

Wang and colleagues describe a fluorescence method for the analysis of Ag^+ in water. When analyzing a solution that contains 1.0×10^{-9} M Ag^+ and 1.1×10^{-7} M Ni^{2+}, the fluorescence intensity (the signal) was +4.9% greater than that obtained for a sample of 1.0×10^{-9} M Ag^+. What is $K_{Ag,Ni}$ for this analytical method? The full citation for the data in this exercise is Wang, L.; Liang, A. N.; Chen, H.; Liu, Y.; Qian, B.; Fu, J. *Anal. Chim. Acta* **2008**, *616*, 170-176.

Answer

Because the signal for Ag^+ in the presence of Ni^{2+} is reported as a relative error, we will assign a value of 100 as the signal for 1×10^{-9} M Ag^+. With a relative error of +4.9%, the signal for the solution of 1×10^{-9} M Ag^+ and 1.1×10^{-7} M Ni^{2+} is 104.9. The sensitivity for Ag^+ is determined using the solution that does not contain Ni^{2+}; thus

$$k_{Ag} = \frac{S_{Ag}}{C_{Ag}} = \frac{100}{1 \times 10^{-9}\ \text{M}} = 1.0 \times 10^{11}\ \text{M}^{-1}$$

Substituting into Equation 3.4.2 values for k_{Ag}, S_{samp} , and the concentrations of Ag^+ and Ni^{2+}

$$104.9 = (1.0 \times 10^{11}\ \text{M}^{-1}) \times (1 \times 10^{-9}\ \text{M}) + k_{Ni} \times (1.1 \times 10^{-7}\ \text{M})$$

and solving gives k_{Ni} as 4.5×10^{7} M^{-1}. The selectivity coefficient is

$$K_{Ag,Ni} = \frac{k_{Ni}}{k_{Ag}} = \frac{4.5 \times 10^{7}\ \text{M}^{-1}}{1.0 \times 10^{11}\ \text{M}^{-1}} = 4.5 \times 10^{-4}$$

A selectivity coefficient provides us with a useful way to evaluate an interferent's potential effect on an analysis. Solving Equation 3.4.3 for k_I

$$k_I = K_{A,I} \times k_A \tag{3.4.4}$$

and substituting in Equation 3.4.1 and Equation 3.4.2, and simplifying gives

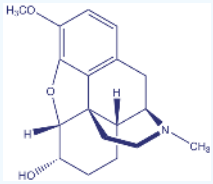
$$S_{samp} = k_A\{n_A + K_{A,I} \times n_I\} \tag{3.4.5}$$

$$S_{samp} = k_A\{C_A + K_{A,I} \times C_I\} \tag{3.4.6}$$

An interferent will not pose a problem as long as the term $K_{A,I} \times n_I$ in Equation 3.4.5 is significantly smaller than n_A, or if $K_{A,I} \times C_I$ in Equation 3.4.6 is significantly smaller than C_A.

EXAMPLE 3.4.2

Barnett and colleagues developed a method to determine the concentration of codeine (structure shown below) in poppy plants [Barnett, N. W.; Bowser, T. A.; Geraldi, R. D.; Smith, B. *Anal. Chim. Acta* **1996**, *318*, 309– 317]. As part of their study they evaluated the effect of several interferents. For example, the authors found that equimolar solutions of codeine and the interferent 6-methoxycodeine gave signals, respectively of 40 and 6 (arbitrary units).



(a) What is the selectivity coefficient for the interferent, 6-methoxycodeine, relative to that for the analyte, codeine.

(b) If we need to know the concentration of codeine with an accuracy of ±0.50%, what is the maximum relative concentration of 6-methoxy-codeine that we can tolerate?

Solution

(a) The signals due to the analyte, S_A, and the interferent, S_I, are

$$S_A = k_A C_A \qquad S_I = k_I C_I$$

Solving these equations for k_A and for k_I, and substituting into Equation 3.4.4 gives

$$K_{A,I} = \frac{S_I/C_I}{S_A/C_I}$$

Because the concentrations of analyte and interferent are equimolar ($C_A = C_I$), the selectivity coefficient is

$$K_{A,I} = \frac{S_I}{S_A} = \frac{6}{40} = 0.15$$

(b) To achieve an accuracy of better than ±0.50% the term $K_{A,I} \times C_I$ in Equation 3.4.6 must be less than 0.50% of C_A; thus

$$K_{A,I} \times C_I \leq 0.0050 \times C_A$$

Solving this inequality for the ratio C_I/C_A and substituting in the value for $K_{A,I}$ from part (a) gives

$$\frac{C_I}{C_A} \leq \frac{0.0050}{K_{A,I}} = \frac{0.0050}{0.15} = 0.033$$

Therefore, the concentration of 6-methoxycodeine must be less than 3.3% of codeine's concentration.

When a method's signal is the result of a chemical reaction—for example, when the signal is the mass of a precipitate—there is a good chance that the method is not very selective and that it is susceptible to an interference.

EXERCISE 3.4.2

Mercury (II) also is an interferent in the fluorescence method for Ag^+ developed by Wang and colleagues (see Practice Exercise 3.4.1). The selectivity coefficient, $K_{Ag,Hg}$ has a value of -1.0×10^{-3}.

(a) What is the significance of the selectivity coefficient's negative sign?

(b) Suppose you plan to use this method to analyze solutions with concentrations of Ag^+ no smaller than 1.0 nM. What is the maximum concentration of Hg^{2+} you can tolerate if your percentage relative errors must be less than ±1.0%?

Answer

(a) A negative value for $K_{Ag,Hg}$ means that the presence of Hg^{2+} decreases the signal from Ag^+.

(b) In this case we need to consider an error of –1%, since the effect of Hg^{2+} is to decrease the signal from Ag^{+}. To achieve this error, the term $K_{A,I} \times C_I$ in Equation 3.4.6 must be less than –1% of C_A; thus

$$K_{\text{Ag,Hg}} \times C_{\text{Hg}} = -0.01 \times C_{\text{Ag}}$$

Substituting in known values for $K_{\text{Ag,Hg}}$ and C_{Ag}, we find that the maximum concentration of Hg^{2+} is 1.0×10^{-8} M.

Problems with selectivity also are more likely when the analyte is present at a very low concentration [Rodgers, L. B. *J. Chem. Educ.* **1986**, *63*, 3–6].

Look back at Figure 1.1.1, which shows Fresenius' analytical method for the determination of nickel in ores. The reason there are so many steps in this procedure is that precipitation reactions generally are not very selective. The method in Figure 1.1.2 includes fewer steps because dimethylglyoxime is a more selective reagent. Even so, if an ore contains palladium, additional steps are needed to prevent the palladium from interfering.

ROBUSTNESS AND RUGGEDNESS

For a method to be useful it must provide reliable results. Unfortunately, methods are subject to a variety of chemical and physical interferences that contribute uncertainty to the analysis. If a method is relatively free from chemical interferences, we can use it to analyze an analyte in a wide variety of sample matrices. Such methods are considered ***robust***.

Random variations in experimental conditions introduces uncertainty. If a method's sensitivity, *k*, is too dependent on experimental conditions, such as temperature, acidity, or reaction time, then a slight change in any of these conditions may give a significantly different result. A ***rugged*** method is relatively insensitive to changes in experimental conditions.

SCALE OF OPERATION

Another way to narrow the choice of methods is to consider three potential limitations: the amount of sample available for the analysis, the expected concentration of analyte in the samples, and the minimum amount of analyte that will produce a measurable signal. Collectively, these limitations define the analytical method's scale of operations.

We can display the scale of operations visually (Figure 3.4.2) by plotting the sample's size on the *x*-axis and the analyte's concentration on the *y*-axis. For convenience, we divide samples into macro (>0.1 g), meso (10 mg–100 mg), micro (0.1 mg–10 mg), and ultramicro (<0.1 mg) sizes, and we divide analytes into major (>1% w/w), minor (0.01% w/w–1% w/w), trace (10^{-7}% w/w–0.01% w/w), and ultratrace (<10^{-7}% w/w) components. Together, the analyte's concentration and the sample's size provide a characteristic description for an analysis. For example, in a microtrace analysis the sample weighs between 0.1 mg and 10 mg and contains a concentration of analyte between 10^{-7}% w/w and 10^{-2}% w/w.

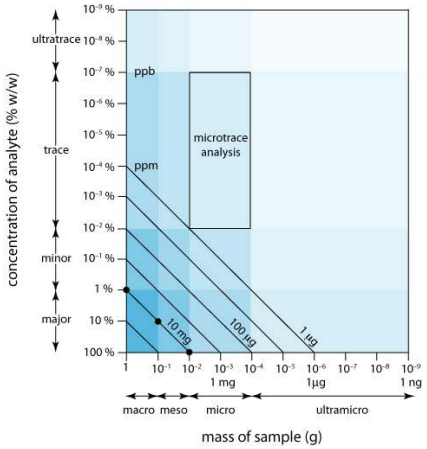


Figure 3.4.2 : Scale of operations for analytical methods. The shaded areas define different types of analyses. The boxed area, for example, represents a microtrace analysis. The diagonal lines show combinations of sample size and analyte concentration that contain the same mass of analyte. The three filled circles (•), for example, indicate analyses that use 10 mg of analyte. See Sandell, E. B.; Elving, P. J. in Kolthoff, I. M.; Elving, P. J., eds. *Treatise on Analytical Chem-istry*, Interscience: New York, Part I, Vol. 1, Chapter 1, pp. 3–6; (b) Potts, L. W. *Quantitative Analysis–Theory and Practice*, Harper and Row: New York, 1987, pp. 12 for more details.

The diagonal lines connecting the axes show combinations of sample size and analyte concentration that contain the same absolute mass of analyte. As shown in Figure 3.4.2 , for example, a 1-g sample that is 1% w/w analyte has the same amount of analyte (10 mg) as a 100-mg sample that is 10% w/w analyte, or a 10-mg sample that is 100% w/w analyte.

We can use Figure 3.4.2 to establish limits for analytical methods. If a method's minimum detectable signal is equivalent to 10 mg of analyte, then it is best suited to a major analyte in a macro or meso sample. Extending the method to an analyte with a concentration of 0.1% w/w requires a sample of 10 g, which rarely is practical due to the complications of carrying such a large amount of material through the analysis. On the other hand, a small sample that contains a trace amount of analyte places significant restrictions on an analysis. For example, a 1-mg sample that is 10^{-4}% w/w in analyte contains just 1 ng of analyte. If we isolate the analyte in 1 mL of solution, then we need an analytical method that reliably can detect it at a concentration of 1 ng/mL.

> It should not surprise you to learn that a total analysis technique typically requires a macro or a meso sample that contains a major analyte. A concentration technique is particularly useful for a minor, trace, or ultratrace analyte in a macro, meso, or micro sample.

EQUIPMENT, TIME, AND COST

Finally, we can compare analytical methods with respect to their equipment needs, the time needed to complete an analysis, and the cost per sample. Methods that rely on instrumentation are equipment-intensive and may require significant operator training. For example, the graphite furnace atomic absorption spectroscopic method for determining lead in water requires a significant capital investment in the instrument and an experienced operator to obtain reliable results. Other methods, such as titrimetry, require less expensive equipment and less training.

The time to complete an analysis for one sample often is fairly similar from method-to-method. This is somewhat misleading, however, because much of this time is spent preparing samples, preparing reagents, and gathering together equipment. Once the samples, reagents, and equipment are in place, the sampling rate may differ substantially. For example, it takes just a few minutes to analyze a single sample for lead using graphite furnace atomic absorption spectroscopy, but several hours to analyze the same sample using gravimetry. This is a significant factor in selecting a method for a laboratory that handles a high volume of samples.

The cost of an analysis depends on many factors, including the cost of equipment and reagents, the cost of hiring analysts, and the number of samples that can be processed per hour. In general, methods that rely on instruments cost more per sample then other methods.

MAKING THE FINAL CHOICE

Unfortunately, the design criteria discussed in this section are not mutually independent [Valcárcel, M.; Ríos, A. *Anal. Chem.* **1993**, *65*, 781A–787A]. Working with smaller samples or improving selectivity often comes at the expense of precision. Minimizing cost and analysis time may decrease accuracy. Selecting a method requires carefully balancing the various design criteria. Usually, the most important design criterion is accuracy, and the best method is the one that gives the most accurate result. When the need for a result is urgent, as is often the case in clinical labs, analysis time may become the critical factor.

In some cases it is the sample's properties that determine the best method. A sample with a complex matrix, for example, may require a method with excellent selectivity to avoid interferences. Samples in which the analyte is present at a trace or ultratrace concentration usually require a concentration method. If the quantity of sample is limited, then the method must not require a large amount of sample.

Determining the concentration of lead in drinking water requires a method that can detect lead at the parts per billion concentration level. Selectivity is important because other metal ions are present at significantly higher concentrations. A method that uses graphite furnace atomic absorption spectroscopy is a common choice for determining lead in drinking water because it meets these specifications. The same method is also useful for determining lead in blood where its ability to detect low concentrations of lead using a few microliters of sample is an important consideration.

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3.5: DEVELOPING THE PROCEDURE

After selecting a method, the next step is to develop a procedure that accomplish our goals for the analysis. In developing a procedure we give attention to compensating for interferences, to selecting and calibrating equipment, to acquiring a representative sample, and to validating the method.

COMPENSATING FOR INTERFERENCES

A method's accuracy depends on its selectivity for the analyte. Even the best method, however, may not be free from interferents that contribute to the measured signal. Potential interferents may be present in the sample itself or in the reagents used during the analysis.

When the sample is free of interferents, the total signal, S_{total}, is a sum of the signal due to the analyte, S_A, and the signal due to interferents in the reagents, S_{reag},

$$S_{total} = S_A + S_{reag} = k_A n_A + S_{reag} \tag{3.5.1}$$

$$S_{total} = S_A + S_{reag} = k_A C_A + S_{reag} \tag{3.5.2}$$

Without an independent determination of S_{reag} we cannot solve Equation 3.5.1 or 3.5.2 for the moles or concentration of analyte.

To determine the contribution of S_{reag} in Equations 3.5.1 and 3.5.2 we measure the signal for a ***method blank***, a solution that does not contain the sample. Consider, for example, a procedure in which we dissolve a 0.1-g sample in a portion of solvent, add several reagents, and dilute to 100 mL with additional solvent. To prepare the method blank we omit the sample and dilute the reagents to 100 mL using the solvent. Because the analyte is absent, S_{total} for the method blank is equal to S_{reag}. Knowing the value for S_{reag} makes it is easy to correct S_{total} for the reagent's contribution to the total signal; thus

$$(S_{total} - S_{reag}) = S_A = k_A n_A$$

$$(S_{total} - S_{reag}) = S_A = k_A C_A$$

By itself, a method blank cannot compensate for an interferent that is part of the sample's matrix. If we happen to know the interferent's identity and concentration, then we can be add it to the method blank; however, this is not a common circumstance and we must, instead, find a method for separating the analyte and interferent before continuing the analysis.

> A method blank also is known as a reagent blank. When the sample is a liquid, or is in solution, we use an equivalent volume of an inert solvent as a substitute for the sample.

CALIBRATION

A simple definition of a quantitative analytical method is that it is a mechanism for converting a measurement, the signal, into the amount of analyte in a sample. Assuming we can correct for interferents, a quantitative analysis is nothing more than solving Equation 3.3.1 or Equation 3.3.2 for n_A or for C_A.

To solve these equations we need the value of k_A. For a total analysis method usually we know the value of k_A because it is defined by the stoichiometry of the chemical reactions responsible for the signal. For a concentration method, however, the value of k_A usually is a complex function of experimental conditions. A ***calibration*** is the process of experimentally determining the value of k_A by measuring the signal for one or more standard samples, each of which contains a known concentration of analyte.

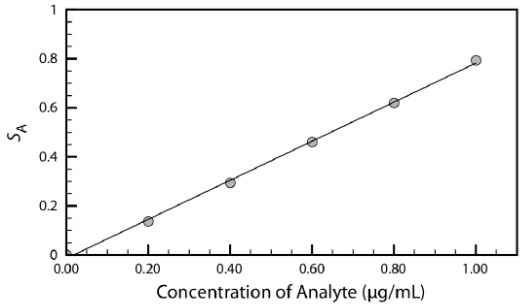


Figure 3.5.1 : Example of a calibration curve. The filled circles (•) are the results for five standard samples, each with a different concentration of analyte, and the line is the best fit to the data determined by a linear regression analysis. See Chapter 5 for a further discussion of calibration curves and an explanation of linear regression.

With a single standard we can calculate the value of k_A using Equation 3.3.1 or Equation 3.3.2. When using several standards with different concentrations of analyte, the result is best viewed visually by plotting S_A versus the concentration of analyte in the standards. Such a plot is

known as a ***calibration curve***, an example of which is shown in Figure 3.5.1 .

SAMPLING

Selecting an appropriate method and executing it properly helps us ensure that our analysis is accurate. If we analyze the wrong sample, however, then the accuracy of our work is of little consequence.

A proper sampling strategy ensures that our samples are representative of the material from which they are taken. Biased or nonrepresentative sampling, and contaminating samples during or after their collection are two examples of sampling errors that can lead to a significant error in accuracy. It is important to realize that sampling errors are independent of errors in the analytical method. As a result, we cannot correct a sampling error in the laboratory by, for example, evaluating a reagent blank.

> Chapter 7 provides a more detailed discussion of sampling, including strategies for obtaining representative samples.

VALIDATION

If we are to have confidence in our procedure we must demonstrate that it can provide acceptable results, a process we call ***validation***. Perhaps the most important part of validating a procedure is establishing that its precision and accuracy are appropriate for the problem we are trying to solve. We also ensure that the written procedure has sufficient detail so that different analysts or laboratories will obtain comparable results. Ideally, validation uses a standard sample whose composition closely matches the samples we will analyze. In the absence of appropriate standards, we can evaluate accuracy by comparing results to those obtained using a method of known accuracy.

> You will find more details about validating analytical methods in Chapter 14.

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3.6: PROTOCOLS

Earlier we defined a protocol as a set of stringent written guidelines that specify an exact procedure that we must follow if an agency is to accept the results of our analysis. In addition to the considerations that went into the procedure's design, a protocol also contains explicit instructions regarding internal and external quality assurance and quality control (***QA/QC***) procedures [Amore, F. *Anal. Chem.* **1979**, *51*, 1105A–1110A; Taylor, J. K. *Anal. Chem.* **1981**, *53*, 1588A–1593A]. The goal of internal QA/QC is to ensure that a laboratory's work is both accurate and precise. External QA/QC is a process in which an external agency certifies a laboratory.

As an example, let's outline a portion of the Environmental Protection Agency's protocol for determining trace metals in water by graphite furnace atomic absorption spectroscopy as part of its Contract Laboratory Program (CLP). The CLP protocol (see Figure 3.6.1) calls for an initial calibration using a method blank and three standards, one of which is at the detection limit. The resulting calibration curve is verified by analyzing initial calibration verification (ICV) and initial calibration blank (ICB) samples. The lab's result for the ICV sample must fall within ±10% of its expected concentration. If the result is outside this limit the analysis is stopped and the problem identified and corrected before continuing.

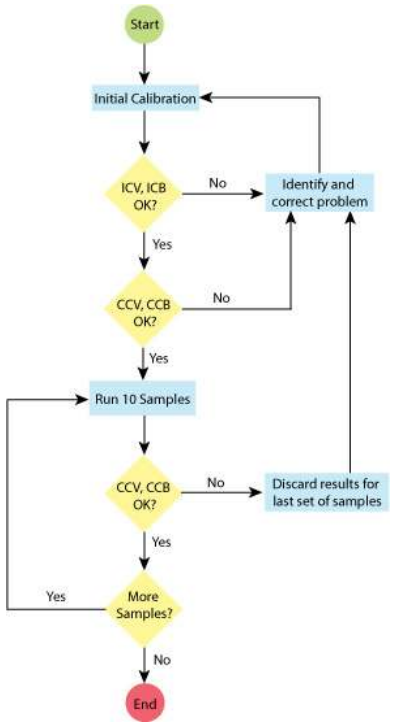


Figure 3.6.1 : Schematic diagram showing a portion of the EPA's protocol for determining trace metals in water using graphite furnace atomic absorption spectrometry. The abbreviations are ICV: initial calibration verification; ICB: initial calibration blank; CCV: continuing calibration verification; CCB: continuing calibration blank.

After a successful analysis of the ICV and ICB samples, the lab reverifies the calibration by analyzing a continuing calibration verification (CCV) sample and a continuing calibration blank (CCB). Results for the CCV also must be within ±10% of its expected concentration. Again, if the lab's result for the CCV is outside the established limits, the analysis is stopped, the problem identified and corrected, and the system recalibrated as described above. Additional CCV and the CCB samples are analyzed before the first sample and after the last sample, and between every set of ten samples. If the result for any CCV or CCB sample is unacceptable, the results for the last set of samples are discarded, the system is recalibrated, and the samples reanalyzed. By following this protocol, each result is bound by successful checks on the calibration. Although not shown in Figure 3.6.1 , the protocol also contains instructions for analyzing duplicate or split samples, and for using spike tests to verify accuracy.

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3.7: THE IMPORTANCE OF ANALYTICAL METHODOLOGY

The importance of the issues raised in this chapter is evident if we examine environmental monitoring programs. The purpose of a monitoring program is to determine the present status of an environmental system, and to assess long term trends in the system's health. These are broad and poorly defined goals. In many cases, an environmental monitoring program begins before the essential questions are known. This is not surprising since it is difficult to formulate questions in the absence of results. Without careful planning, however, a poor experimental design may result in data that has little value.

These concerns are illustrated by the Chesapeake Bay Monitoring Program. This research program, designed to study nutrients and toxic pollutants in the Chesapeake Bay, was initiated in 1984 as a cooperative venture between the federal government, the state governments of Maryland, Virginia, and Pennsylvania, and the District of Columbia. A 1989 review of the program highlights the problems common to many monitoring programs [D'Elia, C. F.; Sanders, J. G.; Capone, D. G. *Envrion. Sci. Technol.* **1989**, *23*, 768–774].

At the beginning of the Chesapeake Bay monitoring program, little attention was given to selecting analytical methods, in large part because the eventual use of the data was not yet specified. The analytical methods initially chosen were standard methods already approved by the Environmental Protection Agency (EPA). In many cases these methods were not useful because they were designed to detect pollutants at their legally mandated maximum allowed concentrations. In unpolluted waters, however, the concentrations of these contaminants often are well below the detection limit of the EPA methods. For example, the detection limit for the EPA approved standard method for phosphate was 7.5 ppb. Since the actual phosphate concentrations in Chesapeake Bay were below the EPA method's detection limit, it provided no useful information. On the other hand, the detection limit for a non-approved variant of the EPA method, a method routinely used by chemical oceanographers, was 0.06 ppb, a more realistic detection limit for their samples. In other cases, such as the elemental analysis for particulate forms of carbon, nitrogen and phosphorous, EPA approved procedures provided poorer reproducibility than nonapproved methods.

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3.8: PROBLEMS

1. When working with a solid sample, often it is necessary to bring the analyte into solution by digesting the sample with a suitable solvent. Any remaining solid impurities are removed by filtration before continuing with the analysis. In a typical total analysis method, the procedure might read

   "After digesting the sample in a beaker using approximately 25 mL of solvent, remove any solid impurities that remain by passing the solution the analyte through filter paper, collecting the filtrate in a clean Erlenmeyer flask. Rinse the beaker with several small portions of solvent, passing these rinsings through the filter paper and collecting them in the same Erlenmeyer flask. Finally, rinse the filter paper with several portions of solvent, collecting the rinsings in the same Erlenmeyer flask."

   For a typical concentration method, however, the procedure might state

   "After digesting the sample in a beaker using 25.00 mL of solvent, remove any solid impurities by filtering a portion of the solution containing the analyte. Collect and discard the first several mL of filtrate before collecting a sample of 5.00 mL for further analysis."

   Explain why these two procedures are different.
2. A certain concentration method works best when the analyte's concentration is approximately 10 ppb.

   (a) If the method requires a sample of 0.5 mL, about what mass of analyte is being measured?

   (b) If the analyte is present at 10% w/v, how would you prepare the sample for analysis?

   (c) Repeat for the case where the analyte is present at 10% w/w.

   (d) Based on your answers to parts (a)–(c), comment on the method's suitability for the determination of a major analyte.
3. An analyst needs to evaluate the potential effect of an interferent, *I*, on the quantitative analysis for an analyte, *A*. She begins by measuring the signal for a sample in which the interferent is absent and the analyte is present with a concentration of 15 ppm, obtaining an average signal of 23.3 (arbitrary units). When she analyzes a sample in which the analyte is absent and the interferent is present with a concentration of 25 ppm, she obtains an average signal of 13.7.

   (a) What is the sensitivity for the analyte?

   (b) What is the sensitivity for the interferent?

   (c) What is the value of the selectivity coefficient?

   (d) Is the method more selective for the analyte or the interferent?

   (e) What is the maximum concentration of interferent relative to that of the analyte if the error in the analysis is to be less than 1%?
4. A sample is analyzed to determine the concentration of an analyte. Under the conditions of the analysis the sensitivity is $17.2\ \text{ppm}^{-1}$. What is the analyte's concentration if S_{total} is 35.2 and S_{reag} is 0.6?
5. A method for the analysis of Ca^{2+} in water suffers from an interference in the presence of Zn^{2+}. When the concentration of Ca^{2+} is 50 times greater than that of Zn^{2+}, an analysis for Ca^{2+} gives a relative error of –2.0%. What is the value of the selectivity coefficient for this method?
6. The quantitative analysis for reduced glutathione in blood is complicated by many potential interferents. In one study, when analyzing a solution of 10.0 ppb glutathione and 1.5 ppb ascorbic acid, the signal was 5.43 times greater than that obtained for the analysis of 10.0 ppb glutathione [Jiménez-Prieto, R.; Velasco, A.; Silva, M; Pérez-Bendito, D. *Anal. Chem. Acta* **1992**, *269*, 273– 279]. What is the selectivity coefficient for this analysis? The same study found that analyzing a solution of 3.5×10^2 ppb methionine and 10.0 ppb glutathione gives a signal that is 0.906 times less than that obtained for the analysis of 10.0 ppb glutathione. What is the selectivity coefficient for this analysis? In what ways do these interferents behave differently?
7. Oungpipat and Alexander described a method for determining the concentration of glycolic acid (GA) in a variety of samples, including physiological fluids such as urine [Oungpipat, W.; Alexander, P. W. *Anal. Chim. Acta* **1994**, *295*, 36–46]. In the presence of only GA, the signal is

$$S_{samp,1} = k_{\text{GA}} C_{\text{GA}}$$

and in the presence of both glycolic acid and ascorbic acid (AA), the signal is

$$S_{samp,2} = k_{\text{GA}} C_{\text{GA}} + k_{\text{AA}} C_{\text{AA}}$$

When the concentration of glycolic acid is $1.0 \times 10^{-4}\ \text{M}$ and the concentration of ascorbic acid is $1.0 \times 10^{-5}\ \text{M}$, the ratio of their signals is

$$\frac{S_{samp,2}}{S_{samp,1}} = 1.44$$

(a) Using the ratio of the two signals, determine the value of the selectivity ratio $K_{\text{GA,AA}}$.

(b) Is the method more selective toward glycolic acid or ascorbic acid?

(c) If the concentration of ascorbic acid is $1.0 \times 10^{-5}\ \text{M}$, what is the smallest concentration of glycolic acid that can be determined such that the error introduced by failing to account for the signal from ascorbic acid is less than 1%?

8. Ibrahim and co-workers developed a new method for the quantitative analysis of hypoxanthine, a natural compound of some nucleic acids [Ibrahim, M. S.; Ahmad, M. E.; Temerk, Y. M.; Kaucke, A. M. *Anal. Chim. Acta* **1996**, *328*, 47–52]. As part of their study they evaluated the method's selectivity for hypoxanthine in the presence of several possible interferents, including ascorbic acid.

(a) When analyzing a solution of $1.12 \times 10^{-6}\ \text{M}$ hypoxanthine the authors obtained a signal of $7.45 \times 10^{-5}\ \text{amps}$. What is the sensitivity for hypoxanthine? You may assume the signal has been corrected for the method blank.

(b) When a solution containing $1.12 \times 10^{-6}\ \text{M}$ hypoxanthine and $6.5 \times 10^{-5}\ \text{M}$ ascorbic acid is analyzed a signal of $4.04 \times 10^{-5}\ \text{amps}$ is obtained. What is the selectivity coefficient for this method?

(c) Is the method more selective for hypoxanthine or for ascorbic acid?

(d) What is the largest concentration of ascorbic acid that may be present if a concentration of $1.12 \times 10^{-6}\ \text{M}$ hypoxanthine is to be determined within 1.0%?

9. Examine a procedure from *Standard Methods for the Analysis of Waters and Wastewaters* (or another manual of standard analytical methods) and identify the steps taken to compensate for interferences, to calibrate equipment and instruments, to standardize the method, and to acquire a representative sample.

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3.9: ADDITIONAL RESOURCES

The International Union of Pure and Applied Chemistry (IUPAC) maintains a web-based compendium of analytical terminology. You can find it at the following web site.

- old.iupac.org/publications/an...al_compendium/

The following papers provide alternative schemes for classifying analytical methods.

- Booksh, K. S.; Kowalski, B. R. "Theory of Analytical Chemistry," *Anal. Chem.* **1994**, *66*, 782A– 791A.
- Phillips, J. B. "Classification of Analytical Methods," *Anal. Chem.* **1981**, *53*, 1463A–1470A.
- Valcárcel, M.; Luque de Castro, M. D. "A Hierarchical Approach to Analytical Chemistry," *Trends Anal. Chem.* **1995**, *14*, 242–250.
- Valcárcel, M.; Simonet, B. M. "Types of Analytical Information and Their Mutual Relationships," *Trends Anal. Chem.* **1995**, *14*, 490–495.

Further details on criteria for evaluating analytical methods are found in the following series of papers.

- Wilson, A. L. "The Performance-Characteristics of Analytical Methods", Part I-*Talanta*, **1970**, *17*, 21–29; Part II-*Talanta*, **1970**, *17*, 31–44; Part III-*Talanta*, **1973**, *20*, 725–732; Part IV-*Talanta*, **1974**, *21*, 1109–1121.

For a point/counterpoint debate on the meaning of sensitivity consult the following two papers and two letters of response.

- Ekins, R.; Edwards, P. "On the Meaning of 'Sensitivity'," *Clin. Chem.* **1997**, *43*, 1824–1831.
- Ekins, R.; Edwards, P. "On the Meaning of 'Sensitivity:' A Rejoinder," *Clin. Chem.* **1998**, *44*, 1773–1776.
- Pardue, H. L. "The Inseparable Triangle: Analytical Sensitivity, Measurement Uncertainty, and Quantitative Resolution," *Clin. Chem.* **1997**, *43*, 1831–1837.
- Pardue, H. L. "Reply to 'On the Meaning of 'Sensitivity:' A Rejoinder'," *Clin. Chem.* **1998**, *44*, 1776–1778.

Several texts provide analytical procedures for specific analytes in well-defined matrices.

- Basset, J.; Denney, R. C.; Jeffery, G. H.; Mendham, J. *Vogel's Textbook of Quantitative Inorganic Analysis*, 4th Edition; Longman: London, 1981.
- Csuros, M. *Environmental Sampling and Analysis for Technicians*, Lewis: Boca Raton, 1994.
- Keith, L. H. (ed) *Compilation of EPA's Sampling and Analysis Methods*, Lewis: Boca Raton, 1996
- Rump, H. H.; Krist, H. *Laboratory Methods for the Examination of Water, Wastewater and Soil*, VCH Publishers: NY, 1988.
- *Standard Methods for the Analysis of Waters and Wastewaters*, 21st Edition, American Public Health Association: Washington, D. C.; 2005.

For a review of the importance of analytical methodology in today's regulatory environment, consult the following text.

- Miller, J. M.; Crowther, J. B. (eds) *Analytical Chemistry in a GMP Environment*, John Wiley & Sons: New York, 2000.

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3.10: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

Every discipline has its own vocabulary and your success in studying ana- lytical chemistry will improve if you master this vocabulary. Be sure you understand the difference between an analyte and its matrix, between a technique and a method, between a procedure and a protocol, and between a total analysis technique and a concentration technique.

In selecting an analytical method we consider criteria such as accu- racy, precision, sensitivity, selectivity, robustness, ruggedness, the amount of available sample, the amount of analyte in the sample, time, cost, and the availability of equipment. These criteria are not mutually independent, and often it is necessary to find an acceptable balance between them.

In developing a procedure or protocol, we give consideration to compensating for interferences, calibrating the method, obtaining an appropriate sample, and validating the analysis. Poorly designed procedures and protocols produce results that are insufficient to meet the needs of the analysis.

KEY TERMS

accuracy	analysis	analyte
calibration	calibration curve	concentration technique
detection limit	determination	interferent
matrix	measurement	method
method blank	precision	procedure
protocol	QA/QC	robust
rugged	selectivity	selectivity coefficient
sensitivity	signal	specificity
technique	total analysis technique	validation

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CHAPTER OVERVIEW

4: OBTAINING AND PREPARING SAMPLES FOR ANALYSIS

When we use an analytical method to solve a problem, there is no guarantee that will obtain accurate or precise results. In designing an analytical method we consider potential sources of determinate error and indeterminate error, and we take appropriate steps—such as reagent blanks and the calibration of instruments—to minimize their effect. Why might a carefully designed analytical method give poor results? One possible reason is that we may have failed to account for errors associated with the sample. If we collect the wrong sample, or if we lose analyte when we prepare the sample for analysis, then we introduce a determinate source of error. If we fail to collect enough samples, or if we collect samples of the wrong size, then the precision of our analysis may suffer. In this chapter we consider how to collect samples and how to prepare them for analysis.

4.1: The Importance of Sampling
4.2: Designing a Sampling Plan
4.3: Implementing the Sampling Plan
4.4: Separating the Analyte From Interferents
4.5: Problems
4.6: Additional Resources
4.7: Chapter Summary and Key Terms

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4.1: THE IMPORTANCE OF SAMPLING

When a manufacturer lists a chemical as ACS Reagent Grade, they must demonstrate that it conforms to specifications set by the American Chemical Society (ACS). For example, the ACS specifications for commercial NaBr require that the concentration of iron is less than 5 ppm. To verify that a production lot meets this standard, the manufacturer collects and analyzes several samples, reporting the average result on the product's label (Figure 7.1.1).



Figure 7.1.1 . Certificate of analysis for a production lot of NaBr. The result for iron meets the ACS specifications, but the result for potassium does not.

If the individual samples do not represent accurately the population from which they are drawn—a population that we call the ***target population***—then even a careful analysis will yield an inaccurate result. Extrapolating a result from a sample to its target population always introduces a determinate sampling error. To minimize this determinate sampling error, we must collect the right sample.

Even if we collect the right sample, indeterminate sampling errors may limit the usefulness of our analysis. Equation 4.1.1 shows that a confidence interval about the mean, $\overline{X}$, is proportional to the standard deviation, *s*, of the analysis

$$\mu = \overline{X} \pm \frac{ts}{\sqrt{n}} \tag{4.1.1}$$

where *n* is the number of samples and *t* is a statistical factor that accounts for the probability that the confidence interval contains the true value, μ.

> Equation 4.1.1 should be familiar to you. See Chapter 4 to review confidence intervals and see Appendix 4 for values of *t*.

Each step of an analysis contributes random error that affects the overall standard deviation. For convenience, let's divide an analysis into two steps—collecting the samples and analyzing the samples—each of which is characterized by a variance. Using a propagation of uncertainty, the relationship between the overall variance, s^2, and the variances due to sampling, s^2_{samp}, and the variance due to the analytical method, s^2_{meth}, is

$$s^2 = s^2_{samp} + s^2_{meth} \tag{4.1.2}$$

> Although Equation 4.1.1 is written in terms of a standard deviation, *s*, a propagation of uncertainty is written in terms of variances, s^2. In this section, and those that follow, we will use both standard deviations and variances to discuss sampling uncertainty. For a review of the propagation of uncertainty, see Chapter 4.3 and Appendix 2.

Equation 4.1.2 shows that the overall variance for an analysis is limited by either the analytical method or sampling, or by both. Unfortunately, analysts often try to minimize the overall variance by improving only the method's precision. This is a futile effort, however, if the standard deviation for sampling is more than three times greater than that for the method [Youden, Y. J. *J. Assoc. Off. Anal. Chem.* **1981**, *50*, 1007–1013]. Figure 7.1.2 shows how the ratio s_{samp}/s_{meth} affects the method's contribution to the overall variance. As shown by the dashed line, if the sample's standard deviation is $3\times$ the method's standard deviation, then indeterminate method errors explain only 10% of the overall variance. If indeterminate sampling errors are significant, decreasing s_{meth} provides only limited improvement in the overall precision.

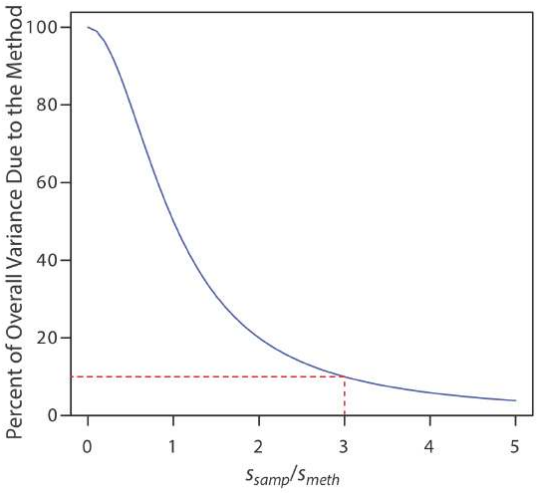


Figure 7.1.2 . The blue curve shows the method's contribution to the overall variance, s^2, as a function of the relative magnitude of the standard deviation in sampling, s_{samp}, and the method's standard deviation, s_{meth}. The dashed red line shows that the method accounts for only 10% of the overall variance when $s_{samp}/s_{meth} = 3 \times s_{meth}$. Understanding the relative importance of potential sources of indeterminate error is important when we consider how to improve the overall precision of the analysis.

EXAMPLE 7.1.1

A quantitative analysis gives a mean concentration of 12.6 ppm for an analyte. The method's standard deviation is 1.1 ppm and the standard deviation for sampling is 2.1 ppm. (a) What is the overall variance for the analysis? (b) By how much does the overall variance change if we improve s_{meth} by 10% to 0.99 ppm? (c) By how much does the overall variance change if we improve s_{samp} by 10% to 1.9 ppm?

Solution

(a) The overall variance is

$$s^2 = s_{samp}^2 + s_{meth}^2 = (2.1 \text{ ppm})^2 + (1.1 \text{ ppm})^2 = 5.6 \text{ ppm}^2$$

(b) Improving the method's standard deviation changes the overall variance to

$$s^2 = (2.1 \text{ ppm})^2 + (0.99 \text{ ppm})^2 = 5.4 \text{ ppm}^2$$

Improving the method's standard deviation by 10% improves the overall variance by approximately 4%.

(c) Changing the standard deviation for sampling

$$s^2 = (1.9 \text{ ppm})^2 + (1.1 \text{ ppm})^2 = 4.8 \text{ ppm}^2$$

improves the overall variance by almost 15%. As expected, because s_{samp} is larger than s_{meth}, we achieve a bigger improvement in the overall variance when we focus our attention on sampling problems.

EXERCISE 7.1.1

Suppose you wish to reduce the overall variance in Example 7.1.1 to 5.0 ppm^2. If you focus on the method, by what percentage do you need to reduce s_{meth}? If you focus on the sampling, by what percentage do you need to reduce s_{samp}?

Answer

To reduce the overall variance by improving the method's standard deviation requires that

$$s^2 = 5.00 \text{ ppm}^2 = s_{samp}^2 + s_{meth}^2 = (2.1\text{ppm})^2 + s_{meth}^2$$

Solving for s_{meth} gives its value as 0.768 ppm. Relative to its original value of 1.1 ppm, this is a reduction of 3.0×10^1 %. To reduce the overall variance by improving the standard deviation for sampling requires that

$$s^2 = 5.00 \text{ ppm}^2 = s_{samp}^2 + s_{meth}^2 = s_{samp}^2 + (1.1 \text{ ppm})^2$$

Solving for s_{samp} gives its value as 1.95 ppm. Relative to its original value of 2.1 ppm, this is reduction of 7.1%.

To determine which step has the greatest effect on the overall variance, we need to measure both s_{samp} and s_{meth}. The analysis of replicate samples provides an estimate of the overall variance. To determine the method's variance we must analyze samples under conditions where we can assume that the sampling variance is negligible; the sampling variance is then determined by difference.

> There are several ways to minimize the standard deviation for sampling. Here are two examples. One approach is to use a standard reference material (SRM) that has been carefully prepared to minimize indeterminate sampling errors. When the sample is homogeneous—as is the case, for example, with an aqueous sample—then another useful approach is to conduct replicate analyses on a single sample.

EXAMPLE 7.1.2

The following data were collected as part of a study to determine the effect of sampling variance on the analysis of drug-animal feed formulations [Fricke, G. H.; Mischler, P. G.; Staffieri, F. P.; Houmyer, C. L. *Anal. Chem.* **1987**, *59*, 1213– 1217].

% drug (w/w)			% drug (w/w)		
0.0114	0.0099	0.0105	0.0105	0.0109	0.0107
0.0102	0.0106	0.0087	0.0103	0.0103	0.0104
0.0100	0.0095	0.0098	0.0101	0.0101	0.013
0.0105	0.0095	0.0097			

The data on the left were obtained under conditions where both s_{samp} and s_{meth} contribute to the overall variance. The data on the right were obtained under conditions where s_{samp} is insignificant. Determine the overall variance, and the standard deviations due to sampling and the analytical method. To which source of indeterminate error—sampling or the method—should we turn our attention if we want to improve the precision of the analysis?

Solution

Using the data on the left, the overall variance, s^2, is 4.71×10^{-7}. To find the method's contribution to the overall variance, s^2_{meth}, we use the data on the right, obtaining a value of 7.00×10^{-8}. The variance due to sampling, s^2_{samp}, is

$$s^2_{samp} = s^2 - s^2_{meth} = 4.71 \times 10^{-7} - 7.00 \times 10^{-8} = 4.01 \times 10^{-7}$$

Converting variances to standard deviations gives s_{samp} as 6.33×10^{-4} and s_{meth} as 2.65×10^{-4}. Because s_{samp} is more than twice as large as s_{meth}, improving the precision of the sampling process will have the greatest impact on the overall precision.

EXERCISE 7.1.2

A polymer's density provides a measure of its crystallinity. The standard deviation for the determination of density using a single sample of a polymer is 1.96×10^{-3} g/cm^3. The standard deviation when using different samples of the polymer is 3.65×10^{-2} g/cm^3. Determine the standard deviations due to sampling and to the analytical method.

Answer

The analytical method's standard deviation is 1.96×10^{-3} g/cm^3 as this is the standard deviation for the analysis of a single sample of the polymer. The sampling variance is

$$s^2_{samp} = s^2 - s^2_{meth} = \left(3.65 \times 10^{-2}\right)^2 - \left(1.96 \times 10^{-3}\right)^2 = 1.33 \times 10^{-3}$$

Converting the variance to a standard deviation gives s_{meth} as 3.64×10^{-2} g/cm^3.

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4.2: DESIGNING A SAMPLING PLAN

A sampling plan must support the goals of an analysis. For example, a material scientist interested in characterizing a metal's surface chemistry is more likely to choose a freshly exposed surface, created by cleaving the sample under vacuum, than a surface previously exposed to the atmosphere. In a qualitative analysis, a sample need not be identical to the original substance provided there is sufficient analyte present to ensure its detection. In fact, if the goal of an analysis is to identify a trace-level component, it may be desirable to discriminate against major components when collecting samples.

> For an interesting discussion of the importance of a sampling plan, see Buger, J. et al. "Do Scientists and Fishermen Collect the Same Size Fish? Possible Implications for Exposure Assessment," *Environ. Res.* **2006**, *101*, 34–41.

For a quantitative analysis, the sample's composition must represent accurately the target population, a requirement that necessitates a careful sampling plan. Among the issues we need to consider are these five questions.

1. From where within the target population should we collect samples?
2. What type of samples should we collect?
3. What is the minimum amount of sample needed for each analysis?
4. How many samples should we analyze?
5. How can we minimize the overall variance for the analysis?

WHERE TO SAMPLE THE TARGET POPULATION

A sampling error occurs whenever a sample's composition is not identical to its target population. If the target population is ***homogeneous***, then we can collect individual samples without giving consideration to where we collect sample. Unfortunately, in most situations the target population is ***heterogeneous*** and attention to where we collect samples is important. For example, due to settling a medication available as an oral suspension may have a higher concentration of its active ingredients at the bottom of the container. The composition of a clinical sample, such as blood or urine, may depend on when it is collected. A patient's blood glucose level, for instance, will change in response to eating and exercise. Other target populations show both a spatial and a temporal heterogeneity. The concentration of dissolved O_2 in a lake is heterogeneous due both to a change in seasons and to point sources of pollution.

> The composition of a homogeneous target population is the same regardless of where we sample, when we sample, or the size of our sample. For a heterogeneous target population, the composition is not the same at different locations, at different times, or for different sample sizes.

If the analyte's distribution within the target population is a concern, then our sampling plan must take this into account. When feasible, homogenizing the target population is a simple solution, although this often is impracticable. In addition, homogenizing a sample destroys information about the analyte's spatial or temporal distribution within the target population, information that may be of importance.

RANDOM SAMPLING

The ideal sampling plan provides an unbiased estimate of the target population's properties. A ***random sampling*** is the easiest way to satisfy this requirement [Cohen, R. D. *J. Chem. Educ.* **1991**, *68*, 902–903]. Despite its apparent simplicity, a truly random sample is difficult to collect. Haphazard sampling, in which samples are collected without a sampling plan, is not random and may reflect an analyst's unintentional biases.

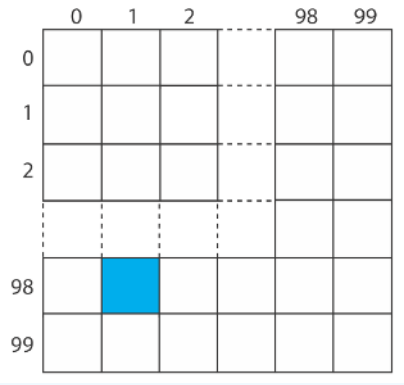
Here is a simple method to ensure that we collect random samples. First, we divide the target population into equal units and assign to each unit a unique number. Then, we use a random number table to select the units to sample. Example 7.2.1 provides an illustrative example. Appendix 14 provides a random number table that you can use to design a sampling plan.

✔ EXAMPLE 7.2.1

To analyze a polymer's tensile strength, individual samples of the polymer are held between two clamps and stretched. To evaluate a production lot, the manufacturer's sampling plan calls for collecting ten 1 cm × 1 cm samples from a 100 cm × 100 cm polymer sheet. Explain how we can use a random number table to ensure that we collect these samples at random.

Solution

As shown by the grid below, we divide the polymer sheet into 10 000 1 cm × 1 cm squares, each identified by its row number and its column number, with numbers running from 0 to 99.



For example, the blue square is in row 98 and in column 1. To select ten squares at random, we enter the random number table in Appendix 14 at an arbitrary point and let the entry's last four digits represent the row number and the column number for the first sample. We then move through the table in a predetermined fashion, selecting random numbers until we have 10 samples. For our first sample, let's use the second entry in the third column of Appendix 14 , which is 76831. The first sample, therefore, is row 68 and column 31. If we proceed by moving down the third column, then the 10 samples are as follows:

sample	number	row	column	sample	number	roq	column
1	76831	68	31	6	41701	17	01
2	66558	65	58	7	38605	86	05
3	33266	32	66	8	64516	45	16
4	12032	20	32	9	13015	30	15
5	14063	40	63	10	12138	21	38

When we collect a random sample we make no assumptions about the target population, which makes this the least biased approach to sampling. On the other hand, a random sample often requires more time and expense than other sampling strategies because we need to collect a greater number of samples to ensure that we adequately sample the target population, particularly when that population is heterogenous [Borgman, L. E.; Quimby, W. F. in Keith, L. H., ed. *Principles of Environmental Sampling*, American Chemical Society: Washington, D. C., 1988, 25–43].

JUDGMENTAL SAMPLING

The opposite of random sampling is selective, or ***judgmental sampling*** in which we use prior information about the target population to help guide our selection of samples. Judgmental sampling is more biased than random sampling, but requires fewer samples. Judgmental sampling is useful if we wish to limit the number of independent variables that might affect our results. For example, if we are studying the bioaccumulation of PCB's in fish, we may choose to exclude fish that are too small, too young, or that appear diseased.

SYSTEMATIC SAMPLING

Random sampling and judgmental sampling represent extremes in bias and in the number of samples needed to characterize the target population. ***Systematic sampling*** falls in between these extremes. In systematic sampling we sample the target population at regular intervals in space or time. Figure 7.2.1 shows an aerial photo of the Great Salt Lake in Utah. A railroad line divides the lake into two sections that have different chemical compositions. To compare the lake's two sections—and to evaluate spatial variations within each section—we use a two-dimensional grid to define sampling locations, collecting samples at the center of each location. When a population's is heterogeneous in time, as is common in clinical and environmental studies, then we might choose to collect samples at regular intervals in time.

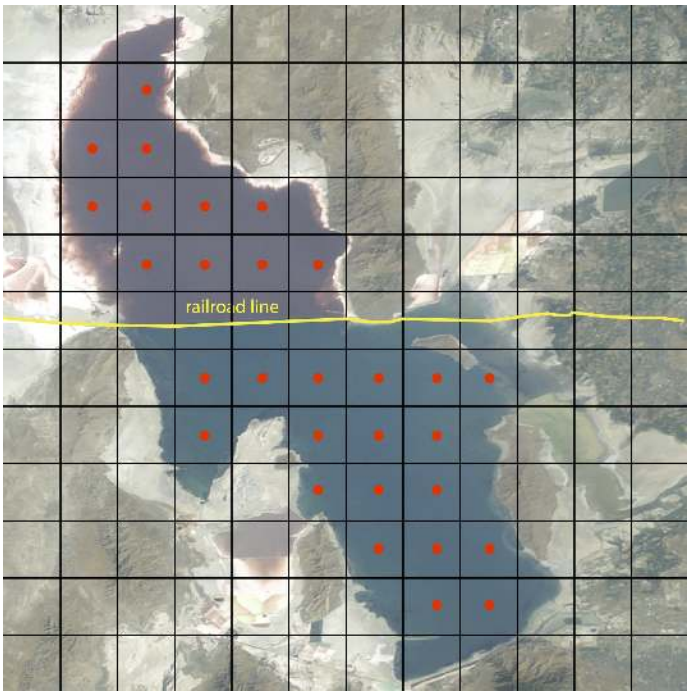


Figure 7.2.1 . Aerial photo of the Great Salt Lake in Utah, taken from the International Space Station at a distance of approximately 380 km. The railroad line divides the lake into two sections that differ in chemical composition. Superimposing a two-dimensional grid divides each section of the lake into sampling units. The red dots at the center of each unit represent sampling sites. Photo courtesy of the Image Science and Analysis Laboratory, NASA Johnson Space Center, Photo Number ISS007-E-13002 (eol.jsc.nasa.gov).

If a target population's properties have a periodic trend, a systematic sampling will lead to a significant bias if our sampling frequency is too small. This is a common problem when sampling electronic signals where the problem is known as aliasing. Consider, for example, a signal that is a simple sign wave. Figure 7.2.2 a shows how an insufficient sampling frequency underestimates the signal's true frequency. The apparent signal, shown by the dashed red line that passes through the five data points, is significantly different from the true signal shown by the solid blue line.

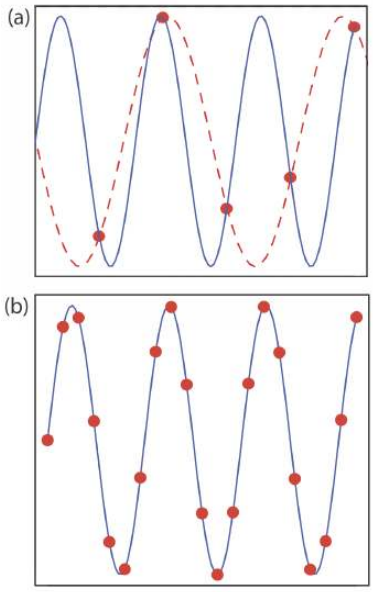


Figure 7.2.2 . Effect of sampling frequency when monitoring a periodic signal. Individual samples are shown by the red dots (•). In (a) the sampling frequency is approximately 1.5 samples per period. The dashed red line shows the apparent signal based on five samples and the solid blue line shows the true signal. In (b) a sampling frequency of approximately 5 samples per period accurately reproduces the true signal.

According to the ***Nyquist theorem***, to determine accurately the frequency of a periodic signal, we must sample the signal at least twice during each cycle or period. If we collect samples at an interval of Δt, then the highest frequency we can monitor accurately is $(2\Delta t)^{-1}$. For example, if we collect one sample each hour, then the highest frequency we can monitor is $(2 \times 1 \text{ hr})^{-1}$ or 0.5 hr^{-1}, a period of less than

2 hr. If our signal's period is less than 2 hours (a frequency of more than 0.5 hr^{-1}), then we must use a faster sampling rate. Ideally, we use a sampling rate that is at least 3–4 times greater than the highest frequency signal of interest. If our signal has a period of one hour, then we should collect a new sample every 15-20 minutes.

SYSTEMATIC–JUDGMENTAL SAMPLING

Combinations of the three primary approaches to sampling also are possible [Keith, L. H. *Environ. Sci. Technol.* **1990**, *24*, 610–617]. One such combination is ***systematic–judgmental sampling***, in which we use prior knowledge about a system to guide a systematic sampling plan. For example, when monitoring waste leaching from a landfill, we expect the plume to move in the same direction as the flow of groundwater—this helps focus our sampling, saving money and time. The systematic–judgmental sampling plan in Figure 7.2.3 includes a rectangular grid for most of the samples and linear transects to explore the plume's limits [Flatman, G. T.; Englund, E. J.; Yfantis, A. A. in Keith, L. H., ed. *Principles of Environmental Sampling*, American Chemical Society: Washington, D. C., 1988, 73–84].

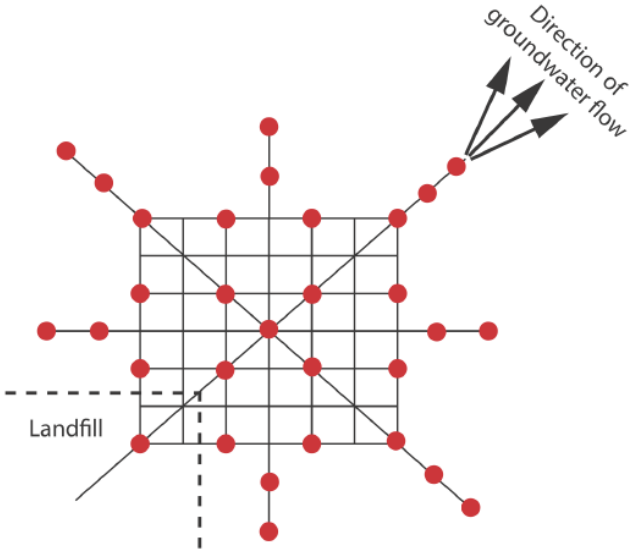


Figure 7.2.3 . Systematic–judgmental sampling plan for monitoring the leaching of pollutants from a landfill. The sampling sites, shown as red dots, are on a systematic grid that straddles the direction of the groundwater's flow. Sampling along the linear transects that extend out from the grid help establish the plume's limits.

STRATIFIED SAMPLING

Another combination of the three primary approaches to sampling is judgmental–random, or ***stratified sampling***. Many target populations consist of distinct units, or strata. For example, suppose we are studying particulate Pb in urban air. Because particulates come in a range of sizes—some visible and some microscopic—and come from many sources—such as road dust, diesel soot, and fly ash to name a few—we can subdivide the target population by size or by source. If we choose a random sampling plan, then we collect samples without considering the different strata, which may bias the sample toward larger particulates. In a stratified sampling we divide the target population into strata and collect random samples from within each stratum. After we analyze the samples from each stratum, we pool their respective means to give an overall mean for the target population. The advantage of stratified sampling is that individual strata usually are more homogeneous than the target population. The overall sampling variance for stratified sampling always is at least as good, and often is better than that obtained by simple random sampling. Because a stratified sampling requires that we collect and analyze samples from several strata, it often requires more time and money.

CONVENIENCE SAMPLING

One additional method of sampling deserves mention. In ***convenience sampling*** we select sample sites using criteria other than minimizing sampling error and sampling variance. In a survey of rural groundwater quality, for example, we can choose to drill wells at sites selected at random or we can choose to take advantage of existing wells; the latter usually is the preferred choice. In this case cost, expedience, and accessibility are more important than ensuring a random sample

WHAT TYPE OF SAMPLE TO COLLECT

Having determined from where to collect samples, the next step in designing a sampling plan is to decide on the type of sample to collect. There are three common methods for obtaining samples: grab sampling, composite sampling, and in situ sampling.

The most common type of sample is a ***grab sample*** in which we collect a portion of the target population at a specific time or location, providing a "snapshot" of the target population. If our target population is homogeneous, a series of random grab samples allows us to

establish its properties. For a heterogeneous target population, systematic grab sampling allows us to characterize how its properties change over time and/or space.

A ***composite sample*** is a set of grab samples that we combine into a single sample before analysis. Because information is lost when we combine individual samples, normally we analyze separately each grab sample. In some situations, however, there are advantages to working with a composite sample.

One situation where composite sampling is appropriate is when our interest is in the target population's average composition over time or space. For example, wastewater treatment plants must monitor and report the average daily composition of the treated water they release to the environment. The analyst can collect and analyze a set of individual grab samples and report the average result, or she can save time and money by combining the grab samples into a single composite sample and report the result of her analysis of the composite sample.

Composite sampling also is useful when a single sample does not supply sufficient material for the analysis. For example, analytical methods for the quantitative analysis of PCB's in fish often require as much as 50 g of tissue, an amount that may be difficult to obtain from a single fish. Combining and homogenizing tissue samples from several fish makes it easy to obtain the necessary 50-g sample.

A significant disadvantage of grab samples and composite samples is that we cannot use them to monitor continuously a time-dependent change in the target population. ***In situ sampling***, in which we insert an analytical sensor into the target population, allows us to monitor the target population without removing individual grab samples. For example, we can monitor the pH of a solution in an industrial production line by immersing a pH electrode in the solution's flow.

✔ EXAMPLE 7.2.2

A study of the relationship between traffic density and the concentrations of Pb, Cd, and Zn in roadside soils uses the following sampling plan [Nabulo, G.; Oryem-Origa, H.; Diamond, M. *Environ. Res.* **2006**, *101*, 42–52]. Samples of surface soil (0–10 cm) are collected at distances of 1, 5, 10, 20, and 30 m from the road. At each distance, 10 samples are taken from different locations and mixed to form a single sample. What type of sampling plan is this? Explain why this is an appropriate sampling plan.

Solution

This is a systematic–judgemental sampling plan using composite samples. These are good choices given the goals of the study. Automobile emissions release particulates that contain elevated concentrations of Pb, Cd, and Zn—this study was conducted in Uganda where leaded gasoline was still in use—which settle out on the surrounding roadside soils as "dry rain." Samples collected near the road and samples collected at fixed distances from the road provide sufficient data for the study, while minimizing the total number of samples. Combining samples from the same distance into a single, composite sample has the advantage of decreasing sampling uncertainty.

HOW MUCH SAMPLE TO COLLECT

To minimize sampling errors, samples must be of an appropriate size. If a sample is too small its composition may differ substantially from that of the target population, which introduces a sampling error. Samples that are too large, however, require more time and money to collect and analyze, without providing a significant improvement in the sampling error.

Let's assume our target population is a homogeneous mixture of two types of particles. Particles of type *A* contain a fixed concentration of analyte, and particles of type *B* are analyte-free. Samples from this target population follow a binomial distribution. If we collect a sample of *n* particles, then the expected number of particles that contains analyte, n_A, is

$$n_A = np$$

where *p* is the probability of selecting a particle of type *A*. The standard deviation for sampling is

$$s_{samp} = \sqrt{np(1-p)} \tag{4.2.1}$$

To calculate the relative standard deviation for sampling, $(s_{samp})_{rel}$, we divide Equation 4.2.1 by n_A, obtaining

$$(s_{samp})_{rel} = \frac{\sqrt{np(1-p)}}{np}$$

Solving for *n* allows us to calculate the number of particles we need to provide a desired relative sampling variance.

$$n = \frac{1-p}{p} \times \frac{1}{(s_{samp})^2_{rel}} \tag{4.2.2}$$

✔ EXAMPLE 7.2.3

Suppose we are analyzing a soil where the particles that contain analyte represent only 1×10^{-7}% of the population. How many particles must we collect to give a percent relative standard deviation for sampling of 1%?

Solution

Since the particles of interest account for 1×10^{-7}% of all particles, the probability, *p*, of selecting one of these particles is 1×10^{-9}. Substituting into Equation 4.2.2 gives

$$n = \frac{1 - \left(1 \times 10^{-9}\right)}{1 \times 10^{-9}} \times \frac{1}{(0.01)^2} = 1 \times 10^{13}$$

To obtain a relative standard deviation for sampling of 1%, we need to collect 1×10^{13} particles.

Depending on the particle size, a sample of 10^{13} particles may be fairly large. Suppose this is equivalent to a mass of 80 g. Working with a sample this large clearly is not practical. Does this mean we must work with a smaller sample and accept a larger relative standard deviation for sampling? Fortunately the answer is no. An important feature of Equation 4.2.2 is that the relative standard deviation for sampling is a function of the number of particles instead of their combined mass. If we crush and grind the particles to make them smaller, then a sample of 10^{13} particles will have a smaller mass. If we assume that a particle is spherical, then its mass is proportional to the cube of its radius.

$$\text{mass} \propto r^3$$

If we decrease a particle's radius by a factor of 2, for example, then we decrease its mass by a factor of 2^3, or 8. This assumes, of course, that the process of crushing and grinding particles does not change the composition of the particles.

EXAMPLE 7.2.4

Assume that a sample of 10^{13} particles from Example 7.2.3 weighs 80 g and that the particles are spherical. By how much must we reduce a particle's radius if we wish to work with 0.6-g samples?

Solution

To reduce the sample's mass from 80 g to 0.6 g, we must change its mass by a factor of

$$\frac{80}{0.6} = 133\times$$

To accomplish this we must decrease a particle's radius by a factor of

$$r^3 = 133\times$$
$$r = 5.1\times$$

Decreasing the radius by a factor of approximately 5 allows us to decrease the sample's mass from 80 g to 0.6 g.

Treating a population as though it contains only two types of particles is a useful exercise because it shows us that we can improve the relative standard deviation for sampling by collecting more particles. Of course, a real population likely contains more than two types of particles, with the analyte present at several levels of concentration. Nevertheless, the sampling of many well-mixed populations approximate binomial sampling statistics because they are homogeneous on the scale at which they are sampled. Under these conditions the following relationship between the mass of a random grab sample, *m*, and the percent relative standard deviation for sampling, *R*, often is valid

$$mR^2 = K_s \tag{4.2.3}$$

where K_s is a sampling constant equal to the mass of a sample that produces a percent relative standard deviation for sampling of ±1% [Ingamells, C. O.; Switzer, P. *Talanta* **1973**, *20*, 547–568].

EXAMPLE 7.2.5

The following data were obtained in a preliminary determination of the amount of inorganic ash in a breakfast cereal.

mass of cereal (g)	0.9956	0.9981	1.0036	0.9994	1.0067
%w/w ash	1.34	1.29	1.32	1.26	1.28

What is the value of K_s and what size sample is needed to give a percent relative standard deviation for sampling of ±2.0%. Predict the percent relative standard deviation and the absolute standard deviation if we collect 5.00-g samples.

Solution

To determine the sampling constant, K_s, we need to know the average mass of the cereal samples and the relative standard deviation for the amount of ash in those samples. The average mass of the cereal samples is 1.0007 g. The average %w/w ash and its absolute standard deviation are, respectively, 1.298 %w/w and 0.03194 %w/w. The percent relative standard deviation, *R*, therefore, is

$$R = \frac{s_{\text{ samp}}}{\overline{X}} = \frac{0.03194\%\text{ w/w}}{1.298\%\text{ w/w}} \times 100 = 2.46\%$$

Solving for K_s gives its value as

$$K_s = mR^2 = (1.0007\text{g})(2.46)^2 = 6.06\text{ g}$$

To obtain a percent relative standard deviation of ±2%, samples must have a mass of at least

$$m = \frac{K_s}{R^2} = \frac{6.06\text{g}}{(2.0)^2} = 1.5\text{ g}$$

If we use 5.00-g samples, then the expected percent relative standard deviation is

$$R = \sqrt{\frac{K_s}{m}} = \sqrt{\frac{6.06\text{g}}{5.00\text{g}}} = 1.10\%$$

and the expected absolute standard deviation is

$$s_{\text{ samp}} = \frac{R\overline{X}}{100} = \frac{(1.10)(1.298\%\text{w/w})}{100} = 0.0143\%\text{w/w}$$

EXERCISE 7.2.1

Olaquindox is a synthetic growth promoter in medicated feeds for pigs. In an analysis of a production lot of feed, five samples with nominal masses of 0.95 g were collected and analyzed, with the results shown in the following table.

mass (g)	0.9530	0.9728	0.9660	0.9402	0.9576
mg olaquindox/kg feed	23.0	23.8	21.0	26.5	21.4

What is the value of K_s and what size samples are needed to obtain a percent relative deviation for sampling of 5.0%? By how much do you need to reduce the average particle size if samples must weigh no more than 1 g?

Answer

To determine the sampling constant, K_s, we need to know the average mass of the samples and the percent relative standard deviation for the concentration of olaquindox in the feed. The average mass for the five samples is 0.95792 g. The average concentration of olaquindox in the samples is 23.14 mg/kg with a standard deviation of 2.200 mg/kg. The percent relative standard deviation, *R*, is

$$R = \frac{s_{\text{ samp}}}{\overline{X}} \times 100 = \frac{2.200\text{ mg/kg}}{23.14\text{ mg/kg}} \times 100 = 9.507 \approx 9.51$$

Solving for K_s gives its value as

$$K_s = mR^2 = (0.95792\text{g})(9.507)^2 = 86.58\text{ g} \approx 86.6\text{ g}$$

To obtain a percent relative standard deviation of 5.0%, individual samples need to have a mass of at least

$$m = \frac{K_s}{R^2} = \frac{86.58\text{ g}}{(5.0)^2} = 3.5\text{ g}$$

To reduce the sample's mass from 3.5 g to 1 g, we must change the mass by a factor of

$$\frac{3.5\text{ g}}{1\text{ g}} = 3.5\times$$

If we assume that the sample's particles are spherical, then we must reduce a particle's radius by a factor of

$$r^3 = 3.5\times$$
$$r = 1.5\times$$

HOW MANY SAMPLES TO COLLECT

In the previous section we considered how much sample we need to minimize the standard deviation due to sampling. Another important consideration is the number of samples to collect. If the results from our analysis of the samples are normally distributed, then the confidence interval for the sampling error is

$$\mu = \overline{X} \pm \frac{t s_{samp}}{\sqrt{n_{samp}}} \tag{4.2.4}$$

where n_{samp} is the number of samples and s_{samp} is the standard deviation for sampling. Rearranging Equation 4.2.4 and substituting e for the quantity $\overline{X} - \mu$, gives the number of samples as

$$n_{samp} = \frac{t^2 s_{samp}^2}{e^2} \tag{4.2.5}$$

Because the value of t depends on n_{samp}, the solution to Equation 4.2.5 is found iteratively.

When we use Equation 4.2.5, we must express the standard deviation for sampling, s_{samp}, and the error, e, in the same way. If s_{samp} is reported as a percent relative standard deviation, then the error, e, is reported as a percent relative error. When you use Equation 4.2.5, be sure to check that you are expressing s_{samp} and e in the same way.

EXAMPLE 7.2.6

In Example 7.2.5 we determined that we need 1.5-g samples to establish an s_{samp} of ±2.0% for the amount of inorganic ash in cereal. How many 1.5-g samples do we need to collect to obtain a percent relative sampling error of ±0.80% at the 95% confidence level?

Solution

Because the value of t depends on the number of samples—a result we have yet to calculate—we begin by letting $n_{samp} = \infty$ and using $t(0.05, \infty)$ for t. From Appendix 4, the value for $t(0.05, \infty)$ is 1.960. Substituting known values into Equation 4.2.5 gives the number of samples as

$$n_{samp} = \frac{(1.960)^2 (2.0)^2}{(0.80)^2} = 24.0 \approx 24$$

Letting $n_{samp} = 24$, the value of $t(0.05, 23)$ from Appendix 4 is 2.073. Recalculating n_{samp} gives

$$n_{samp} = \frac{(2.073)^2 (2.0)^2}{(0.80)^2} = 26.9 \approx 27$$

When $n_{samp} = 27$, the value of $t(0.05, 26)$ from Appendix 4 is 2.060. Recalculating n_{samp} gives

$$n_{samp} = \frac{(2.060)^2 (2.0)^2}{(0.80)^2} = 26.52 \approx 27$$

Because two successive calculations give the same value for n_{samp}, we have an iterative solution to the problem. We need 27 samples to achieve a percent relative sampling error of ±0.80% at the 95% confidence level.

EXERCISE 7.2.2

Assuming that the percent relative standard deviation for sampling in the determination of olaquindox in medicated feed is 5.0% (see Exercise 7.2.1), how many samples do we need to analyze to obtain a percent relative sampling error of ±2.5% at $\alpha = 0.05$?

Answer

Because the value of t depends on the number of samples—a result we have yet to calculate—we begin by letting $n_{samp} = \infty$ and using $t(0.05, \infty)$ for the value of t. From Appendix 4, the value for $t(0.05, \infty)$ is 1.960. Our first estimate for n_{samp} is

$$n_{samp} = \frac{t^2 s_{samp}^2}{e^2} = \frac{(1.96)^2 (5.0)^2}{(2.5)^2} = 15.4 \approx 15$$

Letting $n_{samp} = 15$, the value of $t(0.05,14)$ from Appendix 4 is 2.145. Recalculating n_{samp} gives

$$n_{samp} = \frac{t^2 s_{samp}^2}{e^2} = \frac{(2.145)^2 (5.0)^2}{(2.5)^2} = 18.4 \approx 18$$

Letting n_{samp} = 18, the value of t(0.05,17) from Appendix 4 is 2.103. Recalculating n_{samp} gives

$$n_{samp} = \frac{t^2 s_{samp}^2}{e^2} = \frac{(2.103)^2(5.0)^2}{(2.5)^2} = 17.7 \approx 18$$

Because two successive calculations give the same value for n_{samp}, we need 18 samples to achieve a sampling error of ±2.5% at the 95% confidence interval.

Equation 4.2.5 provides an estimate for the smallest number of samples that will produce the desired sampling error. The actual sampling error may be substantially larger if s_{samp} for the samples we collect during the subsequent analysis is greater than s_{samp} used to calculate n_{samp}. This is not an uncommon problem. For a target population with a relative sampling variance of 50 and a desired relative sampling error of ±5%, Equation 4.2.5 predicts that 10 samples are sufficient. In a simulation using 1000 samples of size 10, however, only 57% of the trials resulted in a sampling error of less than ±5% [Blackwood, L. G. *Environ. Sci. Technol.* **1991**, *25*, 1366–1367]. Increasing the number of samples to 17 was sufficient to ensure that the desired sampling error was achieved 95% of the time.

For an interesting discussion of why the number of samples is important, see Kaplan, D.; Lacetera, N.; Kaplan, C. "Sample Size and Precision in NIH Peer Review," Plos One, 2008, 3(7), 1–3. When reviewing grants, individual reviewers report a score between 1.0 and 5.0 (two significant figures). NIH reports the average score to three significant figures, implying that a difference of 0.01 is significant. If the individual scores have a standard deviation of 0.1, then a difference of 0.01 is significant at $\alpha = 0.05$ only if there are 384 reviews. The authors conclude that NIH review panels are too small to provide a statistically meaningful separation between proposals receiving similar scores.

MINIMIZING THE OVERALL VARIANCE

A final consideration when we develop a sampling plan is how we can minimize the overall variance for the analysis. Equation 7.1.2 shows that the overall variance is a function of the variance due to the method, s_{meth}^2, and the variance due to sampling, s_{samp}^2. As we learned earlier, we can improve the sampling variance by collecting more samples of the proper size. Increasing the number of times we analyze each sample improves the method's variance. If s_{samp}^2 is significantly greater than s_{meth}^2, we can ignore the method's contribution to the overall variance and use Equation 4.2.5 to estimate the number of samples to analyze. Analyzing any sample more than once will not improve the overall variance, because the method's variance is insignificant.

If s_{meth}^2 is significantly greater than s_{samp}^2, then we need to collect and analyze only one sample. The number of replicate analyses, n_{rep}, we need to minimize the error due to the method is given by an equation similar to Equation 4.2.5.

$$n_{rep} = \frac{t^2 s_{meth}^2}{e^2}$$

Unfortunately, the simple situations described above often are the exception. For many analyses, both the sampling variance and the method variance are significant, and both multiple samples and replicate analyses of each sample are necessary. The overall error in this case is

$$e = t\sqrt{\frac{s_{samp}^2}{n_{samp}} + \frac{s_{meth}^2}{n_{samp} n_{rep}}} \tag{4.2.6}$$

Equation 4.2.6 does not have a unique solution as different combinations of n_{samp} and n_{rep} give the same overall error. How many samples we collect and how many times we analyze each sample is determined by other concerns, such as the cost of collecting and analyzing samples, and the amount of available sample.

✔ EXAMPLE 7.2.7

An analytical method has a relative sampling variance of 0.40% and a relative method variance of 0.070%. Evaluate the percent relative error ($\alpha = 0.05$) if you collect 5 samples and analyze each twice, and if you collect 2 samples and analyze each 5 times.

Solution

Both sampling strategies require a total of 10 analyses. From Appendix 4 we find that the value of t(0.05, 9) is 2.262. Using Equation 4.2.6, the relative error for the first sampling strategy is

$$e = 2.262\sqrt{\frac{0.40}{5} + \frac{0.070}{5 \times 2}} = 0.67\%$$

and that for the second sampling strategy is

$$e = 2.262\sqrt{\frac{0.40}{2} + \frac{0.070}{2 \times 5}} = 1.0\%$$

Because the method variance is smaller than the sampling variance, we obtain a smaller relative error if we collect more samples and analyze each sample fewer times.

EXERCISE 7.2.3

An analytical method has a relative sampling variance of 0.10% and a relative method variance of 0.20%. The cost of collecting a sample is $20 and the cost of analyzing a sample is $50. Propose a sampling strategy that provides a maximum relative error of ±0.50% ($\alpha = 0.05$) and a maximum cost of $700.

Answer

If we collect a single sample (cost $20), then we can analyze that sample 13 times (cost $650) and stay within our budget. For this scenario, the percent relative error is

$$e = t\sqrt{\frac{s_{samp}^2}{n_{samp}} + \frac{s_{meth}^2}{n_{samp}n_{rep}}} = 2.179\sqrt{\frac{0.10}{1} + \frac{0.20}{1 \times 13}} = 0.74\%$$

where *t*(0.05, 12) is 2.179. Because this percent relative error is larger than ±0.50%, this is not a suitable sampling strategy.

Next, we try two samples (cost $40), analyzing each six times (cost $600). For this scenario, the percent relative error is

$$e = t\sqrt{\frac{s_{samp}^2}{n_{samp}} + \frac{s_{meth}^2}{n_{samp}n_{rep}}} = 2.2035\sqrt{\frac{0.10}{2} + \frac{0.20}{2 \times 6}} = 0.57\%$$

where *t*(0.05, 11) is 2.2035. Because this percent relative error is larger than ±0.50%, this also is not a suitable sampling strategy.

Next we try three samples (cost $60), analyzing each four times (cost $600). For this scenario, the percent relative error is

$$e = t\sqrt{\frac{s_{samp}^2}{n_{samp}} + \frac{s_{meth}^2}{n_{samp}n_{rep}}} = 2.2035\sqrt{\frac{0.10}{3} + \frac{0.20}{3 \times 4}} = 0.49\%$$

where *t*(0.05, 11) is 2.2035. Because both the total cost ($660) and the percent relative error meet our requirements, this is a suitable sampling strategy.

There are other suitable sampling strategies that meet both goals. The strategy that requires the least expense is to collect eight samples, analyzing each once for a total cost of $560 and a percent relative error of ±0.46%. Collecting 10 samples and analyzing each one time, gives a percent relative error of ±0.39% at a cost of $700.

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4.3: IMPLEMENTING THE SAMPLING PLAN

Implementing a sampling plan usually involves three steps: physically removing the sample from its target population, preserving the sample, and preparing the sample for analysis. Except for in situ sampling, we analyze a sample after we have removed it from its target population. Because sampling exposes the target population to potential contamination, our sampling device must be inert and clean.

Once we remove a sample from its target population, there is a danger that it will undergo a chemical or physical change before we can complete its analysis. This is a serious problem because the sample's properties will no longer e representative of the target population. To prevent this problem, we often preserve samples before we transport them to the laboratory for analysis. Even when we analyze a sample in the field, preservation may still be necessary.

The initial sample is called the primary or ***gross sample***, and it may be a single increment drawn from the target population or a composite of several increments. In many cases we cannot analyze the gross sample without first preparing the sample for analyze by reducing the sample's particle size, by converting the sample into a more readily analyzable form, or by improving its homogeneity.

> Although you may never work with the specific samples highlighted in this section, the case studies presented here may help you in envisioning potential problems associated with your samples.

SOLUTIONS

There are many good examples of solution samples: commercial solvents; beverages, such as milk or fruit juice; natural waters, including lakes, streams, seawater, and rain; bodily fluids, such as blood and urine; and, suspensions, such as those found in many oral medications. Let's use the sampling of natural waters and wastewaters as a case study in how to sample a solution.

SAMPLE COLLECTION

The chemical composition of a surface water—such as a stream, river, lake, estuary, or ocean—is influenced by flow rate and depth. Rapidly flowing shallow streams and rivers, and shallow (<5 m) lakes usually are well mixed and show little stratification with depth. To collect a grab sample we submerge a capped bottle below the surface, remove the cap and allow the bottle to fill completely, and replace the cap. Collecting a sample this way avoids the air–water interface, which may be enriched with heavy metals or contaminated with oil [Duce, R. A.; Quinn, J. G. Olney, C. E.; Piotrowicz, S. R.; Ray, S. J.; Wade, T. L. *Science* **1972**, *176*, 161–163].

Slowly moving streams and rivers, lakes deeper than five meters, estuaries, and oceans may show substantial stratification with depth. Grab samples from near the surface are collected as described above, and samples at greater depths are collected using a sample bottle lowered to the desired depth (Figure 7.3.1).



Figure 7.3.1 . A Niskin sampling bottle for collecting water samples from lakes and oceans. After lowering the bottle to the desired depth, a weight is sent down a winch line, tripping a spring that closes the bottle. Source: modified from NOAA.

Wells for sampling groundwater are purged before we collect samples because the chemical composition of water in a well-casing may differ significantly from that of the groundwater. These differences may result from contaminants introduced while drilling the well or by a change in the groundwater's redox potential following its exposure to atmospheric oxygen. In general, a well is purged by pumping out a volume of water equivalent to several well-casing volumes or by pumping until the water's temperature, pH, or specific conductance is constant. A municipal water supply, such as a residence or a business, is purged before sampling because the chemical composition of water standing in a pipe may differ significantly from the treated water supply. Samples are collected at faucets after flushing the pipes for 2-3 minutes.

Samples from municipal wastewater treatment plants and industrial discharges often are collected as a 24-hour composite. An automatic sampler periodically removes an individual grab sample, adding it to those collected previously. The volume of each sample and the frequency of sampling may be constant, or may vary in response to changes in flow rate.

Sample containers for collecting natural waters and wastewaters are made from glass or plastic. Kimax and Pyrex brand borosilicate glass have the advantage of being easy to sterilize, easy to clean, and inert to all solutions except those that are strongly alkaline. The disadvantages of glass containers are cost, weight, and the ease of breakage. Plastic containers are made from a variety of polymers, including polyethylene, polypropylene, polycarbonate, polyvinyl chloride, and Teflon. Plastic containers are light-weight, durable, and, except for those manufactured from Teflon, inexpensive. In most cases glass or plastic bottles are used interchangeably, although polyethylene bottles generally are preferred because of their lower cost. Glass containers are always used when collecting samples for the analysis of pesticides, oil and grease, and organics because these species often interact with plastic surfaces. Because glass surfaces easily adsorb metal ions, plastic bottles are preferred when collecting samples for the analysis of trace metals.

In most cases the sample bottle has a wide mouth, which makes it easy to fill and to remove the sample. A narrow-mouth sample bottle is used if exposing the sample to the container's cap or to the outside environment is a problem. Unless exposure to plastic is a problem, caps for sample bottles are manufactured from polyethylene. When polyethylene must be avoided, the container's cap includes an inert interior liner of neoprene or Teflon.

SAMPLE PRESERVATION AND PREPARATION

> Here our concern is only with the need to prepare the gross sample by converting it into a form suitable for analysis. Some analytical methods require additional sample preparation steps, such as concentrating or diluting the analyte, or adjusting the analyte's chemical form. We will consider these forms of sample preparation in later chapters that focus on specific analytical methods.

After removing a sample from its target population, its chemical composition may change as a result of chemical, biological, or physical processes. To prevent a change in composition, samples are preserved by controlling the sample's pH and temperature, by limiting its exposure to light or to the atmosphere, or by adding a chemical preservative. After preserving a sample, it is safely stored for later analysis. The maximum holding time between preservation and analysis depends on the analyte's stability and the effectiveness of sample preservation. Table 7.3.1 summarizes preservation methods and maximum holding times for several analytes of importance in the analysis of natural waters and wastewaters.

Table 7.3.1 . Preservation Methods and Maximum Holding Times for Selected Analytes in Natural Waters and Wastewaters

analyte	preservation method	maximum holding time
ammonia	cool to 4ºC; add H_2SO_4 to pH < 2	28 days
chloride	none required	28 days
metals: Cr(VI)	cool to 4ºC	24 hours
metals: Hg	HNO_3 to pH < 2	28 days
metals: all others	HNO_3 to pH < 2	6 months
nitrate	none required	48 hours
organochlorine pesticides	1 mL of 10 mg/mL $HgCl_2$ or immediate extraction with a suitable non-aqueous solvent	7 days without extraction; 40 days with extraction
pH	none required	analyze immediately

Other than adding a preservative, solution samples generally do not need additional preparation before analysis. This is the case for samples of natural waters and wastewaters. Solution samples with particularly complex matricies—blood and milk are two common examples—may need addi- tional processing to separate analytes from interferents, a topic covered later in this chapter.

GASES

Typical examples of gaseous samples include automobile exhaust, emissions from industrial smokestacks, atmospheric gases, and compressed gases. Also included in this category are aerosol particulates—the fine solid particles and liquid droplets that form smoke and smog. Let's use the sampling of urban air as a case study in how to sample a gas.

SAMPLE COLLECTION

One approach for collecting a sample of urban air is to fill a stainless steel canister or a Tedlar/Teflon bag. A pump pulls the air into the container and, after purging, the container is sealed. This method has the advantage of being simple and of collecting a representative sample. Disadvantages include the tendency for some analytes to adsorb to the container's walls, the presence of analytes at concentrations too low to detect with suitable accuracy and precision, and the presence of reactive analytes, such as ozone and nitrogen oxides, that may react with the container or that may otherwise alter the sample's chemical composition during storage. When using a stainless steel canister, cryogenic cooling, which changes the sample from a gaseous state to a liquid state, may limit some of these disadvantages.

Most urban air samples are collected by filtration or by using a trap that contains a solid sorbent. Solid sorbents are used for volatile gases (a vapor pressure more than 10^{-6} atm) and for semi-volatile gases (a vapor pressure between 10^{-6} atm and 10^{-12} atm). Filtration is used to

collect aerosol particulates. Trapping and filtering allow for sampling larger volumes of gas—an important concern for an analyte with a small concentration—and stabilizes the sample between its collection and its analysis.

In solid sorbent sampling, a pump pulls the urban air through a canister packed with sorbent particles. Typically 2–100 L of air are sampled when collecting a volatile compound and 2–500 m^3 when collecting a semi-volatile gas. A variety of inorganic, organic polymer, and carbon sorbents have been used. Inorganic sorbents, such as silica gel, alumina, magnesium aluminum silicate, and molecular sieves, are efficient collectors for polar compounds. Their efficiency at absorbing water, however, limits their capacity for many organic analytes.

> 1 m^3 is equivalent to 10^3 L.

Organic polymeric sorbents include polymeric resins of 2,4-diphenyl-*p*-phenylene oxide or styrene-divinylbenzene for volatile compounds, and polyurethane foam for semi-volatile compounds. These materials have a low affinity for water and are efficient for sampling all but the most highly volatile organic compounds and some lower molecular weight alcohols and ketones. Carbon sorbents are superior to organic polymer resins, which makes them useful for highly volatile organic compounds that will not absorb onto polymeric resins, although removing the compounds may be difficult.

Non-volatile compounds normally are present either as solid particulates or are bound to solid particulates. Samples are collected by pulling a large volume of urban air through a filtering unit and collecting the particulates on glass fiber filters.

The short term exposure of humans, animals, and plants to atmospheric pollutants is more severe than that for pollutants in other matrices. Because the composition of atmospheric gases can vary significantly over a time, the continuous monitoring of atmospheric gases such as O_3, CO, SO_2, NH_3, H_2O_2, and NO_2 by in situ sampling is important [Tanner, R. L. in Keith, L. H., ed. *Principles of Environmental Sampling*, American Chemical Society: Washington, D. C., 1988, 275–286].

SAMPLE PRESERVATION

After collecting a gross sample of urban air, generally there is little need for sample preservation or preparation. The chemical composition of a gas sample usually is stable when it is collected using a solid sorbent, a filter, or by cryogenic cooling. When using a solid sorbent, gaseous compounds are released for analysis by thermal desorption or by extracting with a suitable solvent. If the sorbent is selective for a single analyte, the increase in the sorbent's mass is used to determine the amount of analyte in the sample.

SOLIDS

Typical examples of solid samples include large particulates, such as those found in ores; smaller particulates, such as soils and sediments; tablets, pellets, and capsules used for dispensing pharmaceutical products and animal feeds; sheet materials, such as polymers and rolled metals; and tissue samples from biological specimens. Solids usually are heterogeneous and we must collect samples carefully if they are to be representative of the target population. Let's use the sampling of sediments, soils, and ores as a case study in how to sample solids.

SAMPLE COLLECTION

Sediments from the bottom of streams, rivers, lakes, estuaries, and oceans are collected with a bottom grab sampler or with a corer. A bottom grab sampler (Figure 7.3.2) is equipped with a pair of jaws that close when they contact the sediment, scooping up sediment in the process. Its principal advantages are ease of use and the ability to collect a large sample. Disadvantages include the tendency to lose finer grain sediment particles as water flows out of the sampler, and the loss of spatial information—both laterally and with depth—due to mixing of the sample.



Figure 7.3.2 . Bottom grab sampler being prepared for deployment. Source: NOAA.

An alternative method for collecting sediments is the cylindrical coring device shown in Figure 7.3.3). The corer is dropped into the sediment, collecting a column of sediment and the water in contact with the sediment. With the possible exception of sediment at the surface, which may experience mixing, samples collected with a corer maintain their vertical profile, which preserves information about how the sediment's composition changes with depth.

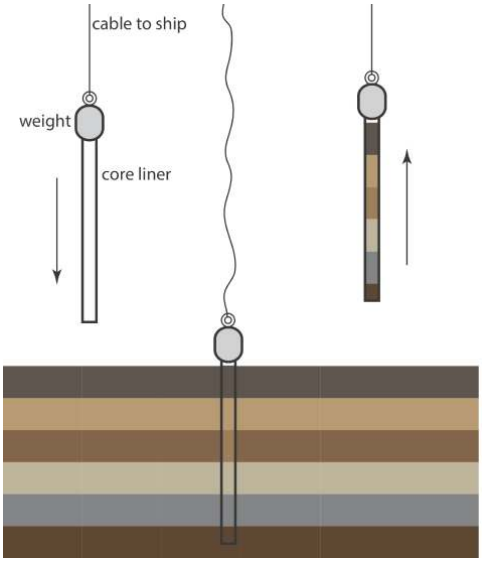


Figure 7.3.3 . Schematic diagram of a gravity corer in operation. The corer's weight is sufficient to penetrate the sediment to a depth of approximately 2 m. Flexible metal leaves on the bottom of the corer are pushed aside by the sediment, which allow it to enter the corer. The leaves bend back and hold the core sample in place as it is hauled back to the surface.

Collecting soil samples at depths of up to 30 cm is accomplished with a scoop or a shovel, although the sampling variance generally is high. A better tool for collecting soil samples near the surface is a soil punch, which is a thin-walled steel tube that retains a core sample after it is pushed into the soil and removed. Soil samples from depths greater than 30 cm are collected by digging a trench and collecting lateral samples with a soil punch. Alternatively, an auger is used to drill a hole to the desired depth and the sample collected with a soil punch.

For particulate materials, particle size often determines the sampling method. Larger particulate solids, such as ores, are sampled using a riffle (Figure 7.3.4), which is a trough with an even number of compartments. Because adjoining compartments empty onto opposite sides of the riffle, dumping a gross sample into the riffle divides it in half. By repeatedly passing half of the separated material back through the riffle, a sample of the desired size is collected.

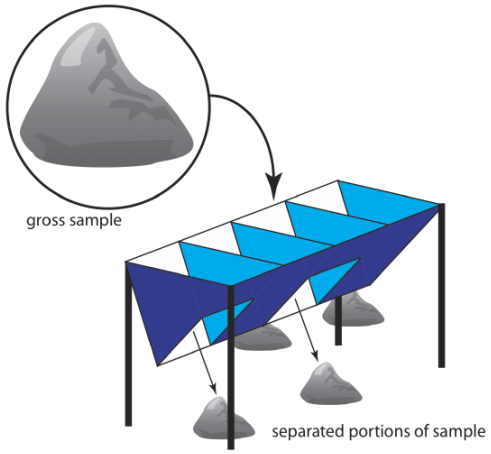


Figure 7.3.4 . Example of a four-unit riffle. Passing the gross sample, shown within the circle, through the riffle divides it into four piles, two on each side. Combining the piles from one side of the riffle provides a new sample, which is passed through the riffle again or kept as the final sample. The piles from the other side of the riffle are discarded.

A sample thief (Figure 7.3.5) is used for sampling smaller particulate materials, such as powders. A typical sample thief consists of two tubes that are nestled together. Each tube has one or more slots aligned down the length of the sample thief. Before inserting the sample thief into the material being sampled, the slots are closed by rotating the inner tube. When the sample thief is in place, rotating the inner tube opens the slots, which fill with individual samples. The inner tube is then rotated to the closed position and the sample thief withdrawn.

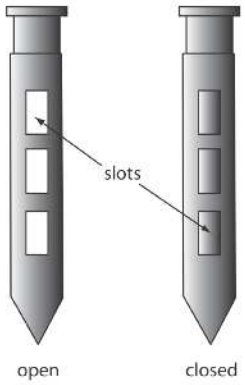


Figure 7.3.5 . Sample thief showing its open and closed positions.

SAMPLE PRESERVATION

Without preservation, a solid sample may undergo a change in composition due to the loss of volatile material, biodegradation, or chemical reactivity (particularly redox reactions). Storing samples at lower temperatures makes them less prone to biodegradation and to the loss of volatile material, but fracturing of solids and phase separations may present problems. To minimize the loss of volatile compounds, the sample container is filled completely, eliminating a headspace where gases collect. Samples that have not been exposed to O_2 particularly are susceptible to oxidation reactions. For example, samples of anaerobic sediments must be prevented from coming into contact with air.

SAMPLE PREPARATION

Unlike gases and liquids, which generally require little sample preparation, a solid sample usually needs some processing before analysis. There are two reasons for this. First, as discussed in Chapter 7.2, the standard deviation for sampling, s_{samp}, is a function of the number of particles in the sample, not the combined mass of the particles. For a heterogeneous material that consists of large particulates, the gross sample may be too large to analyze. For example, a Ni-bearing ore with an average particle size of 5 mm may require a sample that weighs one ton to obtain a reasonable s_{samp}. Reducing the sample's average particle size allows us to collect the same number of particles with a smaller, more manageable mass. Second, many analytical techniques require that the analyte be in solution.

REDUCING PARTICLE SIZE

A reduction in particle size is accomplished by crushing and grinding the gross sample. The resulting particulates are then thoroughly mixed and divided into ***subsamples*** of smaller mass. This process seldom occurs in a single step. Instead, subsamples are cycled through the process several times until a final ***laboratory sample*** is obtained.

Crushing and grinding uses mechanical force to break larger particles into smaller particles. A variety of tools are used depending on the particle's size and hardness. Large particles are crushed using jaw crushers that can reduce particles to diameters of a few millimeters. Ball mills, disk mills, and mortars and pestles are used to further reduce particle size.

A significant change in the gross sample's composition may occur during crushing and grinding. Decreasing particle size increases the available surface area, which increases the risk of losing volatile components. This problem is made worse by the frictional heat that accompanies crushing and grinding. Increasing the surface area also exposes interior portions of the sample to the atmosphere where oxidation may alter the gross sample's composition. Other problems include contamination from the materials used to crush and grind the sample, and differences in the ease with which particles are reduced in size. For example, softer particles are easier to reduce in size and may be lost as dust before the remaining sample is processed. This is a particular problem if the analyte's distribution between different types of particles is not uniform.

The gross sample is reduced to a uniform particle size by intermittently passing it through a sieve. Those particles not passing through the sieve receive additional processing until the entire sample is of uniform size. The resulting material is mixed thoroughly to ensure homogeneity and a subsample obtained with a riffle, or by c***oning and quartering***. As shown in Figure 7.3.6 , the gross sample is piled into a cone, flattened, and divided into four quarters. After discarding two diagonally opposed quarters, the remaining material is cycled through the process of coning and quartering until a suitable laboratory sample remains.

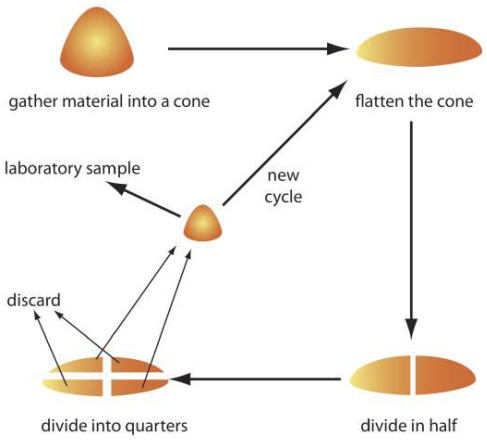


Figure 7.3.6 . Illustration showing the method of coning and quartering for reducing sample size. After gathering the gross sample into a cone, the cone is flattened, divided in half, and then divided into quarters. Two opposing quarters are combined to form the laboratory sample or a subsample that is sent through another cycle. The two remaining quarters are discarded.

BRINGING SOLID SAMPLES INTO SOLUTION

If you are fortunate, your sample will dissolve easily in a suitable solvent, requiring no more effort than gently swirling and heating. Distilled water usually is the solvent of choice for inorganic salts, but organic solvents, such as methanol, chloroform, and toluene, are useful for organic materials.

When a sample is difficult to dissolve, the next step is to try digesting it with an acid or a base. Table 7.3.2 lists several common acids and bases, and summarizes their use. Digestions are carried out in an open container, usually a beaker, using a hot-plate as a source of heat. The main advantage of an open-vessel digestion is cost because it requires no special equipment. Volatile reaction products, however, are lost, which results in a determinate error if they include the analyte.

Table 7.3.2 . Acids and Bases Used for Digesting Samples

solution	uses and properties
HCl (37% w/w)	• dissolves metals more easily reduced than H_2 ($E^o < 0$) • dissolves insoluble carbonate, sulfides, phosphates, fluorides, sulfates, and many oxides
HNO_3 (70% w/w)	• strong oxidizing agent • dissolves most common metals except Al, Au, Pt, and Cr • decomposes organics and biological samples (wet ashing)
H_2SO_4 (98% w/w)	• dissolves many metals and alloys • decomposes organics by oxidation and dehydration
HF (50% w/w)	• dissolves silicates by forming volatile SiF_4
$HClO_4$ (70% w/w)	• hot, concentrated solutions are strong oxidizing agents • dissolves many metals and alloys • decomposes organics (*Caution: reactions with organics often are explosive; use only in a specially equipped hood with a blast shield and after prior decomposition with HNO_3*)
HCl:HNO_3 (3:1 v/v)	• also known as aqua regia • dissolves Au and Pt
NaOH	• dissolves Al and amphoteric oxides of Sn, Pb, Zn, and Cr

Many digestions now are carried out in a closed container using microwave radiation as the source of energy. Vessels for microwave digestion are manufactured using Teflon (or some other fluoropolymer) or fused silica. Both materials are thermally stable, chemically resistant, transparent to microwave radiation, and capable of withstanding elevated pressures. A typical microwave digestion vessel, as shown in Figure 7.3.7 , consists of an insulated vessel body and a cap with a pressure relief valve. The vessels are placed in a microwave oven (a typical oven can accommodate 6–14 vessels) and microwave energy is controlled by monitoring the temperature or pressure within one of the vessels.



Figure 7.3.7 . Microwave digestion unit: on the left is a view of the unit's interior showing the carousel that holds the digestion vessels; on the right is a close-up of a Teflon digestion vessel, which is encased in a thermal sleeve. The pressure relief value, which is part of the vessel's blue cap, contains a membrane that ruptures if the internal pressure becomes too high.

Inorganic samples that resist decomposition by digesting with acids or bases often are brought into solution by fusing with a large excess of an alkali metal salt, called a flux. After mixing the sample and the flux in a crucible, they are heated to a molten state and allowed to cool slowly to room temperature. The resulting melt usually dissolves readily in distilled water or dilute acid. Table 7.3.3 summarizes several common fluxes and their uses. Fusion works when other methods of decomposition do not because of the high temperature and the flux's high concentration in the molten liquid. Disadvantages include contamination from the flux and the crucible, and the loss of volatile materials.

Table 7.3.3 . Common Fluxes for Decomposing Inorganic Samples

flux	melting temperature (°C)	crucible	typical samples
Na_2CO_3	85	Pt	silicates, oxides, phosphate, sulfides
$Li_2B_4O_7$	930	Pt, graphite	aluminosilicates, carbontes
$LiBO_2$	845	Pt, graphite	aluminosilicates, carbonates
NaOH	318	Au, Ag	silicates, silicon carbide
KOH	380	Au, Ag	silicates, silicon carbide
Na_2O_2	—	Ni	silicates, chromium steels, Pt alloys
$K_2S_2O_7$	300	Ni, porcelain	oxides
B_2O_3	577	Pt	silicates, oxides

Finally, we can decompose organic materials by dry ashing. In this method the sample is placed in a suitable crucible and heated over a flame or in a furnace. The carbon present in the sample oxidizes to CO_2, and hydrogen, sulfur, and nitrogen are volatilized as H_2O, SO_2, and N_2. These gases can be trapped and weighed to determine their concentration in the organic material. Often the goal of dry ashing is to remove the organic material, leaving behind an inorganic residue, or ash, that can be further analyzed.

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4.4: SEPARATING THE ANALYTE FROM INTERFERENTS

When an analytical method is selective for the analyte, analyzing a sample is a relatively simple task. For example, a quantitative analysis for glucose in honey is relatively easy to accomplish if the method is selective for glucose, even in the presence of other reducing sugars, such as fructose. Unfortunately, few analytical methods are selective toward a single species.

In the absence of an interferent, the relationship between the sample's signal, S_{samp}, and the analyte's concentration, C_A, is

$$S_{samp} = k_A C_A \tag{4.4.1}$$

where k_A is the analyte's sensitivity.

> In Equation 4.4.1, and the equations that follow, you can replace the analyte's concentration, C_A, with the moles of analyte, n_A, when working with methods, such as gravimetry, that respond to the absolute amount of analyte in a sample. In this case the interferent also is expressed in terms of moles.

If an interferent, is present, then Equation 4.4.1 becomes

$$S_{samp} = k_A C_A + k_I C_I \tag{4.4.2}$$

where k_I and C_I are, respectively, the interferent's sensitivity and concentration. A method's selectivity for the analyte is determined by the relative difference in its sensitivity toward the analyte and the interferent. If k_A is greater than k_I, then the method is more selective for the analyte. The method is more selective for the interferent if k_I is greater than k_A.

Even if a method is more selective for an interferent, we can use it to determine C_A if the interferent's contribution to S_{samp} is insignificant. The ***selectivity coefficient***, $K_{A,I}$, which we introduced in Chapter 3, provides a way to characterize a method's selectivity.

$$K_{A,I} = \frac{k_I}{k_A} \tag{4.4.3}$$

Solving Equation 4.4.3 for k_I, substituting into Equation 4.4.2, and simplifying, gives

$$S_{samp} = k_A \left(C_A + K_{A,I} \times C_I\right) \tag{4.4.4}$$

An interferent, therefore, does not pose a problem as long as the product of its concentration and its selectivity coefficient is significantly smaller than the analyte's concentration.

$$K_{A,I} \times C_I << C_A$$

If we cannot ignore an interferent's contribution to the signal, then we must begin our analysis by separating the analyte and the interferent.

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4.5: PROBLEMS

1. Because of the risk of lead poisoning, the exposure of children to lead-based paint is a significant public health concern. The first step in the quantitative analysis of lead in dried paint chips is to dissolve the sample. Corl evaluated several dissolution techniques [Corl, W. E. *Spectroscopy* **1991**, *6(8)*, 40–43]. Samples of paint were collected and then pulverized using a Pyrex mortar and pestle. Replicate portions of the powdered paint were taken for analysis. The following table shows results for a paint sample and for a standard reference material. Both samples and standards were digested with HNO_3 on a hot plate.

Replicate	% w/w Pb in Sample	% w/w Pb in Standard
1	5.09	11.48
2	6.29	11.62
3	6.64	11.47
4	4.63	11.86

(a) Determine the overall variance, the variance due to the method and the variance due to sampling. (b) What percentage of the overall variance is due to sampling? (c) How might you decrease the variance due to sampling?

2. To analyze a shipment of 100 barrels of an organic solvent, you plan to collect a single sample from each of 10 barrels selected at random. From which barrels should you collect samples if the first barrel is given by the twelfth entry in the random number table in Appendix 14, with subsequent barrels given by every third entry? Assume that entries in the random number table are arranged by rows.

3. The concentration of dissolved O_2 in a lake shows a daily cycle from the effect of photosynthesis, and a yearly cycle due to seasonal changes in temperature. Suggest an appropriate systematic sampling plan to monitor the daily change in dissolved O_2. Suggest an appropriate systematic sampling plan for monitoring the yearly change in dissolved O_2.

4. The data in the following table were collected during a preliminary study of the pH of an industrial wastewater stream.

time (hr)	pH	time (hr)	pH
0.5	4.4	9.0	5.7
1.0	4.8	9.5	5.5
1.5	5.2	10.0	6.5
2.0	5.2	10.5	6.0
2.5	5.6	11.0	5.8
3.0	5.4	11.5	6.0
3.5	5.4	12.0	5.6
4.0	4.4	12.5	5.6
4.5	4.8	13.0	5.4
5.0	4.8	13.5	4.9
5.5	4.2	14.0	5.2
6.0	4.2	14.5	4.4
6.5	3.8	15.0	4.0
7.0	4.0	15.5	4.5
7.5	4.0 0	16.0	4.0
8.0	3.9	16.5	5.0
8.5	4.7	17.0	5.0

Prepare a figure showing how the pH changes as a function of time and suggest an appropriate sampling frequency for a long-term monitoring program.

5. You have been asked to monitor the daily fluctuations in atmospheric ozone in the downtown area of a city to determine if there is relationship between daily traffic patterns and ozone levels. (a) Which of the following sampling plans will you use and why: random, systematic, judgmental, systematic–judgmental, or stratified? (b) Do you plan to collect and analyze a series of grab samples, or will you form a single composite sample? (c) Will your answers to these questions change if your goal is to determine if the average daily ozone level exceeds a threshold value? If yes, then what is your new sampling strategy?

6. The distinction between a homogeneous population and a heterogeneous population is important when we develop a sampling plan. (a) Define homogeneous and heterogeneous. (b) If you collect and analyze a single sample, can you determine if the population is homogeneous or is heterogeneous?

7. Beginning with equation 7.2.2, derive equation 7.2.3. Assume that the particles are spherical with a radius of r and a density of d.

8. The sampling constant for the radioisotope ^{24}Na in homogenized human liver is approximately 35 g [Kratochvil, B.; Taylor, J. K. *Anal. Chem.* **1981**, *53*, 924A–938A]. (a) What is the expected relative standard deviation for sampling if we analyze 1.0-g samples? (b) How

many 1.0-g samples must we analyze to obtain a maximum sampling error of ±5% at the 95% confidence level?

9. Engels and Ingamells reported the following results for the % w/w K_2O in a mixture of amphibolite and orthoclase [Engels, J. C.; Ingamells, C. O. *Geochim. Cosmochim. Acta* **1970**, *34*, 1007–1017].

0.247	0.300	0.236
0.247	0.275	0.212
0.258	0.311	0.304
0.258	0.330	0.187

Each of the 12 samples had a nominal mass of 0.1 g. Using this data, calculate the approximate value for K_s, and then, using this value for K_s, determine the nominal mass of sample needed to achieve a percent relative standard deviation of 2%.

10. The following data was reported for the determination of KH_2PO_4 in a mixture of KH_2PO_4 and NaCl [Guy, R. D.; Ramaley, L.; Wentzell, P. D. *J. Chem. Educ.* **1998**, *75*, 1028–1033].

nominal mass (g)	actual mass (g)	% w/w KH_2PO_4
0.10	0.1039	0.085
	0.1015	1.078
	0.1012	0.413
	0.1010	1.248
	0.1060	0.654
	0.0997	0.507
0.25	0.2515	0.847
	0.2465	0.598
	0.2770	0.431
	0.2460	0.842
	0.2485	0.964
	0.2590	1.178
0.50	0.5084	1.009
	0.4954	0.947
	0.5286	0.618
	0.5232	0.744
	0.4965	0.572
	0.4995	0.709
1.00	1.027	0.696
	0.987	0.843
	0.991	0.535
	0.998	0.750
	0.997	0.711
	1.001	0.639
2.50	2.496	0.766
	2.504	0.769
	2.496	0.682
	2.496	0.609
	2.557	0.589
	2.509	0.617

(a) Prepare a graph of % w/w KH_2PO_4 vs. the actual sample mass. Is this graph consistent with your understanding of the factors that affect sampling variance. (b) For each nominal mass, calculate the percent relative standard deviation, R_{exp}, based on the data. The value of K_s for this analysis is estimated as 350. Use this value of K_s to determine the theoretical percent relative standard deviation, R_{theo}, due to sampling. Considering these calculations, what is your conclusion about the importance of indeterminate sampling errors for this analysis? (c) For each nominal mass, convert R_{theo} to an absolute standard deviation. Plot points on your graph that correspond to ±1 absolute standard deviations about the overall average % w/w KH_2PO_4 for all samples. Draw smooth curves through these two sets of points. Does the sample appear homogeneous on the scale at which it is sampled?

11.In this problem you will collect and analyze data to simulate the sampling process. Obtain a pack of M&M's (or other similar candy). Collect a sample of five candies and count the number that are red (or any other color of your choice). Report the result of your analysis as % red. Return the candies to the bag, mix thoroughly, and repeat the analysis for a total of 20 determinations. Calculate the mean and the standard deviation for your data. Remove all candies from the bag and determine the true % red for the population. Sampling in this

exercise should follow binomial statistics. Calculate the expected mean value and the expected standard deviation, and compare to your experimental results.

12. Determine the error ($\alpha = 0.05$) for the following situations. In each case assume that the variance for a single determination is 0.0025 and that the variance for collecting a single sample is 0.050. (a) Nine samples are collected, each analyzed once. (b) One sample is collected and analyzed nine times. (c) Five samples are collected, each analyzed twice.

13. Which of the sampling schemes in problem 12 is best if you wish to limit the overall error to less than ±0.30 and the cost to collect a single sample is $1 and the cost to analyze a single sample is $10? Which is the best sampling scheme if the cost to collect a single sample is $7 and the cost to analyze a single sample is $3?

14. Maw, Witry, and Emond evaluated a microwave digestion method for Hg against the standard open-vessel digestion method [Maw, R.; Witry, L.; Emond, T. *Spectroscopy* **1994**, *9*, 39–41]. The standard method requires a 2-hr digestion and is operator-intensive. The microwave digestion is complete in approximately 0.5 hr and requires little monitoring by the operator. Samples of baghouse dust from air-pollution-control equipment were collected from a hazardous waste incinerator and digested in triplicate before determining the concentration of Hg in ppm. Results are summarized in the following two tables.

ppm Hg Following Microwave Digestion			
sample	replicate 1	replicate 2	replicate 3
1	7.12	7.66	7.17
2	16.1	15.7	15.6
3	4.89	4.62	4.28
4	9.64	9.03	8.44
a	6.76	7.22	7.50
6	6.19	6.61	7.61
7	9.44	9.56	10.7
8	30.8	29.0	26.3

ppm Hg Following Standard Digestion			
sample	replicate 1	replicate 2	replicate 3
1	5.60	5.54	5.40
2	13.1	13.8	13.0
3	5.39	5.12	5.36
4	6.50	6.52	7.20
a	6.20	6.03	5.77
6	6.25	5.65	5.61
7	15.0	13.9	14.0
8	20.4	16.1	20.0

Does the microwave digestion method yields acceptable results when compared to the standard digestion method?

15. Simpson, Apte, and Batley investigated methods for preserving water samples collected from anoxic (O_2-poor) environments that have high concentrations of dissolved sulfide [Simpson, S. L.: Apte, S. C.; Batley, G. E. *Anal. Chem.* **1998**, *70*, 4202–4205]. They found that preserving water samples with HNO_3 (a common method for preserving aerobic samples) gave significant negative determinate errors when analyzing for Cu^{2+}. Preserving samples by first adding H_2O_2 and then adding HNO_3 eliminated the determinate error. Explain their observations.

16. In a particular analysis the selectivity coefficient, $K_{A,I}$, is 0.816. When a standard sample with an analyte-to-interferent ratio of 5:1 is carried through the analysis, the error when determining the analyte is +6.3%. (a) Determine the apparent recovery for the analyte if R_I =0. (b) Determine the apparent recovery for the interferent if R_A = 0.

17. The amount of Co in an ore is determined using a procedure for which Fe in an interferent. To evaluate the procedure's accuracy, a standard sample of ore known to have a Co/Fe ratio of 10.2 is analyzed. When pure samples of Co and Fe are taken through the procedure the following calibration relationships are obtained

$$S_{Co} = 0.786 \times m_{Co} \text{ and } S_{Fe} = 0.699 \times m_{Fe}$$

where *S* is the signal and *m* is the mass of Co or Fe. When 278.3 mg of Co are taken through the separation step, 275.9 mg are recovered. Only 3.6 mg of Fe are recovered when a 184.9 mg sample of Fe is carried through the separation step. Calculate (a) the recoveries for Co and Fe; (b) the separation factor; (c) the selectivity ratio; (d) the error if no attempt is made to separate the Co and Fe; (e) the error if the separation step is carried out; and (f) the maximum possible recovery for Fe if the recovery for Co is 1.00 and the maximum allowed error is 0.05%.

18. The amount of calcium in a sample of urine is determined by a method for which magnesium is an interferent. The selectivity coefficient, $K_{Ca,Mg}$, for the method is 0.843. When a sample with a Mg/Ca ratio of 0.50 is carried through the procedure, an error of -3.7% is obtained. The error is +5.5% when using a sample with a Mg/Ca ratio of 2.0. (a) Determine the recoveries for Ca and Mg. (b) What is the expected error for a urine sample in which the Mg/Ca ratio is 10.0?

19. Using the formation constants in Appendix 12, show that F^- is an effective masking agent for preventing a reaction between Al^{3+} and EDTA. Assume that the only significant forms of fluoride and EDTA are F^- and Y^{4-}.

20. Cyanide is frequently used as a masking agent for metal ions. Its effectiveness as a masking agent is better in more basic solutions. Explain the reason for this dependence on pH.

21. Explain how we can separate an aqueous sample that contains Cu^{2+}, Sn^{4+}, Pb^{2+}, and Zn^{2+} into its component parts by adjusting the pH of the solution.

22. A solute, *S*, has a distribution ratio between water and ether of 7.5. Calculate the extraction efficiency if we extract a 50.0-mL aqueous sample of *S* using 50.0 mL of ether as (a) a single portion of 50.0 mL; (b) two portions, each of 25.0 mL; (c) four portions, each of 12.5 mL; and (d) five portions, each of 10.0 mL. Assume the solute is not involved in any secondary equilibria.

23. What volume of ether is needed to extract 99.9% of the solute in problem 23 when using (a) 1 extraction; (b) 2 extractions; (c) four extrac- tions; and (d) five extractions.

24. What is the minimum distribution ratio if 99% of the solute in a 50.0-mL sample is extracted using a single 50.0-mL portion of an organic solvent? Repeat for the case where two 25.0-mL portions of the organic solvent are used.

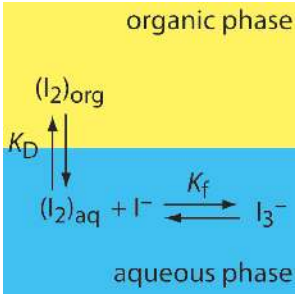
25. A weak acid, HA, with a K_a of 1.0×10^{-5} has a partition coefficient, K_D, of 1.2×10^3 between water and an organic solvent. What restriction on the sample's pH is necessary to ensure that 99.9% of the weak acid in a 50.0-mL sample is extracted using a single 50.0-mL portion of the organic solvent?

26. For problem 25, how many extractions are needed if the sample's pH cannot be decreased below 7.0?

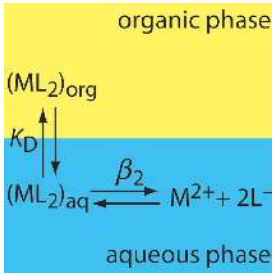
27. A weak base, B, with a K_b of 1.0×10^{-3} has a partition coefficient, K_D, of 5.0×10^2 between water and an organic solvent. What restriction on the sample's pH is necessary to ensure that 99.9% of the weak base in a 50.0-mL sample is extracted when using two 25.0-mL portions of the organic solvent?

28. A sample contains a weak acid analyte, HA, and a weak acid interferent, HB. The acid dissociation constants and the partition coefficients for the weak acids are $K_{a,HA} = 1.0 \times 10^{-3}$, $K_{a,HB} = 1.0 \times 10^{-7}$, $K_{D,HA} = K_{D,HB} = 5.0 \times 10^2$. (a) Calculate the extraction efficiency for HA and HB when a 50.0-mL sample, buffered to a pH of 7.0, is extracted using 50.0 mL of the organic solvent. (b) Which phase is enriched in the analyte? (c) What are the recoveries for the analyte and the interferent in this phase? (d) What is the separation factor? (e) A quantitative analysis is conducted on the phase enriched in analyte. What is the expected relative error if the selectivity coefficient, $K_{HA,HB}$, is 0.500 and the initial ratio of HB/HA is 10.0?

29. The relevant equilibria for the extraction of I_2 from an aqueous solution of KI into an organic phase are shown below. (a) Is the extraction efficiency for I_2 better at higher or at a lower concentrations of I^-? (b) Derive an expression for the distribution ratio for this extraction.



30. The relevant equilibria for the extraction of the metal-ligand complex ML_2 from an aqueous solution into an organic phase are shown below. (a) Derive an expression for the distribution ratio for this extraction. (b) Calculate the extraction efficiency when a 50.0-mL aqueous sample that is 0.15 mM in M^{2+} and 0.12 M in L^- is extracted using 25.0 mL of the organic phase. Assume that K_D is 10.3 and that β_2 is 560.



31. Derive equation 7.7.12 for the extraction scheme outlined in figure 7.7.5.

32. The following information is available for the extraction of Cu^{2+} by CCl_4 and dithizone: $K_{D,c} = 7 \times 10^4$; $\beta_2 = 5 \times 10^{22}$; $K_{a,HL} = 3 \times 10^{-5}$; $K_{D,HL} = 1.1 \times 10^4$; and $n = 2$. What is the extraction efficiency if a 100.0-mL sample of an aqueous solution that is 1.0×10^{-7} M Cu^{2+} and 1 M in HCl is extracted using 10.0 mL of CCl_4 containing 4.0×10^{-4} M dithizone (HL)?

33. Cupferron is a ligand whose strong affinity for metal ions makes it useful as a chelating agent in liquid–liquid extractions. The following table provides pH-dependent distribution ratios for the extraction of Hg^{2+}, Pb^{2+}, and Zn^{2+} from an aqueous solution to an organic solvent.

Distribution Ratios for Hg^{2+}, Pb^{2+}, and Zn^{2+} as a Function of pH

pH	Hg^{2+}	Pb^{2+}	Zn^{2+}
1	3.3	0.0	0.0
2	10.0	0.43	0.0
3	32.3	999	0.0
4	32.3	9999	0.0
5	19.0	9999	0.18
6	4.0	9999	0.33
7	1.0	9999	0.82
8	0.54	9999	1.50
9	0.15	9999	2.57
10	0.05	9999	2.57

(a) Suppose you have a 50.0-mL sample of an aqueous solution that contains Hg^{2+}, Pb^{2+}, and Zn^{2+}. Describe how you can separate these metal ions. (b) Under the conditions for your extraction of Hg^{2+}, what percent of the Hg^{2+} remains in the aqueous phase after three 50.0-mL extractions with the organic solvent? (c) Under the conditions for your extraction of Pb^{2+}, what is the minimum volume of organic solvent needed to extract 99.5% of the Pb^{2+} in a single extraction? (d) Under the conditions for your extraction of Zn^{2+}, how many extractions are needed to remove 99.5% of the Zn^{2+} if each extraction uses 25.0 mL of organic solvent?

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4.6: ADDITIONAL RESOURCES

The following set of experiments and class exercises introduce students to the importance of sampling on the quality of analytical results.

- Bauer, C. F. “Sampling Error Lecture Demonstration,” *J. Chem. Educ.* **1985**, *62*, 253.
- Canaes, L. S.; Brancalion, M. L.; Rossi, A. V.; Rath, S. “Using Candy Samples to Learn About Sampling Techniques and Statistical Evaluation of Data,” *J. Chem. Educ.* **2008**, *85*, 1083–1088.
- Clement, R. E. “Environmental Sampling for Trace Analysis,” *Anal. Chem.* **1992**, *64*, 1076A–1081A.
- Dunn, J. G.; Phillips, D. N.; van Bronswijk, W. “An Exercise to Illustrate the Importance of Sample Preparation in Chemical Analysis,” *J. Chem. Educ.* **1997**, *74*, 1188–1191.
- Fillman, K. L.; Palkendo, J. A. “Collection, Extraction, and Analysis of Lead in Atmospheric Particles,” *J. Chem. Edu.* **2014**, *91*, 590–592.
- Fritz, M. D. “A Demonstration of Sample Segregation,” *J. Chem. Educ.* **2005**, *82*, 255–256.
- Guy, R. D.; Ramaley, L.; Wentzell, P. D. “An Experiment in the Sampling of Solids for Chemical Analysis”, J. Chem. Educ. 1998, 75, 1028–1033.
- Hartman, J. R. “An In-Class Experiment to Illustrate the Importance of Sampling Techniques and Statistical Analysis of Data to Quantitative Analysis Students,” *J. Chem. Educ.* **2000**, *77*, 1017–1018.
- Harvey, D. T. “Two Experiments Illustrating the Importance of Sampling in a Quantitative Chemical Analysis,” *J. Chem. Educ.* **2002**, *79*, 360–363.
- Herrington, B. L. “A Demonstration of the Necessity for Care in Sampling,” *J. Chem. Educ.* **1937**, *14*, 544.
- Kratochvil, B.; Reid, R. S.; Harris, W. E. “Sampling Error in a Particulate Mixture”, *J. Chem. Educ.* **1980**, *57*, 518–520.
- Ross, M. R. “A Classroom Exercise in Sampling Technique,” *J. Chem. Educ.* **2000**, *77*, 1015–1016.
- Settle, F. A.; Pleva, M. “The Weakest Link Exercise,” *Anal. Chem.* **1999**, *71*, 538A–540A.
- Vitt, J. E.; Engstrom, R. C. “Effect of Sample Size on Sampling Error,” *J. Chem. Educ.* **1999**, *76*, 99–100.

The following experiments describe homemade sampling devices for collecting samples in the field.

- Delumyea, R. D.; McCleary, D. L. “A Device to Collect Sediment Cores,” *J. Chem. Educ.* **1993**, *70*, 172–173.
- Rockwell, D. M.; Hansen, T. “Sampling and Analyzing Air Pollution,” *J. Chem. Educ.* **1994**, *71*, 318–322.
- Saxena, S., Upadhyay, R.; Upadhyay, P. “A Simple and Low-Cost Air Sampler,” *J. Chem. Educ.* **1996**, *73*, 787–788.
- Shooter, D. “Nitrogen Dioxide and Its Determination in the Atmosphere,” *J. Chem. Educ.* **1993**, *70*, A133–A140.

The following experiments introduce students to methods for extracting analytes from their matrix.

- “Extract-CleanTM SPE Sample Preparation Guide Volume 1”, Bulletin No. 83, Alltech Associates, Inc. Deerfield, IL.
- Freeman, R. G.; McCurdy, D. L. “Using Microwave Sample Decomposition in Undergraduate Analytical Chemistry,” *J. Chem. Educ.* **1998**, *75*, 1033–1032.
- Snow, N. H.; Dunn, M.; Patel, S. “Determination of Crude Fat in Food Products by Supercritical Fluid Extraction and Gravimetric Analysis,” *J. Chem. Educ.* **1997**, *74*, 1108–1111.
- Yang, M. J.; Orton, M. L.; Pawliszyn, J. “Quantitative Determination of Caffeine in Beverages Using a Combined SPME-GC/MS Method,” *J. Chem. Educ.* **1997**, *74*, 1130–1132.

The following papers provides a general introduction to the terminology used in describing sampling.

- “Terminology—The key to understanding analytical science. Part 2: Sampling and sample preparation,” AMCTB 19, 2005.
- Majors, R. E. “Nomenclature for Sampling in Analytical Chemistry” *LC•GC* **1992**, *10*, 500–506.

Further information on the statistics of sampling is covered in the following papers and textbooks.

- Analytical Methods Committee “What is uncertainty from sampling, and why is it important?” AMCTB 16A, 2004.
- Analytical Methods Committee “Analytical and sampling strategy, fitness for purpose, and computer games,” AMCTB 20, 2005.
- Analytical Methods Committee “Measurement uncertainty arising from sampling: the new Eurachem Guide,” AMCTB No. 31, 2008.
- Analytical Methods Committee “The importance, for regulation, of uncertainty from sampling,” AMCTB 42, 2009.
- Analytical Methods Committee “Estimating sampling uncertainty—how many duplicate samples are needed?” AMCTB 58, 2014.
- Analytical Methods Committee “Random samples,” AMCTB 60, 2014.
- Analytical Methods Committee “Sampling theory and sampling uncertainty,” AMCTB 71, 2015.
- *Sampling for Analytical Purpose, Gy, P. ed., Wiley: NY, 1998.*
- Baiulescu, G. E.; Dumitrescu, P.; Zuaravescu, P. G. *Sampling*, Ellis Horwood: NY, 1991.
- Cohen, R. D. “How the Size of a Random Sample Affects How Accurately It Represents a Population,” *J. Chem. Educ.* **1992**, *74*, 1130–1132.
- Efstathiou, C. E. “On the sampling variance of ultra-dilute solutions,” *Talanta* **2000**, *52*, 711–715.

- Esbensen, K. H.; Wagner, C. “Theory of sampling (TOS) *versus* measurement uncertainty (MU)–A call for integration,” *TRAC-Trend. Anal. Chem.* **2014**, *57*, 93–106.
- Gerlach, R. W.; Dobb, D. E.; Raab, G. A.; Nocerino, J. M. *J. Chemom.* **2002**, *16*, 321–328.
- Gy, P. M. *Sampling of Particulate Materials: Theory and Practice*; Elsevier: Amsterdam, 1979.
- Gy, P. M. *Sampling of Heterogeneous and Dynamic Materials: Theories of Heterogeneity, Sampling and Homogenizing*; Elsevier: Amsterdam, 1992.
- Harrington, B.; Nickerson, B.; Guo, M. X.; Barber, M.; Giamalva, D.; Lee, C.; Scrivens, G. “Sample Preparation Composite and Replicate Strategy for Assay of Solid Oral Drug Products,” *Anal. Chem.* **2014**, *86*, 11930–11936.
- Kratochvil, B.; Taylor, J. K. “Sampling for Chemical Analysis,” *Anal. Chem.* **1981**, *53*, 924A–938A.
- Kratochvil, B.; Goewie, C. E.; Taylor, J. K. “Sampling Theory for Environmental Analysis,” *Trends Anal. Chem.* **1986**, *5*, 253–256.
- Meyer, V. R. *LC•GC* **2002**, *20*, 106–112.
- Rohlf, F. J.; AkÇakaya, H. R.; Ferraro, S. P. “Optimizing Composite Sampling Protocols,” *Environ. Sci. Technol.* **1996**, *30*, 2899–2905.
- Smith, R.; James, G. V. *The Sampling of Bulk Materials*; Royal Society of Chemistry: London, 1981.

The process of collecting a sample presents a variety of difficulties, particularly with respect to the analyte’s integrity. The following papers provide representative examples of sampling problems.

- Barceló, D.; Hennion, M. C. “Sampling of Polar Pesticides from Water Matrices,” *Anal. Chim. Acta* **1997**, *338*, 3–18.
- Batley, G. E.; Gardner, D. “Sampling and Storage of Natural Waters for Trace Metal Analysis,” *Wat. Res.* **1977**, *11*, 745–756.
- Benoit, G.; Hunter, K. S.; Rozan, T. F. “Sources of Trace Metal Contamination Artifacts during Collection, Handling, and Analysis of Freshwaters,” *Anal. Chem.* **1997**, *69*, 1006–1011
- Brittain, H. G. “Particle-Size Distribution II: The Problem of Sampling Powdered Solids,” *Pharm. Technol.* July **2002**, 67–73.
- Ramsey, M. H. “Measurement Uncertainty Arising from Sampling: Implications for the Objectives of Geoanalysis,” *Analyst*, **1997**, *122*, 1255–1260.
- Seiler, T-B; Schulze, T.; Hollert, H. “The risk of altering soil and sediment samples upon extract prepa- ration for analytical and bio-analytical investigations—a review,” *Anal. Bioanal. Chem.* **2008**, 390, 1975–1985.

The following texts and articles provide additional information on methods for separating analytes and inter- ferents.

- “Guide to Solid Phase Extraction,” Bulletin 910, Sigma-Aldrich, 1998.
- “Solid Phase Microextraction: Theory and Optimization of Conditions,” Bulletin 923, Sigma-Aldrich, 1998.
- *Microwave-Enhanced Chemistry: Fundamentals, Sample Preparation, and Applications, Kingston, H. M.; Haswell, S. J., eds.; American Chemical Society: Washington, D.C., 1997.*
- Anderson, R. *Sample Pretreatment and Separation*, Wiley: Chichester, 1987.
- Bettiol, C.; Stievano, L.; Bertelle, M.; Delfino, F.; Argese, E. “Evaluation of microwave-assisted acid extraction procedures for the determination of metal content and potential bioavailability in sediments,” *Appl. Geochem.* **2008**, *23*, 1140–1151.
- Compton, T. R. *Direct Preconcentration Techniques*, Oxford Science Publications: Oxford, 1993.
- Compton, T. R. *Complex-Formation Preconcentration Techniques*, Oxford Science Publications: Oxford, 1993.
- Hinshaw, J. V. “Solid-Phase Microextraction,” *LC•GC Europe* **2003**, *December*, 2–5.
- Karger, B. L.; Snyder, L. R.; Harvath, C. *An Introduction to Separation Science*, Wiley-Interscience: N. Y.; 1973.
- Majors, R. E.; Raynie, D. E. “Sample Preparation and Solid-Phase Extraction”, *LC•GC* **1997**, *15*, 1106–1117.
- Luque de Castro, M. D.; Priego-Capote, F.; Sánchez-Ávila, N. “Is dialysis alive as a membrane-based separation technique?” *Trends Anal. Chem.* **2008**, *27*, 315–326.
- Mary, P.; Studer, V.; Tabeling, P. “Microfluidic Droplet-Based Liquid–Liquid Extraction,” *Anal. Chem.* **2008**, *80*, 2680–2687.
- Miller, J. M. *Separation Methods in Chemical Analysis*, Wiley-Interscience: N. Y.; 1975.
- Morrison, G. H.; Freiser, H. *Solvent Extraction in Analytical Chemistry*, John Wiley and Sons: N. Y.; 1957.
- Pawliszyn, J. *Solid-Phase Microextraction: Theory and Practice*, Wiley: NY, 1997.
- Pawliszyn, J. “Sample Preparation: Quo Vadis?” *Anal. Chem.* **2003**, *75*, 2543–2558.
- Sulcek, Z.; Povondra, P. *Methods of Decomposition in Inorganic Analysis*; CRC Press: Boca Raton, FL, 1989.
- Theis, A. L.; Waldack, A. J.; Hansen, S. M.; Jeannot, M. A. “Headspace Solvent Microextraction,” *Anal. Chem.* **2001**, *73*, 5651–5654.
- Thurman, E. M.; Mills, M. S. *Solid-Phase Extraction: Principles and Practice*, Wiley: NY, 1998.
- Zhang, Z.; Yang, M.; Pawliszyn, J. “Solid-Phase Microextraction,” *Anal. Chem.* **1994**, *66*, 844A–853A.

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4.7: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

An analysis requires a sample and how we acquire that sample is critical. The samples we collect must accurately represent their target population, and our sampling plan must provide a sufficient number of samples of appropriate size so that uncertainty in sampling does not limit the precision of our analysis.

A complete sampling plan requires several considerations, including the type of sample to collect (random, judgmental, systematic, systematic–judgmental, stratified, or convenience); whether to collect grab samples, composite samples, or in situ samples; whether the population is homogeneous or heterogeneous; the appropriate size for each sample; and the number of samples to collect.

Removing a sample from its population may induce a change in its composition due to a chemical or physical process. For this reason, we collect samples in inert containers and we often preserve them at the time of collection.

When an analytical method's selectivity is insufficient, we may need to separate the analyte from potential interferents. Such separations take advantage of physical properties—such as size, mass or density—or chemical properties. Important examples of chemical separations include masking, distillation, and extractions.

KEY TERMS

centrifugation	composite sample	coning and quartering
convenience sampling	density gradient centrifugation	dialysis
distillation	distribution ratio	extraction
extraction efficiency	filtrate	filtration
grab sample	gross sample	heterogeneous
homogeneous	in situ sampling	judgmental sampling
laboratory sample	masking	masking agents
Nyquist theorem	partition coefficient	preconcentration
purge-and-trap	random sampling	recovery
recrystallization	retentate	sampling plan
secondary equilibrium reaction	selectivity coefficient	separation factor
size exclusion chromatography	Soxhlet extractor	stratified sampling
sublimation	subsamples	supercritical fluid
systematic–judgmental sampling	systematic sampling	target population

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CHAPTER OVERVIEW

5: EVALUATING ANALYTICAL DATA

When we use an analytical method we make three separate evaluations of experimental error. First, before we begin the analysis we evaluate potential sources of errors to ensure they will not adversely effect our results. Second, during the analysis we monitor our measurements to ensure that errors remain acceptable. Finally, at the end of the analysis we evaluate the quality of the measurements and results, and compare them to our original design criteria. This chapter provides an introduction to sources of error, to evaluating errors in analytical measurements, and to the statistical analysis of data.

5.1: Characterizing Measurements and Results
5.2: Characterizing Experimental Errors
5.3: Propagation of Uncertainty
5.4: The Distribution of Measurements and Results
5.5: Statistical Analysis of Data
5.6: Statistical Methods for Normal Distributions
5.7: Detection Limits
5.8: Using Excel and R to Analyze Data
5.9: Problems
5.10: Additional Resources
5.11: Chapter Summary and Key Terms

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5.1: CHARACTERIZING MEASUREMENTS AND RESULTS

Let's begin by choosing a simple quantitative problem that requires a single measurement: What is the mass of a penny? You probably recognize that our statement of the problem is too broad. For example, are we interested in the mass of a United States penny or of a Canadian penny, or is the difference relevant? Because a penny's composition and size may differ from country to country, let's narrow our problem to pennies from the United States.

There are other concerns we might consider. For example, the United States Mint produces pennies at two locations (Figure 4.1.1). Because it seems unlikely that a penny's mass depends on where it is minted, we will ignore this concern. Another concern is whether the mass of a newly minted penny is different from the mass of a circulating penny. Because the answer this time is not obvious, let's further narrow our question and ask "What is the mass of a circulating United States Penny?"



Figure 4.1.1 : An uncirculated 2005 Lincoln head penny. The "D" below the date indicates that this penny was produced at the United States Mint at Denver, Colorado. Pennies produced at the Philadelphia Mint do not have a letter below the date. Source: United States Mint image.

A good way to begin our analysis is to gather some preliminary data. Table 4.1.1 shows masses for seven pennies collected from my change jar. In examining this data we see that our question does not have a simple answer. That is, we can not use the mass of a single penny to draw a specific conclusion about the mass of any other penny (although we might reasonably conclude that all pennies weigh at least 3 g). We can, however, characterize this data by reporting the spread of the individual measurements around a central value.

Table 4.1.1 : Masses of Seven Circulating U. S. Pennies

Penny	Mass (g)
1	3.080
2	3.094
3	3.107
4	3.056
5	3.112
6	3.174
7	3.198

MEASURES OF CENTRAL TENDENCY

One way to characterize the data in Table 4.1.1 is to assume that the masses of individual pennies are scattered randomly around a central value that is the best estimate of a penny's expected, or "true" mass. There are two common ways to estimate central tendency: the mean and the median.

MEAN

The ***mean***, $\overline{X}$, is the numerical average for a data set. We calculate the mean by dividing the sum of the individual values by the size of the data set

$$\overline{X} = \frac{\sum_{i=1}^{n} X_i}{n}$$

where X_i is the ith measurement, and n is the size of the data set.

EXAMPLE 4.1.1

What is the mean for the data in Table 4.1.1 ?

Solution

To calculate the mean we add together the results for all measurements

$$3.080 + 3.094 + 3.107 + 3.056 + 3.112 + 3.174 + 3.198 = 21.821 \text{ g}$$

and divide by the number of measurements

$$\overline{X} = \frac{21.821 \text{ g}}{7} = 3.117 \text{ g}$$

The mean is the most common estimate of central tendency. It is not a robust estimate, however, because a single extreme value—one much larger or much smaller than the remainder of the data—influences strongly the mean's value [Rousseeuw, P. J. *J. Chemom.* **1991**, *5*, 1–20]. For example, if we accidently record the third penny's mass as 31.07 g instead of 3.107 g, the mean changes from 3.117 g to 7.112 g!

> An estimate for a statistical parameter is robust if its value is not affected too much by an unusually large or an unusually small measurement.

MEDIAN

The ***median***, $\widetilde{X}$, is the middle value when we order our data from the smallest to the largest value. When the data has an odd number of values, the median is the middle value. For an even number of values, the median is the average of the $n/2$ and the $(n/2) + 1$ values, where n is the size of the data set.

> When $n = 5$, the median is the third value in the ordered data set; for $n = 6$, the median is the average of the third and fourth members of the ordered data set.

EXAMPLE 4.1.2

What is the median for the data in Table 4.1.1 ?

Solution

To determine the median we order the measurements from the smallest to the largest value

$$3.056 \quad 3.080 \quad 3.094 \quad 3.107 \quad 3.112 \quad 3.174 \quad 3.198$$

Because there are seven measurements, the median is the fourth value in the ordered data; thus, the median is 3.107 g.

As shown by Example 4.1.1 and Example 4.1.2 , the mean and the median provide similar estimates of central tendency when all measurements are comparable in magnitude. The median, however, is a more robust estimate of central tendency because it is less sensitive to measurements with extreme values. For example, if we accidently record the third penny's mass as 31.07 g instead of 3.107 g, the median's value changes from 3.107 g to 3.112 g.

MEASURES OF SPREAD

If the mean or the median provides an estimate of a penny's expected mass, then the spread of individual measurements about the mean or median provides an estimate of the difference in mass among pennies or of the uncertainty in measuring mass with a balance. Although we often define the spread relative to a specific measure of central tendency, its magnitude is independent of the central value. Although shifting all measurements in the same direction by adding or subtracting a constant value changes the mean or median, it does not change the spread. There are three common measures of spread: the range, the standard deviation, and the variance.

> Problem 13 at the end of the chapter asks you to show that this is true.

RANGE

The ***range***, w, is the difference between a data set's largest and smallest values.

$$w = X_{\text{largest}} - X_{\text{smallest}}$$

The range provides information about the total variability in the data set, but does not provide information about the distribution of individual values. The range for the data in Table 4.1.1 is

$$w = 3.198 \text{ g} - 3.056 \text{ g} = 0.142 \text{ g}$$

STANDARD DEVIATION

The ***standard deviation***, s, describes the spread of individual values about their mean, and is given as

$$s = \sqrt{\frac{\sum_{i=1}^{n}(X_i - \overline{X})^2}{n-1}} \tag{5.1.1}$$

where X_i is one of the n individual values in the data set, and $\overline{X}$ is the data set's mean value. Frequently, we report the relative standard deviation, s_r, instead of the absolute standard deviation.

$$s_r = \frac{s}{\overline{X}}$$

The percent relative standard deviation, $\%s_r$, is $s_r \times 100$.

The relative standard deviation is important because it allows for a more meaningful comparison between data sets when the individual measurements differ significantly in magnitude. Consider again the data in Table 4.1.1 . If we multiply each value by 10, the absolute standard deviation will increase by 10 as well; the relative standard deviation, however, is the same.

EXAMPLE 4.1.3

Report the standard deviation, the relative standard deviation, and the percent relative standard deviation for the data in Table 4.1.1 ?

Solution

To calculate the standard deviation we first calculate the difference between each measurement and the data set's mean value (3.117), square the resulting differences, and add them together to find the numerator of Equation 5.1.1

$$\begin{aligned}(3.080 - 3.117)^2 &= (-0.037)^2 = 0.001369\\ (3.094 - 3.117)^2 &= (-0.023)^2 = 0.000529\\ (3.107 - 3.117)^2 &= (-0.010)^2 = 0.000100\\ (3.056 - 3.117)^2 &= (-0.061)^2 = 0.003721\\ (3.112 - 3.117)^2 &= (-0.005)^2 = 0.000025\\ (3.174 - 3.117)^2 &= (+0.057)^2 = 0.003249\\ (3.198 - 3.117)^2 &= (+0.081)^2 = \underline{0.006561}\\ &\qquad\qquad\qquad\quad 0.015554\end{aligned}$$

For obvious reasons, the numerator of Equation 5.1.1 is called a sum of squares. Next, we divide this sum of squares by $n - 1$, where n is the number of measurements, and take the square root.

$$s = \sqrt{\frac{0.015554}{7 - 1}} = 0.051 \text{ g}$$

Finally, the relative standard deviation and percent relative standard deviation are

$$s_r = \frac{0.051 \text{ g}}{3.117 \text{ g}} = 0.016$$

$$\%s_r = (0.016) \times 100 = 1.6\%$$

It is much easier to determine the standard deviation using a scientific calculator with built in statistical functions.

Many scientific calculators include two keys for calculating the standard deviation. One key calculates the standard deviation for a data set of n samples drawn from a larger collection of possible samples, which corresponds to Equation 5.1.1 . The other key calculates the standard deviation for all possible samples. The latter is known as the population's standard deviation, which we will cover later in this chapter. Your calculator's manual will help you determine the appropriate key for each.

VARIANCE

Another common measure of spread is the ***variance***, which is the square of the standard deviation. We usually report a data set's standard deviation, rather than its variance, because the mean value and the standard deviation share the same unit. As we will see shortly, the variance is a useful measure of spread because its values are additive.

EXAMPLE 4.1.4

What is the variance for the data in Table 4.1.1 ?

Solution

The variance is the square of the absolute standard deviation. Using the standard deviation from Example 4.1.3 gives the variance as

$$s^2 = (0.051)^2 = 0.0026$$

EXERCISE 4.1.1

The following data were collected as part of a quality control study for the analysis of sodium in serum; results are concentrations of Na^+ in mmol/L.

$$140 \quad 143 \quad 141 \quad 137 \quad 132 \quad 157 \quad 143 \quad 149 \quad 118 \quad 145$$

Report the mean, the median, the range, the standard deviation, and the variance for this data. This data is a portion of a larger data set from Andrew, D. F.; Herzberg, A. M. *Data: A Collection of Problems for the Student and Research Worker*, Springer-Verlag:New York, 1985, pp. 151–155.

Answer

Mean: To find the mean we add together the individual measurements and divide by the number of measurements. The sum of the 10 concentrations is 1405. Dividing the sum by 10, gives the mean as 140.5, or 1.40×10^2 mmol/L.

Median: To find the median we arrange the 10 measurements from the smallest concentration to the largest concentration; thus

$$118 \quad 132 \quad 137 \quad 140 \quad 141 \quad 143 \quad 143 \quad 145 \quad 149 \quad 157$$

The median for a data set with 10 members is the average of the fifth and sixth values; thus, the median is (141 + 143)/2, or 142 mmol/L.

Range: The range is the difference between the largest value and the smallest value; thus, the range is 157 – 118 = 39 mmol/L.

Standard Deviation: To calculate the standard deviation we first calculate the absolute difference between each measurement and the mean value (140.5), square the resulting differences, and add them together. The differences are

$$-0.5 \quad 2.5 \quad 0.5 \quad -3.5 \quad -8.5 \quad 16.5 \quad 2.5 \quad 8.5 \quad -22.5 \quad 4.5$$

and the squared differences are

$$0.25 \quad 6.25 \quad 0.25 \quad 12.25 \quad 72.25 \quad 272.25 \quad 6.25 \quad 72.25 \quad 506.25 \quad 20.25$$

The total sum of squares, which is the numerator of Equation 5.1.1, is 968.50. The standard deviation is

$$s = \sqrt{\frac{968.50}{10-1}} = 10.37 \approx 10.4$$

Variance: The variance is the square of the standard deviation, or 108.

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5.2: CHARACTERIZING EXPERIMENTAL ERRORS

Characterizing a penny's mass using the data in Table 4.1.1 suggests two questions. First, does our measure of central tendency agree with the penny's expected mass? Second, why is there so much variability in the individual results? The first of these questions addresses the accuracy of our measurements and the second addresses the precision of our measurements. In this section we consider the types of experimental errors that affect accuracy and precision.

ERRORS THAT AFFECT ACCURACY

Accuracy is how close a measure of central tendency is to its expected value, μ. We express accuracy either as an absolute error, e

$$e = \overline{X} - \mu \tag{5.2.1}$$

or as a percent relative error, $\%e$

$$\%e = \frac{\overline{X} - \mu}{\mu} \times 100 \tag{5.2.2}$$

Although Equation 5.2.1 and Equation 5.2.2 use the mean as the measure of central tendency, we also can use the median.

> The convention for representing a statistical parameter is to use a Roman letter for a value calculated from experimental data, and a Greek letter for its corresponding expected value. For example, the experimentally determined mean is $\overline{X}$ and its underlying expected value is μ. Likewise, the experimental standard deviation is s and the underlying expected value is σ.

We identify as determinate an error that affects the accuracy of an analysis. Each source of a ***determinate error*** has a specific magnitude and sign. Some sources of determinate error are positive and others are negative, and some are larger in magnitude and others are smaller in magnitude. The cumulative effect of these determinate errors is a net positive or negative error in accuracy.

> It is possible, although unlikely, that the positive and negative determinate errors will offset each other, producing a result with no net error in accuracy.

We assign determinate errors into four categories—sampling errors, method errors, measurement errors, and personal errors—each of which we consider in this section.

SAMPLING ERRORS

A determinate sampling error occurs when our sampling strategy does not provide a us with a representative sample. For example, if we monitor the environmental quality of a lake by sampling from a single site near a point source of pollution, such as an outlet for industrial effluent, then our results will be misleading. To determine the mass of a U. S. penny, our strategy for selecting pennies must ensure that we do not include pennies from other countries.

> An awareness of potential sampling errors especially is important when we work with heterogeneous materials. Strategies for obtaining representative samples are covered in Chapter 5.

METHOD ERRORS

In any analysis the relationship between the signal, S_{total}, and the absolute amount of analyte, n_A, or the analyte's concentration, C_A, is

$$S_{total} = k_A n_A + S_{mb} \tag{5.2.3}$$

$$S_{total} = k_A C_A + S_{mb} \tag{5.2.4}$$

where k_A is the method's sensitivity for the analyte and S_{mb} is the signal from the method blank. A ***method error*** exists when our value for k_A or for S_{mb} is in error. For example, a method in which S_{total} is the mass of a precipitate assumes that k is defined by a pure precipitate of known stoichiometry. If this assumption is not true, then the resulting determination of n_A or C_A is inaccurate. We can minimize a determinate error in k_A by calibrating the method. A method error due to an interferent in the reagents is minimized by using a proper method blank.

MEASUREMENT ERRORS

The manufacturers of analytical instruments and equipment, such as glassware and balances, usually provide a statement of the item's maximum ***measurement error***, or ***tolerance***. For example, a 10-mL volumetric pipet (Figure 4.2.1) has a tolerance of ±0.02 mL, which

means the pipet delivers an actual volume within the range 9.98–10.02 mL at a temperature of 20 °C. Although we express this tolerance as a range, the error is determinate; that is, the pipet's expected volume, μ, is a fixed value within this stated range.



Figure 4.2.1 : Close-up of a 10-mL volumetric pipet showing that it has a tolerance of ±0.02 mL at 20 °C.

Volumetric glassware is categorized into classes based on its relative accuracy. Class A glassware is manufactured to comply with tolerances specified by an agency, such as the National Institute of Standards and Technology or the American Society for Testing and Materials. The tolerance level for Class A glassware is small enough that normally we can use it without calibration. The tolerance levels for Class B glassware usually are twice that for Class A glassware. Other types of volumetric glassware, such as beakers and graduated cylinders, are not used to measure volume accurately. Table 4.2.1 provides a summary of typical measurement errors for Class A volumetric glassware. Tolerances for digital pipets and for balances are provided in Table 4.2.2 and Table 4.2.3 .

Table 4.2.1 : Measurement Errors for Type A Volumetric Glassware

Transfer Pipets		Volumetric Flasks		Burets	
Capacity (mL)	Tolerance (mL)	Capacity (mL)	Tolerance (mL)	Capacity (mL)	Tolerance (mL)
1	±0.006	5	±0.02	10	±0.02
2	±0.006	10	±0.02	25	±0.03
5	±0.01	25	±0.03	50	±0.05
10	±0.02	50	±0.05		
20	±0.03	100	±0.08		
25	±0.03	250	±0.12		
50	±0.05	500	±0.20		
100	±0.08	1000	±0.30		
		2000			

Table 4.2.2 : Measurement Errors for Digital Pipets

Pipet Range	Volume (mL or μL)	Percent Measurement Error
10–100 μL	10	±3.0%
	50	±1.0%
	100	±0.8%
100–1000 μL	100	±3.0%
	500	±1.0%
	1000	±0.6%
1–10 mL	1	±3.0%
	5	±0.8%
	10	±0.6%

The tolerance values for the volumetric glassware in Table 4.2.1 are from the ASTM E288, E542, and E694 standards. The measurement errors for the digital pipets in Table 4.2.2 are from www.eppendorf.com.

Table 4.2.3 : Measurement Errors for Selected Balances

Balance	Capacity (g)	Measurement Error
Precisa 160M	160	±1 mg
A & D ER 120M	120	±0.1 mg
Metler H54	160	±0.01 mg

We can minimize a determinate measurement error by calibrating our equipment. Balances are calibrated using a reference weight whose mass we can trace back to the SI standard kilogram. Volumetric glassware and digital pipets are calibrated by determining the mass of water delivered or contained and using the density of water to calculate the actual volume. It is never safe to assume that a calibration does not change during an analysis or over time. One study, for example, found that repeatedly exposing volumetric glassware to higher temperatures

during machine washing and oven drying, led to small, but significant changes in the glassware's calibration [Castanheira, I.; Batista, E.; Valente, A.; Dias, G.; Mora, M.; Pinto, L.; Costa, H. S. *Food Control* **2006**, *17*, 719–726]. Many instruments drift out of calibration over time and may require frequent recalibration during an analysis.

PERSONAL ERRORS

Finally, analytical work is always subject to ***personal error***, examples of which include the ability to see a change in the color of an indicator that signals the endpoint of a titration, biases, such as consistently overestimating or underestimating the value on an instrument's readout scale, failing to calibrate instrumentation, and misinterpreting procedural directions. You can minimize personal errors by taking proper care.

IDENTIFYING DETERMINATE ERRORS

Determinate errors often are difficult to detect. Without knowing the expected value for an analysis, the usual situation in any analysis that matters, we often have nothing to which we can compare our experimental result. Nevertheless, there are strategies we can use to detect determinate errors.

The magnitude of a constant ***determinate error*** is the same for all samples and is more significant when we analyze smaller samples. Analyzing samples of different sizes, therefore, allows us to detect a constant determinate error. For example, consider a quantitative analysis in which we separate the analyte from its matrix and determine its mass. Let's assume the sample is 50.0% w/w analyte. As we see in Table 4.2.4 , the expected amount of analyte in a 0.100 g sample is 0.050 g. If the analysis has a positive constant determinate error of 0.010 g, then analyzing the sample gives 0.060 g of analyte, or an apparent concentration of 60.0% w/w. As we increase the size of the sample the experimental results become closer to the expected result. An upward or downward trend in a graph of the analyte's experimental concentration versus the sample's mass (Figure 4.2.2) is evidence of a constant determinate error.

Table 4.2.4 : Effect of a Constant Determinate Error on the Analysis of a Sample That is 50.0% w/w Analyte

Mass of Sample (g)	Expected Mass of Analyte (g)	Constant Error (g)	Experimental Mass of Analyte (g)	Experimental Concentration of Analyte (% w/w)
0.100	0.050	0.010	0.060	60.0
0.200	0.100	0.010	0.110	55.0
0.400	0.200	0.010	0.210	52.5
0.800	0.400	0.010	0.410	51.2
1.600	0.800	0.010	0.810	50.6

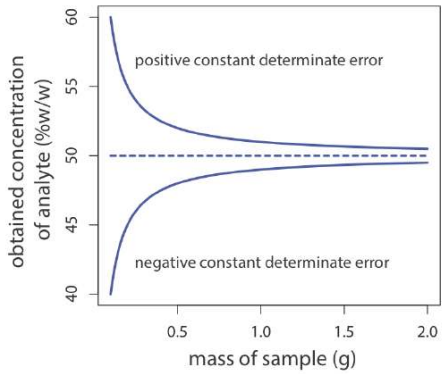


Figure 4.2.2 : Effect of a constant positive determinate error of +0.01 g and a constant negative determinate error of –0.01 g on the determination of an analyte in samples of varying size. The analyte's expected concentration of 50% w/w is shown by the dashed line.

A ***proportional determinate error***, in which the error's magnitude depends on the amount of sample, is more difficult to detect because the result of the analysis is independent of the amount of sample. Table 4.2.5 outlines an example that shows the effect of a positive proportional error of 1.0% on the analysis of a sample that is 50.0% w/w in analyte. Regardless of the sample's size, each analysis gives the same result of 50.5% w/w analyte.

Table 4.2.5 : Effect of a Proportional Determinate Error on the Analysis of a Sample That is 50.0% w/w Analyte

Mass of Sample (g)	Expected Mass of Analyte (g)	Proportional Error (%)	Experimental Mass of Analyte (g)	Experimental Concentration of Analyte (% w/w)
0.100	0.050	1.00	0.0505	50.5
0.200	0.100	1.00	0.101	50.5
0.400	0.200	1.00	0.202	50.5
0.800	0.400	1.00	0.404	50.5
1.600	0.800	1.00	0.808	50.5

One approach for detecting a proportional determinate error is to analyze a standard that contains a known amount of analyte in a matrix similar to our samples. Standards are available from a variety of sources, such as the National Institute of Standards and Technology (where they are called Standard Reference Materials) or the American Society for Testing and Materials. Table 4.2.6 , for example, lists certified values for several analytes in a standard sample of *Gingko biloba* leaves. Another approach is to compare our analysis to an analysis carried out using an independent analytical method that is known to give accurate results. If the two methods give significantly different results, then a determinate error is the likely cause.

Table 4.2.6 : Certified Concentrations for SRM 3246: *Gingko bilbo* (Leaves)

Class of Analyte	Analyte	Mass Fraction (mg/g or ng/g)
Flavonoids/Ginkgolide B (mass fraction in mg/g)	Qurecetin	2.69 ± 0.31
	Kaempferol	3.02 ± 0.41
	Isorhamnetin	$0.517 \pm 0.0.99$
	Total Aglycones	6.22 ± 0.77
Selected Terpenes (mass fraction in mg/g)	Ginkgolide A	0.57 ± 0.28
	Ginkgolide B	0.470 ± 0.090
	Ginkgolide C	0.59 ± 0.22
	Ginkgolide J	0.18 ± 0.10
	Bilobalide	1.52 ± 0.40
	Total Terpene Lactones	3.3 ± 1.1
Selected Toxic Elements (mass fraction in ng/g)	Cadmium	20.8 ± 1.0
	Lead	995 ± 30
	Mercury	23.08 ± 0.17

> The primary purpose of this Standard Reference Material is to validate analytical methods for determining flavonoids, terpene lactones, and toxic elements in *Ginkgo biloba* or other materials with a similar matrix. Values are from the official Certificate of Analysis available at www.nist.gov.

Constant and proportional determinate errors have distinctly different sources, which we can define in terms of the relationship between the signal and the moles or concentration of analyte (Equation 5.2.3 and Equation 5.2.4). An invalid method blank, S_{mb}, is a constant determinate error as it adds or subtracts the same value to the signal. A poorly calibrated method, which yields an invalid sensitivity for the analyte, k_A, results in a proportional determinate error.

ERRORS THAT AFFECT PRECISION

As we saw in Section 4.1, precision is a measure of the spread of individual measurements or results about a central value, which we express as a range, a standard deviation, or a variance. Here we draw a distinction between two types of precision: repeatability and reproducibility. ***Repeatability*** is the precision when a single analyst completes an analysis in a single session using the same solutions, equipment, and instrumentation. ***Reproducibility***, on the other hand, is the precision under any other set of conditions, including between analysts or between laboratory sessions for a single analyst. Since reproducibility includes additional sources of variability, the reproducibility of an analysis cannot be better than its repeatability.

> The ratio of the standard deviation associated with reproducibility to the standard deviation associated with repeatability is called the Horowitz ratio. For a wide variety of analytes in foods, for example, the median Horowtiz ratio is 2.0 with larger values for fatty acids and for trace elements; see Thompson, M.; Wood, R. "The 'Horowitz Ratio'–A Study of the Ratio Between Reproducibility and Repeatability in the Analysis of Foodstuffs," *Anal. Methods*, **2015**, *7*, 375–379.

Errors that affect precision are indeterminate and are characterized by random variations in their magnitude and their direction. Because they are random, positive and negative ***indeterminate errors*** tend to cancel, provided that we make a sufficient number of measurements. In such situations the mean and the median largely are unaffected by the precision of the analysis.

SOURCES OF INDETERMINATE ERROR

We can assign indeterminate errors to several sources, including collecting samples, manipulating samples during the analysis, and making measurements. When we collect a sample, for instance, only a small portion of the available material is taken, which increases the chance that small-scale inhomogeneities in the sample will affect repeatability. Individual pennies, for example, may show variations in mass from several sources, including the manufacturing process and the loss of small amounts of metal or the addition of dirt during circulation. These variations are sources of indeterminate sampling errors.

During an analysis there are many opportunities to introduce indeterminate method errors. If our method for determining the mass of a penny includes directions for cleaning them of dirt, then we must be careful to treat each penny in the same way. Cleaning some pennies more vigorously than others might introduce an indeterminate method error.

Finally, all measuring devices are subject to indeterminate measurement errors due to limitations in our ability to read its scale. For example, a buret with scale divisions every 0.1 mL has an inherent indeterminate error of ±0.01–0.03 mL when we estimate the volume to the hundredth of a milliliter (Figure 4.2.3).

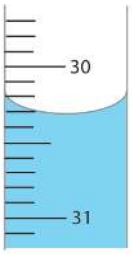


Figure 4.2.3 : Close-up of a buret showing the difficulty in estimating volume. With scale divisions every 0.1 mL it is difficult to read the actual volume to better than ±0.01–0.03 mL.

EVALUATING INDETERMINATE ERROR

Indeterminate errors associated with our analytical equipment or instrumentation generally are easy to estimate if we measure the standard deviation for several replicate measurements, or if we monitor the signal's fluctuations over time in the absence of analyte (Figure 4.2.4) and calculate the standard deviation. Other sources of indeterminate error, such as treating samples inconsistently, are more difficult to estimate.

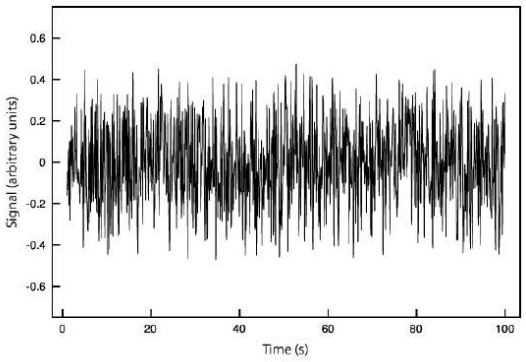


Figure 4.2.4 : Background noise in an instrument showing the random fluctuations in the signal.

To evaluate the effect of an indeterminate measurement error on our analysis of the mass of a circulating United States penny, we might make several determinations of the mass for a single penny (Table 4.2.7). The standard deviation for our original experiment (see Table 4.1.1) is 0.051 g, and it is 0.0024 g for the data in Table 4.2.7 . The significantly better precision when we determine the mass of a single penny suggests that the precision of our analysis is not limited by the balance. A more likely source of indeterminate error is a variability in the masses of individual pennies.

Table 4.2.7 : Replicate Determinations of the Mass of a Single Circulating U. S. Penny

Replicate	Mass (g)	Replicate	Mass (g)
1	3.025	6	3.023
2	3.024	7	3.022
3	3.028	8	3.021
4	3.027	9	3.026
5	3.028	10	3.024

In Section 4.5 we will discuss a statistical method—the *F*-test—that you can use to show that this difference is significant.

ERROR AND UNCERTAINTY

Analytical chemists make a distinction between error and uncertainty [Ellison, S.; Wegscheider, W.; Williams, A. *Anal. Chem.* **1997**, *69*, 607A–613A]. ***Error*** is the difference between a single measurement or result and its expected value. In other words, error is a measure of

bias. As discussed earlier, we divide errors into determinate and indeterminate sources. Although we can find and correct a source of determinate error, the indeterminate portion of the error remains.

Uncertainty expresses the range of possible values for a measurement or result. Note that this definition of uncertainty is not the same as our definition of precision. We calculate precision from our experimental data and use it to estimate the magnitude of indeterminate errors. Uncertainty accounts for all errors—both determinate and indeterminate—that reasonably might affect a measurement or a result. Although we always try to correct determinate errors before we begin an analysis, the correction itself is subject to uncertainty.

Here is an example to help illustrate the difference between precision and uncertainty. Suppose you purchase a 10-mL Class A pipet from a laboratory supply company and use it without any additional calibration. The pipet's tolerance of ±0.02 mL is its uncertainty because your best estimate of its expected volume is 10.00 mL ± 0.02 mL. This uncertainty primarily is determinate. If you use the pipet to dispense several replicate samples of a solution and determine the volume of each sample, the resulting standard deviation is the pipet's precision. Table 4.2.8 shows results for ten such trials, with a mean of 9.992 mL and a standard deviation of ±0.006 mL. This standard deviation is the precision with which we expect to deliver a solution using a Class A 10-mL pipet. In this case the pipet's published uncertainty of ±0.02 mL is worse than its experimentally determined precision of ±0.006 ml. Interestingly, the data in Table 4.2.8 allows us to calibrate this specific pipet's delivery volume as 9.992 mL. If we use this volume as a better estimate of the pipet's expected volume, then its uncertainty is ±0.006 mL. As expected, calibrating the pipet allows us to decrease its uncertainty [Kadis, R. *Talanta* **2004**, *64*, 167–173].

Table 4.2.8 : Experimental Results for Volume Dispensed by a 10–mL Class A Transfer Pipet

Replicate	Volume (ml)	Replicate	Volume (mL)
1	10.002	6	9.983
2	9.993	7	9.991
3	9.984	8	9.990
4	9.996	9	9.988
5	9.989	10	9.999

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5.3: PROPAGATION OF UNCERTAINTY

Suppose we dispense 20 mL of a reagent using the Class A 10-mL pipet whose calibration information is given in Table 4.2.8. If the volume and uncertainty for one use of the pipet is 9.992 ± 0.006 mL, what is the volume and uncertainty if we use the pipet twice?

As a first guess, we might simply add together the volume and the maximum uncertainty for each delivery; thus

(9.992 mL + 9.992 mL) ± (0.006 mL + 0.006 mL) = 19.984 ± 0.012 mL

It is easy to appreciate that combining uncertainties in this way overestimates the total uncertainty. Adding the uncertainty for the first delivery to that of the second delivery assumes that with each use the indeterminate error is in the same direction and is as large as possible. At the other extreme, we might assume that the uncertainty for one delivery is positive and the other is negative. If we subtract the maximum uncertainties for each delivery,

(9.992 mL + 9.992 mL) ± (0.006 mL – 0.006 mL) = 19.984 ± 0.000 mL

we clearly underestimate the total uncertainty.

So what is the total uncertainty? From the discussion above, we reasonably expect that the total uncertainty is greater than ±0.000 mL and that it is less than ±0.012 mL. To estimate the uncertainty we use a mathematical technique known as the propagation of uncertainty. Our treatment of the propagation of uncertainty is based on a few simple rules.

A FEW SYMBOLS

A ***propagation of uncertainty*** allows us to estimate the uncertainty in a result from the uncertainties in the measurements used to calculate that result. For the equations in this section we represent the result with the symbol *R*, and we represent the measurements with the symbols *A*, *B*, and *C*. The corresponding uncertainties are u_R, u_A, u_B, and u_C. We can define the uncertainties for *A*, *B*, and *C* using standard deviations, ranges, or tolerances (or any other measure of uncertainty), as long as we use the same form for all measurements.

> The requirement that we express each uncertainty in the same way is a critically important point. Suppose you have a range for one measurement, such as a pipet's tolerance, and standard deviations for the other measurements. All is not lost. There are ways to convert a range to an estimate of the standard deviation. See Appendix 2 for more details.

UNCERTAINTY WHEN ADDING OR SUBTRACTING

When we add or subtract measurements we propagate their absolute uncertainties. For example, if the result is given by the equation

$$R = A + B - C$$

the the absolute uncertainty in *R* is

$$u_R = \sqrt{u_A^2 + u_B^2 + u_C^2} \tag{5.3.1}$$

✔ EXAMPLE 4.3.1

If we dispense 20 mL using a 10-mL Class A pipet, what is the total volume dispensed and what is the uncertainty in this volume? First, complete the calculation using the manufacturer's tolerance of 10.00 mL±0.02 mL, and then using the calibration data from Table 4.2.8.

Solution

To calculate the total volume we add the volumes for each use of the pipet. When using the manufacturer's values, the total volume is

$$V = 10.00\ \text{mL} + 10.00\ \text{mL} = 20.00\ \text{mL}$$

and when using the calibration data, the total volume is

$$V = 9.992\ \text{mL} + 9.992\ \text{mL} = 19.984\ \text{mL}$$

Using the pipet's tolerance as an estimate of its uncertainty gives the uncertainty in the total volume as

$$u_R = \sqrt{(0.02)^2 + (0.02)^2} = 0.028\ \text{mL} = 0.028\ \text{mL}$$

and using the standard deviation for the data in Table 4.2.8 gives an uncertainty of

$$u_R = \sqrt{(0.006)^2 + (0.006)^2} = 0.0085\ \text{mL}$$

Rounding the volumes to four significant figures gives 20.00 mL ± 0.03 mL when we use the tolerance values, and 19.98 ± 0.01 mL when we use the calibration data.

UNCERTAINTY WHEN MULTIPLYING OR DIVIDING

When we multiple or divide measurements we propagate their relative uncertainties. For example, if the result is given by the equation

$$R = \frac{A \times B}{C}$$

then the relative uncertainty in *R* is

$$\frac{u_R}{R} = \sqrt{\left(\frac{u_A}{A}\right)^2 + \left(\frac{u_B}{B}\right)^2 + \left(\frac{u_C}{C}\right)^2} \tag{5.3.2}$$

EXAMPLE 4.3.2

The quantity of charge, *Q*, in coulombs that passes through an electrical circuit is

$$Q = i \times t$$

where *i* is the current in amperes and *t* is the time in seconds. When a current of 0.15 A ± 0.01 A passes through the circuit for 120 s ± 1 s, what is the total charge and its uncertainty?

Solution

The total charge is

$$Q = (0.15\ \text{A}) \times (120\ \text{s}) = 18\ \text{C}$$

Since charge is the product of current and time, the relative uncertainty in the charge is

$$\frac{u_R}{R} = \sqrt{\left(\frac{0.01}{0.15}\right)^2 + \left(\frac{1}{120}\right)^2} = 0.0672$$

and the charge's absolute uncertainty is

$$u_R = R \times 0.0672 = (18\ \text{C}) \times (0.0672) = 1.2\ \text{C}$$

Thus, we report the total charge as 18 C ± 1 C.

UNCERTAINTY FOR MIXED OPERATIONS

Many chemical calculations involve a combination of adding and subtracting, and of multiply and dividing. As shown in the following example, we can calculate the uncertainty by separately treating each operation using Equation 5.3.1 and Equation 5.3.2 as needed.

EXAMPLE 4.3.3

For a concentration technique, the relationship between the signal and the an analyte's concentration is

$$S_{total} = k_A C_A + S_{mb}$$

What is the analyte's concentration, C_A, and its uncertainty if S_{total} is 24.37 ± 0.02, S_{mb} is 0.96 ± 0.02, and k_A is $0.186 \pm 0.003\ \text{ppm}^{-1}$?

Solution

Rearranging the equation and solving for C_A

$$C_A = \frac{S_{total} - S_{mb}}{k_A} = \frac{24.37 - 0.96}{0.186\ \text{ppm}^{-1}} = \frac{23.41}{0.186\ \text{ppm}^{-1}} = 125.9\ \text{ppm}$$

gives the analyte's concentration as 126 ppm. To estimate the uncertainty in C_A, we first use Equation 5.3.1 to determine the uncertainty for the numerator.

$$u_R = \sqrt{(0.02)^2 + (0.02)^2} = 0.028$$

The numerator, therefore, is 23.41 ± 0.028. To complete the calculation we use Equation 5.3.2 to estimate the relative uncertainty in C_A.

$$\frac{u_R}{R} = \sqrt{\left(\frac{0.028}{23.41}\right)^2 + \left(\frac{0.003}{0.186}\right)^2} = 0.0162$$

The absolute uncertainty in the analyte's concentration is

$$u_R = (125.9 \text{ ppm}) \times (0.0162) = 2.0 \text{ ppm}$$

Thus, we report the analyte's concentration as 126 ppm ± 2 ppm.

EXERCISE 4.3.1

To prepare a standard solution of Cu^{2+} you obtain a piece of copper from a spool of wire. The spool's initial weight is 74.2991 g and its final weight is 73.3216 g. You place the sample of wire in a 500-mL volumetric flask, dissolve it in 10 mL of HNO_3, and dilute to volume. Next, you pipet a 1 mL portion to a 250-mL volumetric flask and dilute to volume. What is the final concentration of Cu^{2+} in mg/L, and its uncertainty? Assume that the uncertainty in the balance is ±0.1 mg and that you are using Class A glassware.

Answer

The first step is to determine the concentration of Cu^{2+} in the final solution. The mass of copper is

$$74.2991 \text{ g} - 73.3216 \text{ g} = 0.9775 \text{ g Cu}$$

The 10 mL of HNO_3 used to dissolve the copper does not factor into our calculation. The concentration of Cu^{2+} is

$$\frac{0.9775 \text{ g Cu}}{0.5000 \text{ L}} \times \frac{1.000 \text{ mL}}{250.0 \text{ mL}} \times \frac{1000 \text{ mg}}{\text{g}} = 7.820 \text{ mg Cu}^{2+}\text{/L}$$

Having found the concentration of Cu^{2+}, we continue with the propagation of uncertainty. The absolute uncertainty in the mass of Cu wire is

$$u_{\text{g Cu}} = \sqrt{(0.0001)^2 + (0.0001)^2} = 0.00014 \text{ g}$$

The relative uncertainty in the concentration of Cu^{2+} is

$$\frac{u_{\text{mg/L}}}{7.820 \text{ mg/L}} = \sqrt{\left(\frac{0.00014}{0.9775}\right)^2 + \left(\frac{0.20}{500.0}\right)^2 + \left(\frac{0.006}{1.000}\right)^2 + \left(\frac{0.12}{250.0}\right)^2} = 0.00603$$

Solving for $u_{\text{mg/L}}$ gives the uncertainty as 0.0472. The concentration and uncertainty for Cu^{2+} is 7.820 mg/L ± 0.047 mg/L.

UNCERTAINTY FOR OTHER MATHEMATICAL FUNCTIONS

Many other mathematical operations are common in analytical chemistry, including the use of powers, roots, and logarithms. Table 4.3.1 provides equations for propagating uncertainty for some of these function where *A* and *B* are independent measurements and where *k* is a constant whose value has no uncertainty.

Table 4.3.1 : Propagation of Uncertainty for Selected Mathematical Functions

Function	u_R	Function	u_R
$R = kA$	$u_R = ku_A$	$R = \ln(A)$	$u_R = \frac{u_A}{A}$
$R = A + B$	$u_R = \sqrt{u_A^2 + u_B^2}$	$R = \log(A)$	$u_R = 0.4343 \times \frac{u_A}{A}$
$R = A - B$	$u_R = \sqrt{u_A^2 + u_B^2}$	$R = e^A$	$\frac{u_R}{R} = u_A$
$R = A \times B$	$\frac{u_R}{R} = \sqrt{\left(\frac{u_A}{A}\right)^2 + \left(\frac{u_B}{B}\right)^2}$	$R = 10^A$	$\frac{u_R}{R} = 2.303 \times u_A$
$R = \frac{A}{B}$	$\frac{u_R}{R} = \sqrt{\left(\frac{u_A}{A}\right)^2 + \left(\frac{u_B}{B}\right)^2}$	$R = A^k$	$\frac{u_R}{R} = k \times \frac{u_A}{A}$

EXAMPLE 4.3.4

If the pH of a solution is 3.72 with an absolute uncertainty of ±0.03, what is the $[H^+]$ and its uncertainty?

Solution

The concentration of H^+ is

$$[H^+] = 10^{-\text{pH}} = 10^{-3.72} = 1.91 \times 10^{-4} \text{ M}$$

or 1.9×10^{-4} M to two significant figures. From Table 4.3.1 the relative uncertainty in $[H^+]$ is

$$\frac{u_R}{R} = 2.303 \times u_A = 2.303 \times 0.03 = 0.069$$

The uncertainty in the concentration, therefore, is

$$(1.91 \times 10^{-4}\ \text{M}) \times (0.069) = 1.3 \times 10^{-5}\ \text{M}$$

We report the $[H^+]$ as $1.9(\pm 0.1) \times 10^{-4}$ M, which is equivalent to $1.9 \times 10^{-4}\ \text{M} \pm 0.1 \times 10^{-4}\ \text{M}$.

? EXERCISE 4.3.2

A solution of copper ions is blue because it absorbs yellow and orange light. Absorbance, *A*, is defined as

$$A = -\log T = -\log\left(\frac{P}{P_o}\right)$$

where, *T* is the transmittance, P_o is the power of radiation as emitted from the light source and *P* is its power after it passes through the solution. What is the absorbance if P_o is 3.80×10^2 and *P* is 1.50×10^2 ? If the uncertainty in measuring P_o and *P* is 15, what is the uncertainty in the absorbance?

Answer

The first step is to calculate the absorbance, which is

$$A = -\log T = -\log\frac{P}{P_o} = -\log\frac{1.50 \times 10^2}{3.80 \times 10^2} = 0.4037 \approx 0.404$$

Having found the absorbance, we continue with the propagation of uncertainty. First, we find the uncertainty for the ratio P/P_o, which is the transmittance, T.

$$\frac{u_T}{T} = \sqrt{\left(\frac{15}{3.80 \times 10^2}\right)^2 + \left(\frac{15}{1.50 \times 10^2}\right)^2} = 0.1075$$

Finally, from Table 4.3.1 the uncertainty in the absorbance is

$$u_A = 0.4343 \times \frac{u_T}{T} = (0.4343) \times (0.1075) = 4.669 \times 10^{-2}$$

The absorbance and uncertainty is 0.40 ± 0.05 absorbance units.

IS CALCULATING UNCERTAINTY ACTUALLY USEFUL?

Given the effort it takes to calculate uncertainty, it is worth asking whether such calculations are useful. The short answer is, yes. Let's consider three examples of how we can use a propagation of uncertainty to help guide the development of an analytical method.

One reason to complete a propagation of uncertainty is that we can compare our estimate of the uncertainty to that obtained experimentally. For example, to determine the mass of a penny we measure its mass twice—once to tare the balance at 0.000 g and once to measure the penny's mass. If the uncertainty in each measurement of mass is ±0.001 g, then we estimate the total uncertainty in the penny's mass as

$$u_R = \sqrt{(0.001)^2 + (0.001)^2} = 0.0014\ \text{g}$$

If we measure a single penny's mass several times and obtain a standard deviation of ±0.050 g, then we have evidence that the measurement process is out of control. Knowing this, we can identify and correct the problem.

We also can use a propagation of uncertainty to help us decide how to improve an analytical method's uncertainty. In Example 4.3.3 , for instance, we calculated an analyte's concentration as 126 ppm ± 2 ppm, which is a percent uncertainty of 1.6%. Suppose we want to decrease the percent uncertainty to no more than 0.8%. How might we accomplish this? Looking back at the calculation, we see that the concentration's relative uncertainty is determined by the relative uncertainty in the measured signal (corrected for the reagent blank)

$$\frac{0.028}{23.41} = 0.0012 \text{ or } 0.12\%$$

and the relative uncertainty in the method's sensitivity, k_A,

$$\frac{0.003 \text{ ppm}^{-1}}{0.186 \text{ ppm}^{-1}} = 0.016 \text{ or } 1.6\%$$

Of these two terms, the uncertainty in the method's sensitivity dominates the overall uncertainty. Improving the signal's uncertainty will not improve the overall uncertainty of the analysis. To achieve an overall uncertainty of 0.8% we must improve the uncertainty in k_A to ±0.0015 ppm^{-1}.

EXERCISE 4.3.3

Verify that an uncertainty of ±0.0015 ppm^{-1} for k_A is the correct result.

Answer

An uncertainty of 0.8% is a relative uncertainty in the concentration of 0.008; thus, letting u be the uncertainty in k_A

$$0.008 = \sqrt{\left(\frac{0.028}{23.41}\right)^2 + \left(\frac{u}{0.186}\right)^2}$$

Squaring both sides of the equation gives

$$6.4 \times 10^{-5} = \left(\frac{0.028}{23.41}\right)^2 + \left(\frac{u}{0.186}\right)^2$$

Solving for the uncertainty in k_A gives its value as 1.47×10^{-3} or ±0.0015 ppm^{-1}.

Finally, we can use a propagation of uncertainty to determine which of several procedures provides the smallest uncertainty. When we dilute a stock solution usually there are several combinations of volumetric glassware that will give the same final concentration. For instance, we can dilute a stock solution by a factor of 10 using a 10-mL pipet and a 100-mL volumetric flask, or using a 25-mL pipet and a 250-mL volumetric flask. We also can accomplish the same dilution in two steps using a 50-mL pipet and 100-mL volumetric flask for the first dilution, and a 10-mL pipet and a 50-mL volumetric flask for the second dilution. The overall uncertainty in the final concentration—and, therefore, the best option for the dilution—depends on the uncertainty of the volumetric pipets and volumetric flasks. As shown in the following example, we can use the tolerance values for volumetric glassware to determine the optimum dilution strategy [Lam, R. B.; Isenhour, T. L. *Anal. Chem.* **1980**, *52*, 1158–1161].

EXAMPLE 4.3.5 :

Which of the following methods for preparing a 0.0010 M solution from a 1.0 M stock solution provides the smallest overall uncertainty?

(a) A one-step dilution that uses a 1-mL pipet and a 1000-mL volumetric flask.

(b) A two-step dilution that uses a 20-mL pipet and a 1000-mL volumetric flask for the first dilution, and a 25-mL pipet and a 500-mL volumetric flask for the second dilution.

Solution

The dilution calculations for case (a) and case (b) are

$$\text{case (a)}: 1.0 \text{ M} \times \frac{1.000 \text{ mL}}{1000.0 \text{ mL}} = 0.0010 \text{ M}$$

$$\text{case (b)}: 1.0 \text{ M} \times \frac{20.00 \text{ mL}}{1000.0 \text{ mL}} \times \frac{25.00 \text{ mL}}{500.0 \text{mL}} = 0.0010 \text{ M}$$

Using tolerance values from Table 4.2.1, the relative uncertainty for case (a) is

$$u_R = \sqrt{\left(\frac{0.006}{1.000}\right)^2 + \left(\frac{0.3}{1000.0}\right)^2} = 0.006$$

and for case (b) the relative uncertainty is

$$u_R = \sqrt{\left(\frac{0.03}{20.00}\right)^2 + \left(\frac{0.3}{1000}\right)^2 + \left(\frac{0.03}{25.00}\right)^2 + \left(\frac{0.2}{500.0}\right)^2} = 0.002$$

> Since the relative uncertainty for case (b) is less than that for case (a), the two-step dilution provides the smallest overall uncertainty. Of course we must balance the smaller uncertainty for case (b) against the increased opportunity for introducing a determinate error when making two dilutions instead of just one dilution, as in case (a).

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5.4: THE DISTRIBUTION OF MEASUREMENTS AND RESULTS

Earlier we reported results for a determination of the mass of a circulating United States penny, obtaining a mean of 3.117 g and a standard deviation of 0.051 g. Table 4.4.1 shows results for a second, independent determination of a penny's mass, as well as the data from the first experiment. Although the means and standard deviations for the two experiments are similar, they are not identical. The difference between the two experiments raises some interesting questions. Are the results for one experiment better than the results for the other experiment? Do the two experiments provide equivalent estimates for the mean and the standard deviation? What is our best estimate of a penny's expected mass? To answer these questions we need to understand how we might predict the properties of all pennies using the results from an analysis of a small sample of pennies. We begin by making a distinction between populations and samples.

Table 4.4.1 : Results for Two Determinations of the Mass of a Circulating U. S. Penny

First Experiment		Second Experiment	
Penny	Mass (g)	Penny	Mass (g)
1	3.080	1	3.052
2	3.094	2	3.141
3	3.107	3	3.083
4	3.056	4	3.083
5	3.112	5	3.048
6	3.174		
7	3.198		
$\overline{X}$	3.117		3.081
s	0.051		0.037

POPULATIONS AND SAMPLES

A ***population*** is the set of all objects in the system we are investigating. For the data in Table 4.4.1 , the population is all United States pennies in circulation. This population is so large that we cannot analyze every member of the population. Instead, we select and analyze a limited subset, or ***sample*** of the population. The data in Table 4.4.1 , for example, shows the results for two such samples drawn from the larger population of all circulating United States pennies.

PROBABILITY DISTRIBUTIONS FOR POPULATIONS

Table 4.4.1 provides the means and the standard deviations for two samples of circulating United States pennies. What do these samples tell us about the population of pennies? What is the largest possible mass for a penny? What is the smallest possible mass? Are all masses equally probable, or are some masses more common?

To answer these questions we need to know how the masses of individual pennies are distributed about the population's average mass. We represent the distribution of a population by plotting the probability or frequency of obtaining a specific result as a function of the possible results. Such plots are called ***probability distributions***.

There are many possible probability distributions; in fact, the probability distribution can take any shape depending on the nature of the population. Fortunately many chemical systems display one of several common probability distributions. Two of these distributions, the binomial distribution and the normal distribution, are discussed in this section.

THE BINOMIAL DISTRIBUTION

The binomial distribution describes a population in which the result is the number of times a particular event occurs during a fixed number of trials. Mathematically, the binomial distribution is defined as

$$P(X,N) = \frac{N!}{X!(N-X)!} \times p^X \times (1-p)^{N-X}$$

where $P(X , N)$ is the probability that an event occurs X times during N trials, and p is the event's probability for a single trial. If you flip a coin five times, $P(2,5)$ is the probability the coin will turn up "heads" exactly twice.

> The term $N!$ reads as N-factorial and is the product $N \times (N-1) \times (N-2) \times \cdots \times 1$. For example, 4! is $4 \times 3 \times 2 \times 1 = 24$. Your calculator probably has a key for calculating factorials.

A binomial distribution has well-defined measures of central tendency and spread. The expected mean value is

$$\mu = Np$$

and the expected spread is given by the variance

$$\sigma^2 = Np(1-p)$$

or the standard deviation.

$$\sigma = \sqrt{Np(1-p)}$$

The binomial distribution describes a population whose members have only specific, discrete values. When you roll a die, for example, the possible values are 1, 2, 3, 4, 5, or 6. A roll of 3.45 is not possible. As shown in Worked Example 4.4.1 , one example of a chemical system that obeys the binomial distribution is the probability of finding a particular isotope in a molecule.

EXAMPLE 4.4.1

Carbon has two stable, non-radioactive isotopes, ^{12}C and ^{13}C, with relative isotopic abundances of, respectively, 98.89% and 1.11%.

(a) What are the mean and the standard deviation for the number of ^{13}C atoms in a molecule of cholesterol ($C_{27}H_{44}O$)?

(b) What is the probability that a molecule of cholesterol has no atoms of ^{13}C?

Solution

The probability of finding an atom of ^{13}C in a molecule of cholesterol follows a binomial distribution, where X is the number of ^{13}C atoms, N is the number of carbon atoms in a molecule of cholesterol, and p is the probability that an atom of carbon in ^{13}C.

For (a), the mean number of ^{13}C atoms in a molecule of cholesterol is

$$\mu = Np = 27 \times 0.0111 = 0.300$$

with a standard deviation of

$$\sigma = \sqrt{Np(1-p)} = \sqrt{27 \times 0.0111 \times (1 - 0.0111)} = 0.544$$

For (b), the probability of finding a molecule of cholesterol without an atom of ^{13}C is

$$P(0,27) = \frac{27!}{0!\,(27-0)!} \times (0.0111)^0 \times (1-0.0111)^{27-0} = 0.740$$

There is a 74.0% probability that a molecule of cholesterol will not have an atom of ^{13}C, a result consistent with the observation that the mean number of ^{13}C atoms per molecule of cholesterol, 0.300, is less than one.

A portion of the binomial distribution for atoms of ^{13}C in cholesterol is shown in Figure 4.4.1 . Note in particular that there is little probability of finding more than two atoms of ^{13}C in any molecule of cholesterol.

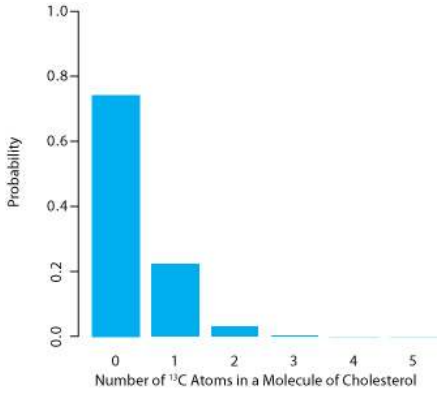


Figure 4.4.1 : Portion of the binomial distribution for the number of naturally occurring ^{13}C atoms in a molecule of cholesterol. Only 3.6% of cholesterol molecules contain more than one atom of ^{13}C, and only 0.33% contain more than two atoms of ^{13}C.

THE NORMAL DISTRIBUTION

A binomial distribution describes a population whose members have only certain discrete values. This is the case with the number of ^{13}C atoms in cholesterol. A molecule of cholesterol, for example, can have two ^{13}C atoms, but it can not have 2.5 atoms of ^{13}C. A population is continuous if its members may take on any value. The efficiency of extracting cholesterol from a sample, for example, can take on any value between 0% (no cholesterol is extracted) and 100% (all cholesterol is extracted).

The most common continuous distribution is the Gaussian, or ***normal distribution***, the equation for which is

$$f(X) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(X-\mu)^2}{2\sigma^2}}$$

where μ is the expected mean for a population with n members

$$\mu = \frac{\sum_{i=1}^{n} X_i}{n}$$

and σ^2 is the population's variance.

$$\sigma^2 = \frac{\sum_{i=1}^{n} (X_i - \mu)^2}{n} \tag{5.4.1}$$

Examples of three normal distributions, each with an expected mean of 0 and with variances of 25, 100, or 400, respectively, are shown in Figure 4.4.2 . Two features of these normal distribution curves deserve attention. First, note that each normal distribution has a single maximum that corresponds to μ, and that the distribution is symmetrical about this value. Second, increasing the population's variance increases the distribution's spread and decreases its height; the area under the curve, however, is the same for all three distributions.

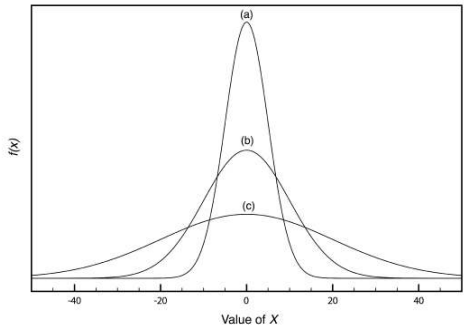


Figure 4.4.2 : Normal distribution curves for: (a) $\mu = 0$; $\sigma^2 = 25$ (b) $\mu = 0$; $\sigma^2 = 100$ (c) $\mu = 0$; $\sigma^2 = 400$.

The area under a normal distribution curve is an important and useful property as it is equal to the probability of finding a member of the population within a particular range of values. In Figure 4.4.2 , for example, 99.99% of the population shown in curve (a) have values of X between –20 and +20. For curve (c), 68.26% of the population's members have values of X between –20 and +20.

Because a normal distribution depends solely on μ and σ^2, the probability of finding a member of the population between any two limits is the same for all normally distributed populations. Figure 4.4.3 , for example, shows that 68.26% of the members of a normal distribution have a value within the range $\mu \pm 1\sigma$, and that 95.44% of population's members have values within the range $\mu \pm 2\sigma$. Only 0.27% members of a population have values that exceed the expected mean by more than $\pm\ 3\sigma$. Additional ranges and probabilities are gathered together in the probability table included in Appendix 3. As shown in Example 4.4.2 , if we know the mean and the standard deviation for a normally distributed population, then we can determine the percentage of the population between any defined limits.

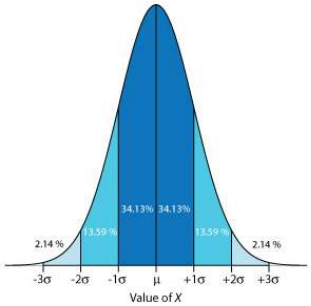


Figure 4.4.3 : Normal distribution curve showing the area under the curve for several different ranges of values of X.

EXAMPLE 4.4.2

The amount of aspirin in the analgesic tablets from a particular manufacturer is known to follow a normal distribution with $\mu = 250$ mg and $\sigma = 5$. In a random sample of tablets from the production line, what percentage are expected to contain between 243 and 262 mg of aspirin?

Solution

We do not determine directly the percentage of tablets between 243 mg and 262 mg of aspirin. Instead, we first find the percentage of tablets with less than 243 mg of aspirin and the percentage of tablets having more than 262 mg of aspirin. Subtracting these results from

100%, gives the percentage of tablets that contain between 243 mg and 262 mg of aspirin.

To find the percentage of tablets with less than 243 mg of aspirin or more than 262 mg of aspirin we calculate the deviation, *z*, of each limit from μ in terms of the population's standard deviation, σ

$$z = \frac{X - \mu}{\sigma}$$

where *X* is the limit in question. The deviation for the lower limit is

$$z_{lower} = \frac{243 - 250}{5} = -1.4$$

and the deviation for the upper limit is

$$z_{upper} = \frac{262 - 250}{5} = +2.4$$

Using the table in Appendix 3, we find that the percentage of tablets with less than 243 mg of aspirin is 8.08%, and that the percentage of tablets with more than 262 mg of aspirin is 0.82%. Therefore, the percentage of tablets containing between 243 and 262 mg of aspirin is

$$100.00\% - 8.08\% - 0.82\% = 91.10\%$$

Figure 4.4.4 shows the distribution of aspiring in the tablets, with the area in blue showing the percentage of tablets containing between 243 mg and 262 mg of aspirin.

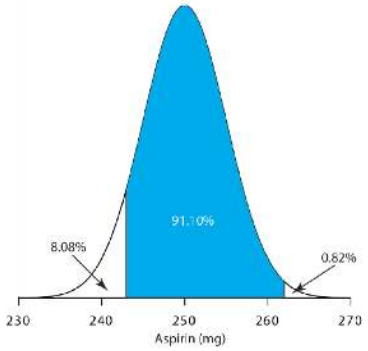


Figure 4.4.4 : Normal distribution for the population of aspirin tablets in Example 4.4.2 . The population's mean and standard deviation are 250 mg and 5 mg, respectively. The shaded area shows the percentage of tablets containing between 243 mg and 262 mg of aspirin.

? EXERCISE 4.4.1

What percentage of aspirin tablets will contain between 240 mg and 245 mg of aspirin if the population's mean is 250 mg and the population's standard deviation is 5 mg.

Answer

To find the percentage of tablets that contain less than 245 mg of aspirin we first calculate the deviation, *z*,

$$z = \frac{245 - 250}{5} = -1.00$$

and then look up the corresponding probability in Appendix 3, obtaining a value of 15.87%. To find the percentage of tablets that contain less than 240 mg of aspirin we find that

$$z = \frac{240 - 250}{5} = -2.00$$

which corresponds to 2.28%. The percentage of tablets containing between 240 and 245 mg of aspiring is 15.87% – 2.28% = 13.59%.

CONFIDENCE INTERVALS FOR POPULATIONS

If we select at random a single member from a population, what is its most likely value? This is an important question, and, in one form or another, it is at the heart of any analysis in which we wish to extrapolate from a sample to the sample's parent population. One of the most important features of a population's probability distribution is that it provides a way to answer this question.

Figure 4.4.3 shows that for a normal distribution, 68.26% of the population's members have values within the range $\mu \pm 1\sigma$. Stating this another way, there is a 68.26% probability that the result for a single sample drawn from a normally distributed population is in the interval $\mu \pm 1\sigma$. In general, if we select a single sample we expect its value, X_i is in the range

$$X_i = \mu \pm z\sigma \tag{5.4.2}$$

where the value of z is how confident we are in assigning this range. Values reported in this fashion are called ***confidence intervals***. Equation 5.4.2, for example, is the confidence interval for a single member of a population. Table 4.4.2 gives the confidence intervals for several values of z. For reasons discussed later in the chapter, a 95% confidence level is a common choice in analytical chemistry.

When z = 1, we call this the 68.26% confidence interval.

Table 4.4.2 : Confidence Intervals for a Normal Distribution

z	Confidence Interval
0.50	38.30
1.00	68.26
1.50	86.64
1.96	95.00
2.00	95.44
2.50	98.76
3.00	99.73
3.50	99.95

EXAMPLE 4.4.3

What is the 95% confidence interval for the amount of aspirin in a single analgesic tablet drawn from a population for which μ is 250 mg and for which σ is 5?

Solution

Using Table 4.4.2 , we find that z is 1.96 for a 95% confidence interval. Substituting this into Equation 5.4.2 gives the confidence interval for a single tablet as

$$X_i = \mu \pm 1.96\sigma = 250 \text{ mg} \pm (1.96 \times 5) = 250 \text{ mg} \pm 10\text{mg}$$

A confidence interval of 250 mg ± 10 mg means that 95% of the tablets in the population contain between 240 and 260 mg of aspirin.

Alternatively, we can rewrite Equation 5.4.2 so that it gives the confidence interval is for μ based on the population's standard deviation and the value of a single member drawn from the population.

$$\mu = X_i \pm z\sigma \tag{5.4.3}$$

EXAMPLE 4.4.4

The population standard deviation for the amount of aspirin in a batch of analgesic tablets is known to be 7 mg of aspirin. If you randomly select and analyze a single tablet and find that it contains 245 mg of aspirin, what is the 95% confidence interval for the population's mean?

Solution

The 95% confidence interval for the population mean is given as

$$\mu = X_i \pm z\sigma = 245 \text{ mg} \pm (1.96 \times 7) \text{ mg} = 245 \text{ mg} \pm 14 \text{ mg}$$

Therefore, based on this one sample, we estimate that there is 95% probability that the population's mean, μ, lies within the range of 231 mg to 259 mg of aspirin.

Note the qualification that the prediction for μ is based on one sample; a different sample likely will give a different 95% confidence interval. Our result here, therefore, is an estimate for μ based on this one sample.

It is unusual to predict the population's expected mean from the analysis of a single sample; instead, we collect n samples drawn from a population of known σ, and report the mean, $\overline{X}$. The standard deviation of the mean, $\sigma_{\overline{X}}$, which also is known as the ***standard error of the mean***, is

$$\sigma_{\overline{X}} = \frac{\sigma}{\sqrt{n}}$$

The confidence interval for the population's mean, therefore, is

$$\mu = \overline{\overline{X}} \pm \frac{z\sigma}{\sqrt{n}}$$

EXAMPLE 4.4.5

What is the 95% confidence interval for the analgesic tablets in Example 4.4.4 , if an analysis of five tablets yields a mean of 245 mg of aspirin?

Solution

In this case the confidence interval is

$$\mu = 245 \text{ mg} \pm \frac{1.96 \times 7}{\sqrt{5}} \text{ mg} = 245 \text{ mg} \pm 6 \text{ mg}$$

We estimate a 95% probability that the population's mean is between 239 mg and 251 mg of aspirin. As expected, the confidence interval when using the mean of five samples is smaller than that for a single sample.

EXERCISE 4.4.2

An analysis of seven aspirin tablets from a population known to have a standard deviation of 5, gives the following results in mg aspirin per tablet:

$$246 \quad 249 \quad 255 \quad 251 \quad 251 \quad 247 \quad 250$$

What is the 95% confidence interval for the population's expected mean?

Answer

The mean is 249.9 mg aspirin/tablet for this sample of seven tablets. For a 95% confidence interval the value of z is 1.96, which makes the confidence interval

$$249.9 \pm \frac{1.96 \times 5}{\sqrt{7}} = 249.9 \pm 3.7 \approx 250 \text{ mg} \pm 4 \text{ mg}$$

PROBABILITY DISTRIBUTIONS FOR SAMPLES

In Examples 4.4.2 –4.4.5 we assumed that the amount of aspirin in analgesic tablets is normally distributed. Without analyzing every member of the population, how can we justify this assumption? In a situation where we cannot study the whole population, or when we cannot predict the mathematical form of a population's probability distribution, we must deduce the distribution from a limited sampling of its members.

SAMPLE DISTRIBUTIONS AND THE CENTRAL LIMIT THEOREM

Let's return to the problem of determining a penny's mass to explore further the relationship between a population's distribution and the distribution of a sample drawn from that population. The two sets of data in Table 4.4.1 are too small to provide a useful picture of a sample's distribution, so we will use the larger sample of 100 pennies shown in Table 4.4.3 . The mean and the standard deviation for this sample are 3.095 g and 0.0346 g, respectively.

Table 4.4.3 : Masses for a Sample of 100 Circulating U. S. Pennies

Penny	Weight (g)	Penny	Weight (g)	Penny	Weight (g)	Penny	Weight (g)
1	3.126	26	3.073	51	3.101	76	3.086
2	3.140	27	3.084	52	3.049	77	3.123
3	3.092	28	3.148	53	3.082	78	3.115
4	3.095	29	3.047	54	3.142	79	3.055
5	3.080	30	3.121	55	3.082	80	3.057
6	3.065	31	3.116	56	3.066	81	3.097
7	3.117	32	3.005	57	3.128	82	3.066
8	3.034	33	3.115	58	3.112	83	3.113
9	3.126	34	3.103	59	3.085	84	3.102
10	3.057	35	3.086	60	3.086	85	3.033
11	3.053	36	3.103	61	3.084	86	3.112
12	3.099	37	3.049	62	3.104	87	3.103
13	3.065	38	2.998	63	3.107	88	3.198
14	3.059	39	3.063	64	3.093	89	3.103
15	3.068	40	3.055	65	3.126	90	3.126
16	3.060	41	3.181	66	3.138	91	3.111
17	3.078	42	3.108	67	3.131	92	3.126
18	3.125	43	3.114	68	3.120	93	3.052
19	3.090	44	3.121	69	3.100	94	3.113
20	3.100	45	3.105	70	3.099	95	3.085
21	3.055	46	3.078	71	3.097	96	3.117
22	3.105	47	3.147	72	3.091	97	3.142
23	3.063	48	3.104	73	3.077	98	3.031
24	3.083	49	3.146	74	3.178	99	3.083
25	3.065	50	3.095	75	3.054	100	3.104

A ***histogram*** (Figure 4.4.5) is a useful way to examine the data in Table 4.4.3 . To create the histogram, we divide the sample into intervals, by mass, and determine the percentage of pennies within each interval (Table 4.4.4). Note that the sample's mean is the midpoint of the histogram.

Table 4.4.4 : Frequency Distribution for the Data in Table 4.4.3

Mass Interval	Frequency (as % of Sample)	Mass Interval	Frequency (as % of Sample)
2.991 – 3.009	2	3.105 – 3.123	19
3.010 – 3.028	0	3.124 – 3.142	12
3.029 – 3.047	4	3.143 – 3.161	3
3.048 – 3.066	19	3.162 – 3.180	1
3.067 – 3.085	14	3.181 – 3.199	2
3.086 – 3.104	24	3.200 – 3.218	0

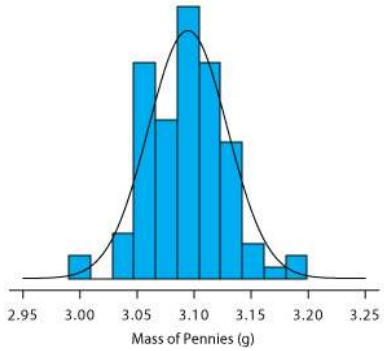


Figure 4.4.5 : The blue bars show a histogram for the data in Table 4.4.3 . The height of each bar corresponds to the percentage of pennies within one of the mass intervals in Table 4.4.4 . Superimposed on the histogram is a normal distribution curve based on the assumption that μ and σ^2 for the population are equivalent to $\overline{X}$ and σ^2 for the sample. The total area of the histogram's bars and the area under the normal distribution curve are equal.

Figure 4.4.5 also includes a normal distribution curve for the population of pennies, based on the assumption that the mean and the variance for the sample are appropriate estimates for the population's mean and variance. Although the histogram is not perfectly symmetric in shape, it provides a good approximation of the normal distribution curve, suggesting that the sample of 100 pennies is normally distributed. It is easy to imagine that the histogram will approximate more closely a normal distribution if we include additional pennies in our sample.

We will not offer a formal proof that the sample of pennies in Table 4.4.3 and the population of all circulating U. S. pennies are normally distributed; however, the evidence in Figure 4.4.5 strongly suggests this is true. Although we cannot claim that the results of all experiments are normally distributed, in most cases our data are normally distributed. According to the ***central limit theorem***, when a measurement is subject to a variety of indeterminate errors, the results for that measurement will approximate a normal distribution [Mark, H.; Workman, J. *Spectroscopy* **1988**, *3*, 44–48]. The central limit theorem holds true even if the individual sources of indeterminate error are not normally distributed. The chief limitation to the central limit theorem is that the sources of indeterminate error must be independent and of similar magnitude so that no one source of error dominates the final distribution.

An additional feature of the central limit theorem is that a distribution of means for samples drawn from a population with any distribution will approximate closely a normal distribution if the size of each sample is sufficiently large. For example, Figure 4.4.6 shows the distribution for two samples of 10 000 drawn from a uniform distribution in which every value between 0 and 1 occurs with an equal frequency. For samples of size n = 1, the resulting distribution closely approximates the population's uniform distribution. The distribution of the means for samples of size n = 10, however, closely approximates a normal distribution.

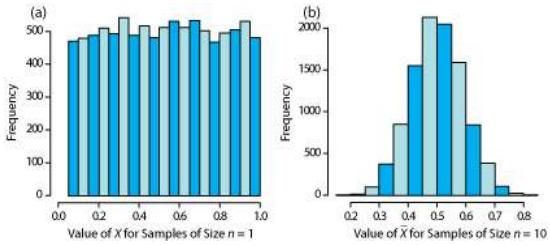


Figure 4.4.6 : Histograms for (a) 10 000 samples of size n = 1 drawn from a uniform distribution with a minimum value of 0 and a maximum value of 1, and (b) the means for 10000 samples of size n = 10 drawn from the same uniform distribution. For (a) the mean of the 10 000 samples is 0.5042, and for (b) the mean of the 10 000 samples is 0.5006. Note that for (a) the distribution closely approximates a uniform distribution in which every possible result is equally likely, and that for (b) the distribution closely approximates a normal distribution.

You might reasonably ask whether this aspect of the central limit theorem is important as it is unlikely that we will complete 10 000 analyses, each of which is the average of 10 individual trials. This is deceiving. When we acquire a sample of soil, for example, it consists of many individual particles each of which is an individual sample of the soil. Our analysis of this sample, therefore, gives the mean for this large number of individual soil particles. Because of this, the central limit theorem is relevant. For a discussion of circumstances where the central limit theorem may not apply, see "Do You Reckon It's Normally Distributed?", the full reference for which is Majewsky, M.; Wagner, M.; Farlin, J. *Sci. Total Environ.* **2016**, *548–549*, 408–409.

DEGREES OF FREEDOM

Did you notice the differences between the equation for the variance of a population and the variance of a sample? If not, here are the two equations:

$$\sigma^2 = \frac{\sum_{i=1}^{n}(X_i - \mu)^2}{n}$$

$$s^2 = \frac{\sum_{i=1}^{n}(X_i - \overline{X})^2}{n-1}$$

Both equations measure the variance around the mean, using μ for a population and $\overline{X}$ for a sample. Although the equations use different measures for the mean, the intention is the same for both the sample and the population. A more interesting difference is between the denominators of the two equations. When we calculate the population's variance we divide the numerator by the population's size, *n*; for the sample's variance, however, we divide by *n* – 1, where *n* is the sample's size. Why do we divide by *n* – 1 when we calculate the sample's variance?

A variance is the average squared deviation of individual results relative to the mean. When we calculate an average we divide the sum by the number of independent measurements, or ***degrees of freedom***, in the calculation. For the population's variance, the degrees of freedom is equal to the population's size, *n*. When we measure every member of a population we have complete information about the population.

When we calculate the sample's variance, however, we replace μ with $\overline{X}$, which we also calculate using the same data. If there are *n* members in the sample, we can deduce the value of the nth member from the remaining *n* – 1 members and the mean. For example, if \(*n* = 5\) and we know that the first four samples are 1, 2, 3 and 4, and that the mean is 3, then the fifth member of the sample must be

$$X_5 = (\overline{X} \times n) - X_1 - X_2 - X_3 - X_4 = (3 \times 5) - 1 - 2 - 3 - 4 = 5$$

Because we have just four independent measurements, we have lost one degree of freedom. Using *n* – 1 in place of *n* when we calculate the sample's variance ensures that s^2 is an unbiased estimator of σ^2.

> Here is another way to think about degrees of freedom. We analyze samples to make predictions about the underlying population. When our sample consists of *n* measurements we cannot make more than *n* independent predictions about the population. Each time we estimate a parameter, such as the population's mean, we lose a degree of freedom. If there are *n* degrees of freedom for calculating the sample's mean, then *n* – 1 degrees of freedom remain when we calculate the sample's variance.

CONFIDENCE INTERVALS FOR SAMPLES

Earlier we introduced the confidence interval as a way to report the most probable value for a population's mean, μ

$$\mu = \overline{X} \pm \frac{z\sigma}{\sqrt{n}} \tag{5.4.4}$$

where $\overline{X}$ is the mean for a sample of size *n*, and σ is the population's standard deviation. For most analyses we do not know the population's standard deviation. We can still calculate a confidence interval, however, if we make two modifications to Equation 5.4.4.

The first modification is straightforward—we replace the population's standard deviation, σ, with the sample's standard deviation, *s*. The second modification is not as obvious. The values of *z* in Table 4.4.2 are for a normal distribution, which is a function of $sigma^2$, not s^2. Although the sample's variance, s^2, is an unbiased estimate of the population's variance, σ^2, the value of s^2 will only rarely equal σ^2. To account for this uncertainty in estimating σ^2, we replace the variable *z* in Equation 5.4.4 with the variable *t*, where *t* is defined such that $t \geq z$ at all confidence levels.

$$\mu = \overline{X} \pm \frac{ts}{\sqrt{n}} \tag{5.4.5}$$

Values for *t* at the 95% confidence level are shown in Table 4.4.5 . Note that *t* becomes smaller as the number of degrees of freedom increases, and that it approaches *z* as *n* approaches infinity. The larger the sample, the more closely its confidence interval for a sample (Equation 5.4.5) approaches the confidence interval for the population (Equation 5.4.3). Appendix 4 provides additional values of *t* for other confidence levels.

Table 4.4.5 : Values of t for a 95% Confidence Interval

Degrees of Freedom	*t*	Degrees of Freedom	*t*	Degrees of Freedom	*t*	Degrees of Freedom	*t*
1	12.706	6	2.447	12	2.179	30	2.042
2	4.303	7	2.365	14	2.145	40	2.021
3	3.181	8	2.306	16	2.120	60	2.000
4	2.776	9	2.262	18	2.101	100	1.984
5	2.571	10	2.228	20	2.086	\(\infty	1.960

✔ EXAMPLE 4.4.6

What are the 95% confidence intervals for the two samples of pennies in Table 4.4.1 ?

Solution

The mean and the standard deviation for first experiment are, respectively, 3.117 g and 0.051 g. Because the sample consists of seven measurements, there are six degrees of freedom. The value of *t* from Table 4.4.5 , is 2.447. Substituting into Equation 5.4.5 gives

$$\mu = 3.117\ \text{g} \pm \frac{2.447 \times 0.051\ \text{g}}{\sqrt{7}} = 3.117\ \text{g} \pm 0.047\ \text{g}$$

For the second experiment the mean and the standard deviation are 3.081 g and 0.073 g, respectively, with four degrees of freedom. The 95% confidence interval is

$$\mu = 3.081\ \text{g} \pm \frac{2.776 \times 0.037\ \text{g}}{\sqrt{5}} = 3.081\ \text{g} \pm 0.046\ \text{g}$$

Based on the first experiment, the 95% confidence interval for the population's mean is 3.070–3.164 g. For the second experiment, the 95% confidence interval is 3.035–3.127 g. Although the two confidence intervals are not identical—remember, each confidence interval provides a different estimate for μ—the mean for each experiment is contained within the other experiment's confidence interval. There also is an appreciable overlap of the two confidence intervals. Both of these observations are consistent with samples drawn from the same population.

Note that our comparison of these two confidence intervals at this point is somewhat vague and unsatisfying. We will return to this point in the next section, when we consider a statistical approach to comparing the results of experiments.

? EXERCISE 4.4.3

What is the 95% confidence interval for the sample of 100 pennies in Table 4.4.3 ? The mean and the standard deviation for this sample are 3.095 g and 0.0346 g, respectively. Compare your result to the confidence intervals for the samples of pennies in Table 4.4.1 .

Answer

With 100 pennies, we have 99 degrees of freedom for the mean. Although Table 4.4.3 does not include a value for *t*(0.05, 99), we can approximate its value by using the values for *t*(0.05, 60) and *t*(0.05, 100) and by assuming a linear change in its value.

$$t(0.05, 99) = t(0.05, 60) - \frac{39}{40}\{t(0.05, 60) - t(0.05, 100\})$$

$$t(0.05, 99) = 2.000 - \frac{39}{40}\{2.000 - 1.984\} = 1.9844$$

The 95% confidence interval for the pennies is

$$3.095 \pm \frac{1.9844 \times 0.0346}{\sqrt{100}} = 3.095\ \text{g} \pm 0.007\ \text{g}$$

From Example 4.4.6 , the 95% confidence intervals for the two samples in Table 4.4.1 are 3.117 g ± 0.047 g and 3.081 g ± 0.046 g. As expected, the confidence interval for the sample of 100 pennies is much smaller than that for the two smaller samples of pennies. Note, as well, that the confidence interval for the larger sample fits within the confidence intervals for the two smaller samples.

A CAUTIONARY STATEMENT

There is a temptation when we analyze data simply to plug numbers into an equation, carry out the calculation, and report the result. This is never a good idea, and you should develop the habit of reviewing and evaluating your data. For example, if you analyze five samples and report an analyte's mean concentration as 0.67 ppm with a standard deviation of 0.64 ppm, then the 95% confidence interval is

$$\mu = 0.67\ \text{ppm} \pm \frac{2.776 \times 0.64\ \text{ppm}}{\sqrt{5}} = 0.67\ \text{ppm} \pm 0.79\ \text{ppm}$$

This confidence interval estimates that the analyte's true concentration is between –0.12 ppm and 1.46 ppm. Including a negative concentration within the confidence interval should lead you to reevaluate your data or your conclusions. A closer examination of your data may convince you that the standard deviation is larger than expected, making the confidence interval too broad, or you may conclude that the analyte's concentration is too small to report with confidence.

> We will return to the topic of detection limits near the end of this chapter.

Here is a second example of why you should closely examine your data: results obtained on samples drawn at random from a normally distributed population must be random. If the results for a sequence of samples show a regular pattern or trend, then the underlying population either is not normally distributed or there is a time-dependent determinate error. For example, if we randomly select 20 pennies and find that the mass of each penny is greater than that for the preceding penny, then we might suspect that our balance is drifting out of calibration.

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5.5: STATISTICAL ANALYSIS OF DATA

A confidence interval is a useful way to report the result of an analysis because it sets limits on the expected result. In the absence of determinate error, a confidence interval based on a sample's mean indicates the range of values in which we expect to find the population's mean. When we report a 95% confidence interval for the mass of a penny as 3.117 g ± 0.047 g, for example, we are stating that there is only a 5% probability that the penny's expected mass is less than 3.070 g or more than 3.164 g.

Because a confidence interval is a statement of probability, it allows us to consider comparative questions, such as these: "Are the results for a newly developed method to determine cholesterol in blood significantly different from those obtained using a standard method?" or "Is there a significant variation in the composition of rainwater collected at different sites downwind from a coal-burning utility plant?" In this section we introduce a general approach to the statistical analysis of data. Specific statistical tests are presented in Section 4.6.

> The reliability of significance testing recently has received much attention—see Nuzzo, R. "Scientific Method: Statistical Errors," *Nature*, **2014**, *506*, 150–152 for a general discussion of the issues—so it is appropriate to begin this section by noting the need to ensure that our data and our research question are compatible so that we do not read more into a statistical analysis than our data allows; see Leek, J. T.; Peng, R. D. "What is the Question? *Science*, **2015**, *347*, 1314-1315 for a use-ul discussion of six common research questions.
>
> In the context of analytical chemistry, significance testing often accompanies an exploratory data analysis (Is there a reason to suspect that there is a difference between these two analytical methods when applied to a common sample?) or an inferential data analysis (Is there a reason to suspect that there is a relationship between these two independent measurements?). A statistically significant result for these types of analytical research questions generally leads to the design of additional experiments better suited to making predictions or to explaining an underlying causal relationship. A significance test is the first step toward building a greater understanding of an analytical problem, not the final answer to that problem.

SIGNIFICANCE TESTING

Let's consider the following problem. To determine if a medication is effective in lowering blood glucose concentrations, we collect two sets of blood samples from a patient. We collect one set of samples immediately before we administer the medication, and collect the second set of samples several hours later. After analyzing the samples, we report their respective means and variances. How do we decide if the medication was successful in lowering the patient's concentration of blood glucose?

One way to answer this question is to construct a normal distribution curve for each sample, and to compare the two curves to each other. Three possible outcomes are shown in Figure 4.5.1 . In Figure 4.5.1 a, there is a complete separation of the two normal distribution curves, which suggests the two samples are significantly different from each other. In Figure 4.5.1 b, the normal distribution curves for the two samples almost completely overlap, which suggests that the difference between the samples is insignificant. Figure 4.5.1 c, however, presents us with a dilemma. Although the means for the two samples seem different, the overlap of their normal distribution curves suggests that a significant number of possible outcomes could belong to either distribution. In this case the best we can do is to make a statement about the probability that the samples are significantly different from each other.

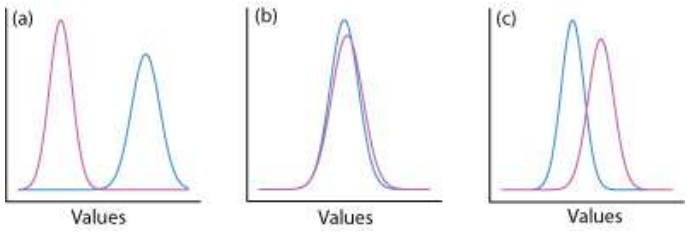


Figure 4.5.1 : Three examples of the possible relationships between the normal distribution curves for two samples. In (a) the curves do not overlap, which suggests that the samples are significantly different from each other. In (b) the two curves are almost identical, suggesting the samples are indistinguishable. The partial overlap of the curves in (c) means that the best we can do is evaluate the probability that there is a difference between the samples.

The process by which we determine the probability that there is a significant difference between two samples is called significance testing or hypothesis testing. Before we discuss specific examples we will first establish a general approach to conducting and interpreting a significance test.

CONSTRUCTING A SIGNIFICANCE TEST

The purpose of a ***significance test*** is to determine whether the difference between two or more results is sufficiently large that it cannot be explained by indeterminate errors. The first step in constructing a significance test is to state the problem as a yes or no question, such as "Is this medication effective at lowering a patient's blood glucose levels?" A null hypothesis and an alternative hypothesis define the two possible answers to our yes or no question. The ***null hypothesis***, H_0, is that indeterminate errors are sufficient to explain any differences between our results. The ***alternative hypothesis***, H_A, is that the differences in our results are too great to be explained by random error and that they must be determinate in nature. We test the null hypothesis, which we either retain or reject. If we reject the null hypothesis, then we must accept the alternative hypothesis and conclude that the difference is significant.

Failing to reject a null hypothesis is not the same as accepting it. We retain a null hypothesis because we have insufficient evidence to prove it incorrect. It is impossible to prove that a null hypothesis is true. This is an important point and one that is easy to forget. To appreciate this point let's return to our sample of 100 pennies in Table 4.4.3. After looking at the data we might propose the following null and alternative hypotheses.

H_0: The mass of a circulating U.S. penny is between 2.900 g and 3.200 g

H_A: The mass of a circulating U.S. penny may be less than 2.900 g or more than 3.200 g

To test the null hypothesis we find a penny and determine its mass. If the penny's mass is 2.512 g then we can reject the null hypothesis and accept the alternative hypothesis. Suppose that the penny's mass is 3.162 g. Although this result increases our confidence in the null hypothesis, it does not prove that the null hypothesis is correct because the next penny we sample might weigh less than 2.900 g or more than 3.200 g.

After we state the null and the alternative hypotheses, the second step is to choose a confidence level for the analysis. The confidence level defines the probability that we will reject the null hypothesis when it is, in fact, true. We can express this as our confidence that we are correct in rejecting the null hypothesis (e.g. 95%), or as the probability that we are incorrect in rejecting the null hypothesis. For the latter, the confidence level is given as α, where

$$\alpha = 1 - \frac{\text{confidence interval (\%)}}{100} \tag{5.5.1}$$

For a 95% confidence level, α is 0.05.

> In this textbook we use α to represent the probability that we incorrectly reject the null hypothesis. In other textbooks this probability is given as *p* (often read as "p- value"). Although the symbols differ, the meaning is the same.

The third step is to calculate an appropriate test statistic and to compare it to a critical value. The test statistic's critical value defines a breakpoint between values that lead us to reject or to retain the null hypothesis, which is the fourth, and final, step of a significance test. How we calculate the test statistic depends on what we are comparing, a topic we cover in Section 4.6. The last step is to either retain the null hypothesis, or to reject it and accept the alternative hypothesis.

> The four steps for a statistical analysis of data using a significance test:
>
> 1. Pose a question, and state the null hypothesis, H_0, and the alternative hypothesis, H_A.
> 2. Choose a confidence level for the statistical analysis.
> 3. Calculate an appropriate test statistic and compare it to a critical value.
> 4. Either retain the null hypothesis, or reject it and accept the alternative hypothesis.

ONE-TAILED AND TWO-TAILED SIGNIFICANCE TESTS

Suppose we want to evaluate the accuracy of a new analytical method. We might use the method to analyze a Standard Reference Material that contains a known concentration of analyte, μ. We analyze the standard several times, obtaining a mean value, $\overline{X}$, for the analyte's concentration. Our null hypothesis is that there is no difference between $\overline{X}$ and μ

$$H_0 \colon \overline{X} = \mu$$

If we conduct the significance test at $\alpha = 0.05$, then we retain the null hypothesis if a 95% confidence interval around $\overline{X}$ contains μ. If the alternative hypothesis is

$$H_A \colon \overline{X} \neq \mu$$

then we reject the null hypothesis and accept the alternative hypothesis if μ lies in the shaded areas at either end of the sample's probability distribution curve (Figure 4.5.2 a). Each of the shaded areas accounts for 2.5% of the area under the probability distribution curve, for a total

of 5%. This is a ***two-tailed significance test*** because we reject the null hypothesis for values of μ at either extreme of the sample's probability distribution curve.

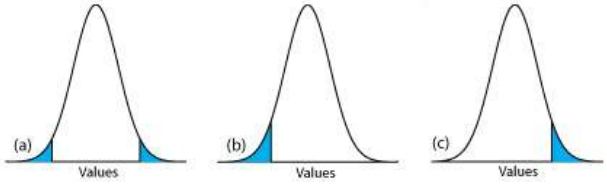


Figure 4.5.2 : Examples of (a) two-tailed, and (b, c) one-tailed, significance test of $\overline{X}$ and μ. The probability distribution curves, which are normal distributions, are based on the sample's mean and standard deviation. For α = 0.05, the blue areas account for 5% of the area under the curve. If the value of μ falls within the blue areas, then we reject the null hypothesis and accept the alternative hypothesis. We retain the null hypothesis if the value of μ falls within the unshaded area of the curve.

We also can write the alternative hypothesis in two additional ways

$$H_A: \overline{\overline{X}} > \mu$$

$$H_A: \overline{\overline{X}} < \mu$$

rejecting the null hypothesis if n falls within the shaded areas shown in Figure 4.5.2 b or Figure 4.5.2 c, respectively. In each case the shaded area represents 5% of the area under the probability distribution curve. These are examples of a ***one-tailed significance test***.

For a fixed confidence level, a two-tailed significance test is the more conservative test because rejecting the null hypothesis requires a larger difference between the parameters we are comparing. In most situations we have no particular reason to expect that one parameter must be larger (or must be smaller) than the other parameter. This is the case, for example, when we evaluate the accuracy of a new analytical method. A two-tailed significance test, therefore, usually is the appropriate choice.

We reserve a one-tailed significance test for a situation where we specifically are interested in whether one parameter is larger (or smaller) than the other parameter. For example, a one-tailed significance test is appropriate if we are evaluating a medication's ability to lower blood glucose levels. In this case we are interested only in whether the glucose levels after we administer the medication are less than the glucose levels before we initiated treatment. If a patient's blood glucose level is greater after we administer the medication, then we know the answer—the medication did not work—and do not need to conduct a statistical analysis.

ERROR IN SIGNIFICANCE TESTING

Because a significance test relies on probability, its interpretation is subject to error. In a significance test, a defines the probability of rejecting a null hypothesis that is true. When we conduct a significance test at $\alpha = 0.05$, there is a 5% probability that we will incorrectly reject the null hypothesis. This is known as a ***type 1 error***, and its risk is always equivalent to α. A type 1 error in a two-tailed or a one-tailed significance tests corresponds to the shaded areas under the probability distribution curves in Figure 4.5.2 .

A second type of error occurs when we retain a null hypothesis even though it is false. This is as a ***type 2 error***, and the probability of its occurrence is β. Unfortunately, in most cases we cannot calculate or estimate the value for β. The probability of a type 2 error, however, is inversely proportional to the probability of a type 1 error.

Minimizing a type 1 error by decreasing α increases the likelihood of a type 2 error. When we choose a value for α we must compromise between these two types of error. Most of the examples in this text use a 95% confidence level ($\alpha = 0.05$) because this usually is a reasonable compromise between type 1 and type 2 errors for analytical work. It is not unusual, however, to use a more stringent (e.g. $\alpha = 0.01$) or a more lenient (e.g. $\alpha = 0.10$) confidence level when the situation calls for it.

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5.6: STATISTICAL METHODS FOR NORMAL DISTRIBUTIONS

The most common distribution for our results is a normal distribution. Because the area between any two limits of a normal distribution curve is well defined, constructing and evaluating significance tests is straightforward.

COMPARING $\overline{X}$ TO μ

One way to validate a new analytical method is to analyze a sample that contains a known amount of analyte, μ. To judge the method's accuracy we analyze several portions of the sample, determine the average amount of analyte in the sample, $\overline{X}$, and use a significance test to compare $\overline{X}$ to μ. Our null hypothesis is that the difference between $\overline{X}$ and μ is explained by indeterminate errors that affect the determination of $\overline{X}$. The alternative hypothesis is that the difference between $\overline{X}$ and μ is too large to be explained by indeterminate error.

$$H_0: \overline{X} = \mu$$

$$H_A: \overline{X} \neq \mu$$

The test statistic is t_{exp}, which we substitute into the confidence interval for μ given by Equation 4.4.5

$$\mu = \overline{X} \pm \frac{t_{exp} s}{\sqrt{n}} \tag{5.6.1}$$

Rearranging this equation and solving for t_{exp}

$$t_{exp} = \frac{|\mu - \overline{X}|\sqrt{n}}{s} \tag{5.6.2}$$

gives the value for t_{exp} when μ is at either the right edge or the left edge of the sample's confidence interval (Figure 4.6.1 a)

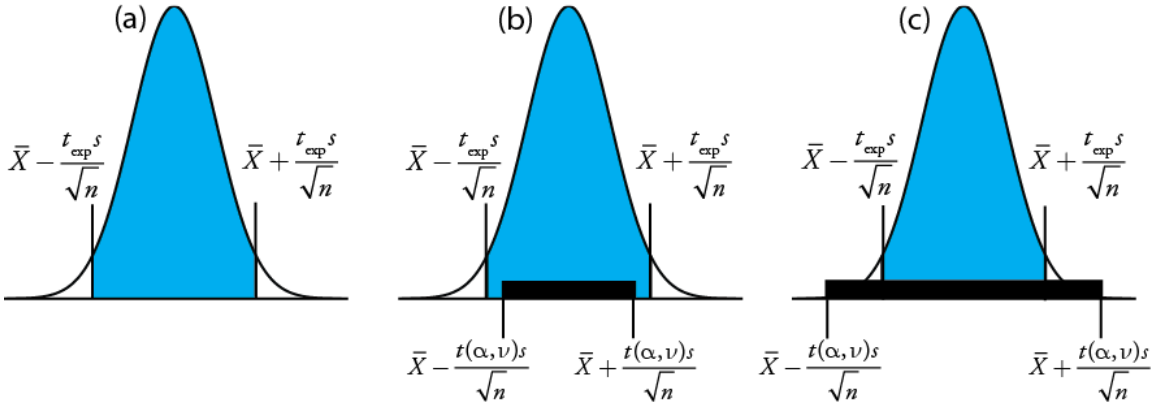


Figure 4.6.1 : Relationship between a confidence interval and the result of a significance test. (a) The shaded area under the normal distribution curve shows the sample's confidence interval for μ based on t_{exp}. The solid bars in (b) and (c) show the expected confidence intervals for μ explained by indeterminate error given the choice of α and the available degrees of freedom, ν. For (b) we reject the null hypothesis because portions of the sample's confidence interval fall outside the confidence interval explained by indeterminate error. In the case of (c) we retain the null hypothesis because the confidence interval explained by indeterminate error completely encompasses the sample's confidence interval.

To determine if we should retain or reject the null hypothesis, we compare the value of t_{exp} to a critical value, $t(\alpha,\nu)$, where α is the confidence level and ν is the degrees of freedom for the sample. The critical value $t(\alpha,\nu)$ defines the largest confidence interval explained by indeterminate error. If $t_{exp} > t(\alpha,\nu)$, then our sample's confidence interval is greater than that explained by indeterminate errors (Figure 4.6.1 b). In this case, we reject the null hypothesis and accept the alternative hypothesis. If $t_{exp} \leq t(\alpha,\nu)$, then our sample's confidence interval is smaller than that explained by indeterminate error, and we retain the null hypothesis (Figure 4.6.1 c). Example 4.6.1 provides a typical application of this significance test, which is known as a **t-test** of $\overline{X}$ to μ.

You will find values for $t(\alpha,\nu)$ in Appendix 4.

Another name for the *t*-test is Student's *t*-test. Student was the pen name for William Gossett (1876-1927) who developed the *t*-test while working as a statistician for the Guiness Brewery in Dublin, Ireland. He published under the name Student because the brewery did not want its competitors to know they were using statistics to help improve the quality of their products.

EXAMPLE 4.6.1

Before determining the amount of Na_2CO_3 in a sample, you decide to check your procedure by analyzing a standard sample that is 98.76% w/w Na_2CO_3. Five replicate determinations of the %w/w Na_2CO_3 in the standard gave the following results

$$98.71\% \quad 98.59\% \quad 98.62\% \quad 98.44\% \quad 98.58\%$$

Using $\alpha = 0.05$, is there any evidence that the analysis is giving inaccurate results?

Solution

The mean and standard deviation for the five trials are

$$\overline{X} = 98.59 \qquad s = 0.0973$$

Because there is no reason to believe that the results for the standard must be larger or smaller than μ, a two-tailed *t*-test is appropriate. The null hypothesis and alternative hypothesis are

$$H_0 : \overline{X} = \mu \qquad H_A : \overline{X} \neq \mu$$

The test statistic, t_{exp}, is

$$t_{exp} = \frac{|\mu - \overline{X}|\sqrt{n}}{s} = \frac{|98.76 - 98.59|\sqrt{5}}{0.0973} = 3.91$$

The critical value for *t*(0.05, 4) from Appendix 4 is 2.78. Since t_{exp} is greater than *t*(0.05, 4), we reject the null hypothesis and accept the alternative hypothesis. At the 95% confidence level the difference between $\overline{X}$ and μ is too large to be explained by indeterminate sources of error, which suggests there is a determinate source of error that affects the analysis.

There is another way to interpret the result of this *t*-test. Knowing that t_{exp} is 3.91 and that there are 4 degrees of freedom, we use Appendix 4 to estimate the α value corresponding to a $t(\alpha, 4)$ of 3.91. From Appendix 4, *t*(0.02, 4) is 3.75 and *t*(0.01, 4) is 4.60. Although we can reject the null hypothesis at the 98% confidence level, we cannot reject it at the 99% confidence level. For a discussion of the advantages of this approach, see J. A. C. Sterne and G. D. Smith "Sifting the evidence—what's wrong with significance tests?" *BMJ* **2001**, *322*, 226–231.

EXERCISE 4.6.1

To evaluate the accuracy of a new analytical method, an analyst determines the purity of a standard for which μ is 100.0%, obtaining the following results.

$$99.28\% \quad 103.93\% \quad 99.43\% \quad 99.84\% \quad 97.60\% \quad 96.70\% \quad 98.02\%$$

Is there any evidence at $\alpha = 0.05$ that there is a determinate error affecting the results?

Answer

The null hypothesis is $H_0 : \overline{X} = \mu$ and the alternative hypothesis is $H_A : \overline{X} \neq \mu$. The mean and the standard deviation for the data are 99.26% and 2.35%, respectively. The value for t_{exp} is

$$t_{exp} = \frac{|100.0 - 99.26|\sqrt{7}}{2.35} = 0.833$$

and the critical value for *t*(0.05, 6) is 2.477. Because t_{exp} is less than *t*(0.05, 6) we retain the null hypothesis and have no evidence for a significant difference between $\overline{X}$ and μ.

Earlier we made the point that we must exercise caution when we interpret the result of a statistical analysis. We will keep returning to this point because it is an important one. Having determined that a result is inaccurate, as we did in Example 4.6.1 , the next step is to identify and to correct the error. Before we expend time and money on this, however, we first should examine critically our data. For example, the smaller the value of *s*, the larger the value of t_{exp}. If the standard deviation for our analysis is unrealistically small, then the probability of a type 2 error increases. Including a few additional replicate analyses of the standard and reevaluating the *t*-test may strengthen our evidence for a determinate error, or it may show us that there is no evidence for a determinate error.

COMPARING s^2 TO σ^2

If we analyze regularly a particular sample, we may be able to establish an expected variance, σ^2, for the analysis. This often is the case, for example, in a clinical lab that analyze hundreds of blood samples each day. A few replicate analyses of a single sample gives a sample variance, s^2, whose value may or may not differ significantly from σ^2.

We can use an *F*-test to evaluate whether a difference between s^2 and σ^2 is significant. The null hypothesis is $H_0\colon s^2 = \sigma^2$ and the alternative hypothesis is $H_A\colon s^2 \neq \sigma^2$. The test statistic for evaluating the null hypothesis is F_{exp}, which is given as either

$$F_{exp} = \frac{s^2}{\sigma^2} \text{ if } s^2 > \sigma^2 \text{ or } F_{exp} = \frac{\sigma^2}{s^2} \text{ if } \sigma^2 > s^2 \tag{5.6.3}$$

depending on whether s^2 is larger or smaller than σ^2. This way of defining F_{exp} ensures that its value is always greater than or equal to one.

If the null hypothesis is true, then F_{exp} should equal one; however, because of indeterminate errors F_{exp} usually is greater than one. A critical value, $F(\alpha, \nu_{num}, \nu_{den})$, is the largest value of F_{exp} that we can attribute to indeterminate error given the specified significance level, α, and the degrees of freedom for the variance in the numerator, ν_{num}, and the variance in the denominator, ν_{den}. The degrees of freedom for s^2 is $n - 1$, where n is the number of replicates used to determine the sample's variance, and the degrees of freedom for σ^2 is defined as infinity, ∞. Critical values of *F* for $\alpha = 0.05$ are listed in Appendix 5 for both one-tailed and two-tailed *F*-tests.

EXAMPLE 4.6.2

A manufacturer's process for analyzing aspirin tablets has a known variance of 25. A sample of 10 aspirin tablets is selected and analyzed for the amount of aspirin, yielding the following results in mg aspirin/tablet.

254 249 252 252 249 249 250 247 251 252

Determine whether there is evidence of a significant difference between the sample's variance and the expected variance at $\alpha = 0.05$.

Solution

The variance for the sample of 10 tablets is 4.3. The null hypothesis and alternative hypotheses are

$$H_0\colon s^2 = \sigma^2 \qquad H_A\colon s^2 \neq \sigma^2$$

and the value for F_{exp} is

$$F_{exp} = \frac{\sigma^2}{s^2} = \frac{25}{4.3} = 5.8$$

The critical value for *F*(0.05, ∞, 9) from Appendix 5 is 3.333. Since F_{exp} is greater than *F*(0.05, ∞, 9), we reject the null hypothesis and accept the alternative hypothesis that there is a significant difference between the sample's variance and the expected variance. One explanation for the difference might be that the aspirin tablets were not selected randomly.

COMPARING VARIANCES FOR TWO SAMPLES

We can extend the *F*-test to compare the variances for two samples, *A* and *B*, by rewriting Equation 5.6.3 as

$$F_{exp} = \frac{s_A^2}{s_B^2}$$

defining *A* and *B* so that the value of *F*exp is greater than or equal to 1.

EXAMPLE 4.6.3

Table 4.4.1 shows results for two experiments to determine the mass of a circulating U.S. penny. Determine whether there is a difference in the variances of these analyses at $\alpha = 0.05$.

Solution

The standard deviations for the two experiments are 0.051 for the first experiment (*A*) and 0.037 for the second experiment (*B*). The null and alternative hypotheses are

$$H_0\colon s_A^2 = s_B^2 \qquad H_A\colon s_A^2 \neq s_B^2$$

and the value of F_{exp} is

$$F_{exp} = \frac{s_A^2}{s_B^2} = \frac{(0.051)^2}{(0.037)^2} = \frac{0.00260}{0.00137} = 1.90$$

From Appendix 5, the critical value for $F(0.05, 6, 4)$ is 9.197. Because $F_{exp} < F(0.05, 6, 4)$, we retain the null hypothesis. There is no evidence at $\alpha = 0.05$ to suggest that the difference in variances is significant.

EXERCISE 4.6.2

To compare two production lots of aspirin tablets, we collect an analyze samples from each, obtaining the following results (in mg aspirin/tablet).

$$\text{Lot 1: } 256 \quad 248 \quad 245 \quad 245 \quad 244 \quad 248 \quad 261$$

$$\text{Lot 2: } 241 \quad 258 \quad 241 \quad 244 \quad 256 \quad 254$$

Is there any evidence at $\alpha = 0.05$ that there is a significant difference in the variances for these two samples?

Answer

The standard deviations are 6.451 mg for Lot 1 and 7.849 mg for Lot 2. The null and alternative hypotheses are

$$H_0: s^2_{\text{Lot 1}} = s^2_{\text{Lot 2}} \qquad H_A: s^2_{\text{Lot 1}} \neq s^2_{\text{Lot 2}}$$

and the value of F_{exp} is

$$F_{exp} = \frac{(7.849)^2}{(6.451)^2} = 1.480$$

The critical value for $F(0.05, 5, 6)$ is 5.988. Because $F_{exp} < F(0.05, 5, 6)$, we retain the null hypothesis. There is no evidence at $\alpha = 0.05$ to suggest that the difference in the variances is significant.

COMPARING MEANS FOR TWO SAMPLES

Three factors influence the result of an analysis: the method, the sample, and the analyst. We can study the influence of these factors by conducting experiments in which we change one factor while holding constant the other factors. For example, to compare two analytical methods we can have the same analyst apply each method to the same sample and then examine the resulting means. In a similar fashion, we can design experiments to compare two analysts or to compare two samples.

It also is possible to design experiments in which we vary more than one of these factors. We will return to this point in Chapter 14.

Before we consider the significance tests for comparing the means of two samples, we need to make a distinction between ***unpaired data*** and ***paired data***. This is a critical distinction and learning to distinguish between these two types of data is important. Here are two simple examples that highlight the difference between unpaired data and paired data. In each example the goal is to compare two balances by weighing pennies.

- Example 1: We collect 10 pennies and weigh each penny on each balance. This is an example of paired data because we use the same 10 pennies to evaluate each balance.
- Example 2: We collect 10 pennies and divide them into two groups of five pennies each. We weigh the pennies in the first group on one balance and we weigh the second group of pennies on the other balance. Note that no penny is weighed on both balances. This is an example of unpaired data because we evaluate each balance using a different sample of pennies.

In both examples the samples of 10 pennies were drawn from the same population; the difference is how we sampled that population. We will learn why this distinction is important when we review the significance test for paired data; first, however, we present the significance test for unpaired data.

One simple test for determining whether data are paired or unpaired is to look at the size of each sample. If the samples are of different size, then the data must be unpaired. The converse is not true. If two samples are of equal size, they may be paired or unpaired.

UNPAIRED DATA

Consider two analyses, A and B with means of $\overline{X}_A$ and $\overline{X}_B$, and standard deviations of s_A and s_B. The confidence intervals for μ_A and for μ_B are

$$\mu_A = \overline{X}_A \pm \frac{t s_A}{\sqrt{n_A}} \tag{5.6.4}$$

$$\mu_B = \overline{X}_B \pm \frac{ts_B}{\sqrt{n_B}} \tag{5.6.5}$$

where n_A and n_B are the sample sizes for *A* and for *B*. Our null hypothesis, H_0: $\mu_A = \mu_B$, is that and any difference between μ_A and μ_B is the result of indeterminate errors that affect the analyses. The alternative hypothesis, H_A: $\mu_A \neq \mu_B$, is that the difference between $\mu_A$and μ_B is too large to be explained by indeterminate error.

To derive an equation for t_{exp}, we assume that μ_A equals μ_B, and combine Equation 5.6.4 and Equation 5.6.5

$$\overline{X}_A \pm \frac{t_{exp} s_A}{\sqrt{n_A}} = \overline{X}_B \pm \frac{t_{exp} s_B}{\sqrt{n_B}}$$

Solving for $|\overline{X}_A - \overline{X}_B|$ and using a propagation of uncertainty, gives

$$|\overline{X}_A - \overline{X}_B| = t_{exp} \times \sqrt{\frac{s_A^2}{n_A} + \frac{s_B^2}{n_B}} \tag{5.6.6}$$

Finally, we solve for t_{exp}

$$t_{exp} = \frac{|\overline{X}_A - \overline{X}_B|}{\sqrt{\frac{s_A^2}{n_A} + \frac{s_B^2}{n_B}}} \tag{5.6.7}$$

and compare it to a critical value, $t(\alpha, \nu)$, where α is the probability of a type 1 error, and ν is the degrees of freedom.

> Problem 9 asks you to use a propagation of uncertainty to show that Equation 5.6.6 is correct.

Thus far our development of this *t*-test is similar to that for comparing $\overline{X}$ to μ, and yet we do not have enough information to evaluate the *t*-test. Do you see the problem? With two independent sets of data it is unclear how many degrees of freedom we have.

Suppose that the variances s_A^2 and s_B^2 provide estimates of the same σ^2. In this case we can replace s_A^2 and s_B^2 with a pooled variance, s_{pool}^2, that is a better estimate for the variance. Thus, Equation 5.6.7 becomes

$$t_{exp} = \frac{|\overline{X}_A - \overline{X}_B|}{s_{pool} \times \sqrt{\frac{1}{n_A} + \frac{1}{n_B}}} = \frac{|\overline{X}_A - \overline{X}_B|}{s_{pool}} \times \sqrt{\frac{n_A n_B}{n_A + n_B}} \tag{5.6.8}$$

where s_{pool}, the pooled standard deviation, is

$$s_{pool} = \sqrt{\frac{(n_A - 1)s_A^2 + (n_B - 1)s_B^2}{n_A + n_B - 2}} \tag{5.6.9}$$

The denominator of Equation 5.6.9 shows us that the degrees of freedom for a pooled standard deviation is $n_A + n_B - 2$, which also is the degrees of freedom for the *t*-test. Note that we lose two degrees of freedom because the calculations for s_A^2 and s_B^2 require the prior calculation of $\overline{X}_A$ amd $\overline{X}_B$.

> So how do you determine if it is okay to pool the variances? Use an *F*-test.

If s_A^2 and s_B^2 are significantly different, then we calculate t_{exp} using Equation 5.6.7. In this case, we find the degrees of freedom using the following imposing equation.

$$\nu = \frac{\left(\frac{s_A^2}{n_A} + \frac{s_B^2}{n_B}\right)^2}{\frac{\left(\frac{s_A^2}{n_A}\right)^2}{n_A+1} + \frac{\left(\frac{s_B^2}{n_B}\right)^2}{n_B+1}} - 2 \tag{5.6.10}$$

Because the degrees of freedom must be an integer, we round to the nearest integer the value of ν obtained using Equation 5.6.10.

> Equation 5.6.10, which is from Miller, J.C.; Miller, J.N. *Statistics for Analytical Chemistry*, 2nd Ed., Ellis-Horward: Chichester, UK, 1988. In the 6th Edition, the authors note that several different equations have been suggested for the number of degrees of freedom for

t when s_A and s_B differ, reflecting the fact that the determination of degrees of freedom an approximation. An alternative equation—which is used by statistical software packages, such as R, Minitab, Excel—is

$$\nu = \frac{\left(\frac{s_A^2}{n_A} + \frac{s_B^2}{n_B}\right)^2}{\frac{\left(\frac{s_A^2}{n_A}\right)^2}{n_A - 1} + \frac{\left(\frac{s_B^2}{n_B}\right)^2}{n_B - 1}} = \frac{\left(\frac{s_A^2}{n_A} + \frac{s_B^2}{n_B}\right)^2}{\frac{s_A^4}{n_A^2(n_A - 1)} + \frac{s_B^4}{n_B^2(n_B - 1)}}$$

For typical problems in analytical chemistry, the calculated degrees of freedom is reasonably insensitive to the choice of equation.

Regardless of whether we calculate t_{exp} using Equation 5.6.7 or Equation 5.6.8, we reject the null hypothesis if t_{exp} is greater than $t(\alpha, \nu)$ and retain the null hypothesis if t_{exp} is less than or equal to $t(\alpha, \nu)$.

EXAMPLE 4.6.4

Table 4.4.1 provides results for two experiments to determine the mass of a circulating U.S. penny. Determine whether there is a difference in the means of these analyses at $\alpha = 0.05$.

Solution

First we use an *F*-test to determine whether we can pool the variances. We completed this analysis in Example 4.6.3 , finding no evidence of a significant difference, which means we can pool the standard deviations, obtaining

$$s_{pool} = \sqrt{\frac{(7-1)(0.051)^2 + (5-1)(0.037)^2}{7+5-2}} = 0.0459$$

with 10 degrees of freedom. To compare the means we use the following null hypothesis and alternative hypotheses

$$H_0: \mu_A = \mu_B \qquad H_A: \mu_A \neq \mu_B$$

Because we are using the pooled standard deviation, we calculate t_{exp} using Equation 5.6.8.

$$t_{exp} = \frac{|3.117 - 3.081|}{0.0459} \times \sqrt{\frac{7 \times 5}{7+5}} = 1.34$$

The critical value for *t*(0.05, 10), from Appendix 4, is 2.23. Because t_{exp} is less than *t*(0.05, 10) we retain the null hypothesis. For $\alpha = 0.05$ we do not have evidence that the two sets of pennies are significantly different.

EXAMPLE 4.6.5

One method for determining the %w/w Na_2CO_3 in soda ash is to use an acid–base titration. When two analysts analyze the same sample of soda ash they obtain the results shown here.

Analyst A:	86.82%	87.04%	86.93%	87.01%	86.20%	87.00%
Analyst B:	81.01%	86.15%	81.73%	83.19%	80.27%	83.93%

Determine whether the difference in the mean values is significant at $\alpha = 0.05$.

Solution

We begin by reporting the mean and standard deviation for each analyst.

$$\overline{X}_A = 86.83\% \qquad s_A = 0.32\%$$

$$\overline{X}_B = 82.71\% \qquad s_B = 2.16\%$$

To determine whether we can use a pooled standard deviation, we first complete an *F*-test using the following null and alternative hypotheses.

$$H_0: s_A^2 = s_B^2 \qquad H_A: s_A^2 \neq s_B^2$$

Calculating F_{exp}, we obtain a value of

$$F_{exp} = \frac{(2.16)^2}{(0.32)^2} = 45.6$$

Because F_{exp} is larger than the critical value of 7.15 for $F(0.05, 5, 5)$ from Appendix 5, we reject the null hypothesis and accept the alternative hypothesis that there is a significant difference between the variances; thus, we cannot calculate a pooled standard deviation.

To compare the means for the two analysts we use the following null and alternative hypotheses.

$$H_0: \overline{X}_A = \overline{X}_B \qquad H_A: \overline{X}_A \neq \overline{X}_B$$

Because we cannot pool the standard deviations, we calculate t_{exp} using Equation 5.6.7 instead of Equation 5.6.8

$$t_{exp} = \frac{|86.83 - 82.71|}{\sqrt{\frac{(0.32)^2}{6} + \frac{(2.16)^2}{6}}} = 4.62$$

and calculate the degrees of freedom using Equation 5.6.10.

$$\nu = \frac{\left(\frac{(0.32)^2}{6} + \frac{(2.16)^2}{6}\right)^2}{\frac{\left(\frac{(0.32)^2}{6}\right)^2}{6+1} + \frac{\left(\frac{(2.16)^2}{6}\right)^2}{6+1}} - 2 = 5.3 \approx 5$$

From Appendix 4, the critical value for $t(0.05, 5)$ is 2.57. Because t_{exp} is greater than $t(0.05, 5)$ we reject the null hypothesis and accept the alternative hypothesis that the means for the two analysts are significantly different at $\alpha = 0.05$.

? EXERCISE 4.6.3

To compare two production lots of aspirin tablets, you collect samples from each and analyze them, obtaining the following results (in mg aspirin/tablet).

Lot 1: 256 248 245 245 244 248 261

Lot 2: 241 258 241 244 256 254

Is there any evidence at $\alpha = 0.05$ that there is a significant difference in the variance between the results for these two samples? This is the same data from Exercise 4.6.2 .

Answer

To compare the means for the two lots, we use an unpaired t-test of the null hypothesis $H_0: \overline{X}_{\text{Lot 1}} = \overline{X}_{\text{Lot 2}}$ and the alternative hypothesis $H_A: \overline{X}_{\text{Lot 1}} \neq \overline{X}_{\text{Lot 2}}$. Because there is no evidence to suggest a difference in the variances (see Exercise 4.6.2) we pool the standard deviations, obtaining an s_{pool} of

$$s_{pool} = \sqrt{\frac{(7-1)(6.451)^2 + (6-1)(7.849)^2}{7+6-2}} = 7.121$$

The means for the two samples are 249.57 mg for Lot 1 and 249.00 mg for Lot 2. The value for t_{exp} is

$$t_{exp} = \frac{|249.57 - 249.00|}{7.121} \times \sqrt{\frac{7 \times 6}{7+6}} = 0.1439$$

The critical value for $t(0.05, 11)$ is 2.204. Because t_{exp} is less than $t(0.05, 11)$, we retain the null hypothesis and find no evidence at $\alpha = 0.05$ that there is a significant difference between the means for the two lots of aspirin tablets.

PAIRED DATA

Suppose we are evaluating a new method for monitoring blood glucose concentrations in patients. An important part of evaluating a new method is to compare it to an established method. What is the best way to gather data for this study? Because the variation in the blood glucose levels amongst patients is large we may be unable to detect a small, but significant difference between the methods if we use different patients to gather data for each method. Using paired data, in which the we analyze each patient's blood using both methods, prevents a large variance within a population from adversely affecting a t-test of means.

Typical blood glucose levels for most non-diabetic individuals ranges between 80–120 mg/dL (4.4–6.7 mM), rising to as high as 140 mg/dL (7.8 mM) shortly after eating. Higher levels are common for individuals who are pre-diabetic or diabetic.

When we use paired data we first calculate the difference, d_i, between the paired values for each sample. Using these difference values, we then calculate the average difference, $\bar{d}$, and the standard deviation of the differences, s_d. The null hypothesis, $H_0: d = 0$, is that there is no difference between the two samples, and the alternative hypothesis, $H_A: d \neq 0$, is that the difference between the two samples is significant.

The test statistic, t_{exp}, is derived from a confidence interval around $\bar{d}$

$$t_{exp} = \frac{|\bar{d}|\sqrt{n}}{s_d}$$

where n is the number of paired samples. As is true for other forms of the t-test, we compare t_{exp} to $t(\alpha, \nu)$, where the degrees of freedom, ν, is $n - 1$. If t_{exp} is greater than $t(\alpha, \nu)$, then we reject the null hypothesis and accept the alternative hypothesis. We retain the null hypothesis if t_{exp} is less than or equal to t(a, o). This is known as a ***paired t-test.***

EXAMPLE 4.6.6

Marecek et. al. developed a new electrochemical method for the rapid determination of the concentration of the antibiotic monensin in fermentation vats [Marecek, V.; Janchenova, H.; Brezina, M.; Betti, M. *Anal. Chim. Acta* **1991**, *244*, 15–19]. The standard method for the analysis is a test for microbiological activity, which is both difficult to complete and time-consuming. Samples were collected from the fermentation vats at various times during production and analyzed for the concentration of monensin using both methods. The results, in parts per thousand (ppt), are reported in the following table.

Sample	Microbiological	Electrochemical
1	129.5	132.3
2	89.6	91.0
3	76.6	73.6
4	52.2	58.2
5	110.8	104.2
6	50.4	49.9
7	72.4	82.1
8	141.4	154.1
9	75.0	73.4
10	34.1	38.1
11	60.3	60.1

Is there a significant difference between the methods at $\alpha = 0.05$?

Solution

Acquiring samples over an extended period of time introduces a substantial time-dependent change in the concentration of monensin. Because the variation in concentration between samples is so large, we use a paired t-test with the following null and alternative hypotheses.

$$H_0: \bar{d} = 0 \qquad H_A: \bar{d} \neq 0$$

Defining the difference between the methods as

$$d_i = (X_{\text{elect}})_i - (X_{\text{micro}})_i$$

we calculate the difference for each sample.

sample	1	2	3	4	5	6	7	8	9	10	11
d_i	2.8	1.4	–3.0	6.0	–6.6	–0.5	9.7	12.7	–1.6	4.0	–0.2

The mean and the standard deviation for the differences are, respectively, 2.25 ppt and 5.63 ppt. The value of t_{exp} is

$$t_{exp} = \frac{|2.25|\sqrt{11}}{5.63} = 1.33$$

which is smaller than the critical value of 2.23 for t(0.05, 10) from Appendix 4. We retain the null hypothesis and find no evidence for a significant difference in the methods at $\alpha = 0.05$.

EXERCISE 4.6.4

Suppose you are studying the distribution of zinc in a lake and want to know if there is a significant difference between the concentration of Zn^{2+} at the sediment-water interface and its concentration at the air-water interface. You collect samples from six locations—near the lake's center, near its drainage outlet, etc.—obtaining the results (in mg/L) shown in the table. Using this data, determine if there is a significant difference between the concentration of Zn^{2+} at the two interfaces at $\alpha = 0.05$. Complete this analysis treating the data as (a) unpaired and as (b) paired. Briefly comment on your results.

Location	Air-Water Interface	Sediment-Water Interface
1	0.430	0.415
2	0.266	0.238
3	0.457	0.390
4	0.531	0.410
5	0.707	0.605
6	0.716	0.609

Complete this analysis treating the data as (a) unpaired and as (b) paired. Briefly comment on your results.

Answer

Treating as Unpaired Data: The mean and the standard deviation for the concentration of Zn^{2+} at the air-water interface are 0.5178 mg/L and 0.1732 mg/L, respectively, and the values for the sediment-water interface are 0.4445 mg/L and 0.1418 mg/L, respectively. An *F*-test of the variances gives an F_{exp} of 1.493 and an $F(0.05, 5, 5)$ of 7.146. Because F_{exp} is smaller than $F(0.05, 5, 5)$, we have no evidence at $\alpha = 0.05$ to suggest that the difference in variances is significant. Pooling the standard deviations gives an s_{pool} of 0.1582 mg/L. An unpaired *t*-test gives t_{exp} as 0.8025. Because t_{exp} is smaller than $t(0.05, 11)$, which is 2.204, we have no evidence that there is a difference in the concentration of Zn^{2+} between the two interfaces.

Treating as Paired Data: To treat as paired data we need to calculate the difference, d_i, between the concentration of Zn^{2+} at the air-water interface and at the sediment-water interface for each location, where

$$d_i = \left([Zn^{2+}]_{\text{air-water}}\right)_i - \left([Zn^{2+}]_{\text{sed-water}}\right)_i$$

The mean difference is 0.07333 mg/L with a standard deviation of 0.0441 mg/L. The null hypothesis and the alternative hypothesis are

$$H_0: \bar{d} = 0 \qquad H_A: \bar{d} \neq 0$$

and the value of t_{exp} is

$$t_{exp} = \frac{|0.07333|\sqrt{6}}{0.0441} = 4.073$$

Because t_{exp} is greater than $t(0.05, 5)$, which is 2.571, we reject the null hypothesis and accept the alternative hypothesis that there is a significant difference in the concentration of Zn^{2+} between the air-water interface and the sediment-water interface.

The difference in the concentration of Zn^{2+} between locations is much larger than the difference in the concentration of Zn^{2+} between the interfaces. Because out interest is in studying the difference between the interfaces, the larger standard deviation when treating the data as unpaired increases the probability of incorrectly retaining the null hypothesis, a type 2 error.

One important requirement for a paired *t*-test is that the determinate and the indeterminate errors that affect the analysis must be independent of the analyte's concentration. If this is not the case, then a sample with an unusually high concentration of analyte will have an unusually large d_i. Including this sample in the calculation of $\bar{d}$ and s_d gives a biased estimate for the expected mean and standard deviation. This rarely is a problem for samples that span a limited range of analyte concentrations, such as those in Example 4.6.6 or Exercise 4.6.4 . When paired data span a wide range of concentrations, however, the magnitude of the determinate and indeterminate sources of error may not be independent of the analyte's concentration; when true, a paired *t*-test may give misleading results because the paired data with the largest absolute determinate and indeterminate errors will dominate $\bar{d}$. In this situation a regression analysis, which is the subject of the next chapter, is more appropriate method for comparing the data.

OUTLIERS

Earlier in the chapter we examined several data sets consisting of the mass of a circulating United States penny. Table 4.6.1 provides one more data set. Do you notice anything unusual in this data? Of the 112 pennies included in Table 4.4.1 and Table 4.4.3, no penny weighed less than 3 g. In Table 4.6.1, however, the mass of one penny is less than 3 g. We might ask whether this penny's mass is so different from the other pennies that it is in error.

Table 4.6.1 : Mass (g) for Additional Sample of Circulating U. S. Pennies

3.067	2.514	3.094
3.049	3.048	3.109
3.039	3.079	3.102

A measurement that is not consistent with other measurements is called outlier. An ***outlier*** might exist for many reasons: the outlier might belong to a different population (Is this a Canadian penny?); the outlier might be a contaminated or otherwise altered sample (Is the penny damaged or unusually dirty?); or the outlier may result from an error in the analysis (Did we forget to tare the balance?). Regardless of its source, the presence of an outlier compromises any meaningful analysis of our data. There are many significance tests that we can use to identify a potential outlier, three of which we present here.

DIXON'S *Q*-TEST

One of the most common significance tests for identifying an outlier is ***Dixon's Q-test***. The null hypothesis is that there are no outliers, and the alternative hypothesis is that there is an outlier. The *Q*-test compares the gap between the suspected outlier and its nearest numerical neighbor to the range of the entire data set (Figure 4.6.2).

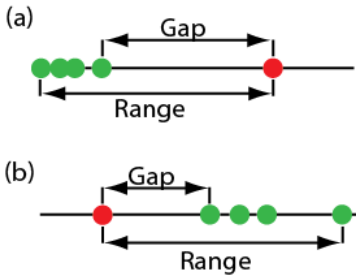


Figure 4.6.2 : Dotplots showing the distribution of two data sets containing a possible outlier. In (a) the possible outlier's value is larger than the remaining data, and in (b) the possible outlier's value is smaller than the remaining data.

The test statistic, Q_{exp}, is

$$Q_{\text{exp}} = \frac{\text{gap}}{\text{range}} = \frac{|\text{outlier's value} - \text{nearest value}|}{\text{largest value} - \text{smallest value}}$$

This equation is appropriate for evaluating a single outlier. Other forms of Dixon's *Q*-test allow its extension to detecting multiple outliers [Rorabacher, D. B. *Anal. Chem.* **1991**, *63*, 139–146].

The value of Q_{exp} is compared to a critical value, $Q(\alpha, n)$, where α is the probability that we will reject a valid data point (a type 1 error) and *n* is the total number of data points. To protect against rejecting a valid data point, usually we apply the more conservative two-tailed *Q*-test, even though the possible outlier is the smallest or the largest value in the data set. If Q_{exp} is greater than $Q(\alpha, n)$, then we reject the null hypothesis and may exclude the outlier. We retain the possible outlier when Q_{exp} is less than or equal to $Q(\alpha, n)$. Table 4.6.2 provides values for $Q(\alpha, n)$ for a data set that has 3–10 values. A more extensive table is in Appendix 6. Values for $Q(\alpha, n)$ assume an underlying normal distribution.

Table 4.6.2 : Dixon's Q-Test

n	*Q*(0.05, *n*)
3	0.970
4	0.829
5	0.710
6	0.625
7	0.568
8	0.526
9	0.493
10	0.466

GRUBB'S TEST

Although Dixon's *Q*-test is a common method for evaluating outliers, it is no longer favored by the International Standards Organization (ISO), which recommends the ***Grubb's test***. There are several versions of Grubb's test depending on the number of potential outliers. Here we will consider the case where there is a single suspected outlier.

> For details on this recommendation, see International Standards ISO Guide 5752-2 "Accuracy (trueness and precision) of measurement methods and results–Part 2: basic methods for the determination of repeatability and reproducibility of a standard measurement

method," 1994.

The test statistic for Grubb's test, G_{exp}, is the distance between the sample's mean, $\overline{X}$, and the potential outlier, X_{out}, in terms of the sample's standard deviation, s.

$$G_{exp} = \frac{|X_{out} - \overline{X}|}{s}$$

We compare the value of G_{exp} to a critical value $G(\alpha, n)$, where α is the probability that we will reject a valid data point and n is the number of data points in the sample. If G_{exp} is greater than $G(\alpha, n)$, then we may reject the data point as an outlier, otherwise we retain the data point as part of the sample. Table 4.6.3 provides values for $G(0.05, n)$ for a sample containing 3–10 values. A more extensive table is in Appendix 7. Values for $G(\alpha, n)$ assume an underlying normal distribution.

Table 4.6.3 : Grubb's Test

n	$G(0.05, n)$
3	1.115
4	1.481
5	1.715
6	1.887
7	2.020
8	2.126
9	2.215
10	2.290

CHAUVENET'S CRITERION

Our final method for identifying an outlier is ***Chauvenet's criterion***. Unlike Dixon's Q-Test and Grubb's test, you can apply this method to any distribution as long as you know how to calculate the probability for a particular outcome. Chauvenet's criterion states that we can reject a data point if the probability of obtaining the data point's value is less than $(2n)^{-1}$, where n is the size of the sample. For example, if n = 10, a result with a probability of less than $(2 \times 10)^{-1}$, or 0.05, is considered an outlier.

To calculate a potential outlier's probability we first calculate its standardized deviation, z

$$z = \frac{|X_{out} - \overline{X}|}{s}$$

where X_{out} is the potential outlier, $\overline{X}$ is the sample's mean and s is the sample's standard deviation. Note that this equation is identical to the equation for G_{exp} in the Grubb's test. For a normal distribution, we can find the probability of obtaining a value of z using the probability table in Appendix 3.

✔ EXAMPLE 4.6.7

Table 4.6.1 contains the masses for nine circulating United States pennies. One entry, 2.514 g, appears to be an outlier. Determine if this penny is an outlier using a Q-test, Grubb's test, and Chauvenet's criterion. For the Q-test and Grubb's test, let $\alpha = 0.05$.

Solution

For the Q-test the value for Qexp is

$$Q_{exp} = \frac{|2.514 - 3.039|}{3.109 - 2.514} = 0.882$$

From Table 4.6.2 , the critical value for $Q(0.05, 9)$ is 0.493. Because Q_{exp} is greater than $Q(0.05, 9)$, we can assume the penny with a mass of 2.514 g likely is an outlier.

For Grubb's test we first need the mean and the standard deviation, which are 3.011 g and 0.188 g, respectively. The value for G_{exp} is

$$G_{exp} = \frac{|2.514 - 3.011}{0.188} = 2.64$$

Using Table 4.6.3 , we find that the critical value for $G(0.05, 9)$ is 2.215. Because G_{exp} is greater than $G(0.05, 9)$, we can assume that the penny with a mass of 2.514 g likely is an outlier.

For Chauvenet's criterion, the critical probability is $(2 \times 9)^{-1}$, or 0.0556. The value of z is the same as G_{exp}, or 2.64. Using Appendix 3, the probability for z = 2.64 is 0.00415. Because the probability of obtaining a mass of 0.2514 g is less than the critical probability, we can assume the penny with a mass of 2.514 g likely is an outlier.

You should exercise caution when using a significance test for outliers because there is a chance you will reject a valid result. In addition, you should avoid rejecting an outlier if it leads to a precision that is much better than expected based on a propagation of uncertainty. Given these concerns it is not surprising that some statisticians caution against the removal of outliers [Deming, W. E. *Statistical Analysis of Data*; Wiley: New York, 1943 (republished by Dover: New York, 1961); p. 171].

> You also can adopt a more stringent requirement for rejecting data. When using the Grubb's test, for example, the ISO 5752 guidelines suggests retaining a value if the probability for rejecting it is greater than $\alpha = 0.05$, and flagging a value as a "straggler" if the probability for rejecting it is between $\alpha = 0.05$ and $\alpha = 0.01$. A "straggler" is retained unless there is compelling reason for its rejection. The guidelines recommend using $\alpha = 0.01$ as the minimum criterion for rejecting a possible outlier.

On the other hand, testing for outliers can provide useful information if we try to understand the source of the suspected outlier. For example, the outlier in Table 4.6.1 represents a significant change in the mass of a penny (an approximately 17% decrease in mass), which is the result of a change in the composition of the U.S. penny. In 1982 the composition of a U.S. penny changed from a brass alloy that was 95% w/w Cu and 5% w/w Zn (with a nominal mass of 3.1 g), to a pure zinc core covered with copper (with a nominal mass of 2.5 g) [Richardson, T. H. *J. Chem. Educ.* **1991**, *68*, 310–311]. The pennies in Table 4.6.1 , therefore, were drawn from different populations.

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5.7: DETECTION LIMITS

The International Union of Pure and Applied Chemistry (IUPAC) defines a method's detection limit as the smallest concentration or absolute amount of analyte that has a signal significantly larger than the signal from a suitable blank [IUPAC Compendium of Chemical Technology, Electronic Version]. Although our interest is in the amount of analyte, in this section we will define the detection limit in terms of the analyte's signal. Knowing the signal you can calculate the analyte's concentration, C_A, or the moles of analyte, n_A, using the equations

$$S_A = k_A C_A \text{ or } S_A = k_A n_A$$

where k is the method's sensitivity.

> See Chapter 3 for a review of these equations.

Let's translate the IUPAC definition of the detection limit into a mathematical form by letting S_{mb} represent the average signal for a method blank, and letting σ_{mb} represent the method blank's standard deviation. The null hypothesis is that the analyte is not present in the sample, and the alternative hypothesis is that the analyte is present in the sample. To detect the analyte, its signal must exceed S_{mb} by a suitable amount; thus,

$$(S_A)_{DL} = S_{mb} \pm z\sigma_{mb} \tag{5.7.1}$$

where $(S_A)_{DL}$ is the analyte's detection limit.

> If σ_{mb} is not known, we can replace it with s_{mb}; Equation 5.7.1 then becomes
>
> $$(S_A)_{DL} = S_{mb} \pm ts_{mb}$$
>
> You can make similar adjustments to other equations in this section. See, for example, Kirchner, C. J. "Estimation of Detection Limits for Environme tal Analytical Procedures," in Currie, L. A. (ed) *Detection in Analytical Chemistry: Importance, Theory, and Practice*; American Chemical Society: Washington, D. C., 1988.

The value we choose for z depends on our tolerance for reporting the analyte's concentration even if it is absent from the sample (a type 1 error). Typically, z is set to three, which, from Appendix 3, corresponds to a probability, α, of 0.00135. As shown in Figure 4.7.1 a, there is only a 0.135% probability of detecting the analyte in a sample that actually is analyte-free.

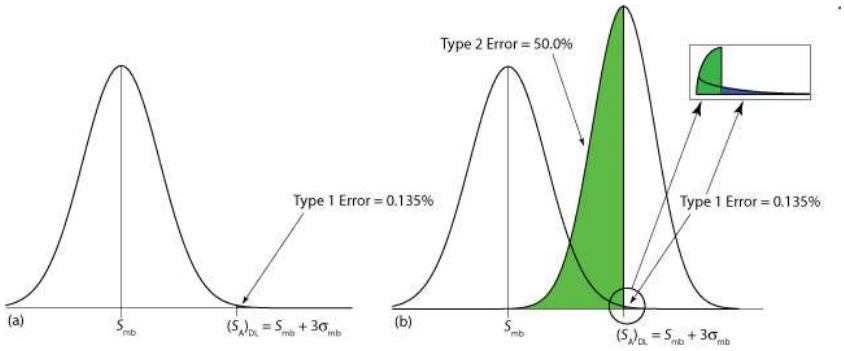


Figure 4.7.1 : Normal distribution curves showing the probability of type 1 and type 2 errors for the IUPAC detection limit. (a) The normal distribution curve for the method blank, with S_{mb} = 0 and σ_{mb} = 1. The minimum detectable signal for the analyte, $(S_A)_{DL}$, has a type 1 error of 0.135%. (b) The normal distribution curve for the analyte at its detection limit, $(S_A)_{DL}$= 3, is superimposed on the normal distribution curve for the method blank. The standard deviation for the analyte's signal, σ_A, is 0.8, The area in green represents the probability of a type 2 error, which is 50%. The inset shows, in blue, the probability of a type 1 error, which is 0.135%.

A detection limit also is subject to a type 2 error in which we fail to find evidence for the analyte even though it is present in the sample. Consider, for example, the situation shown in Figure 4.7.1 b where the signal for a sample that contains the analyte is exactly equal to $(S_A)_{DL}$. In this case the probability of a type 2 error is 50% because half of the sample's possible signals are below the detection limit. We correctly detect the analyte at the IUPAC detection limit only half the time. The IUPAC definition for the detection limit is the smallest signal for which we can say, at a significance level of α, that an analyte is present in the sample; however, failing to detect the analyte does not mean it is not present in the sample.

The detection limit often is represented, particularly when discussing public policy issues, as a distinct line that separates detectable concentrations of analytes from concentrations we cannot detect. This use of a detection limit is incorrect [Rogers, L. B. *J. Chem. Educ.*

1986, *63*, 3–6]. As suggested by Figure 4.7.1 , for an analyte whose concentration is near the detection limit there is a high probability that we will fail to detect the analyte.

An alternative expression for the detection limit, the ***limit of identification***, minimizes both type 1 and type 2 errors [Long, G. L.; Winefordner, J. D. *Anal. Chem.* **1983**, *55*, 712A–724A]. The analyte's signal at the limit of identification, $(S_A)_{\text{LOI}}$, includes an additional term, $z\sigma_A$, to account for the distribution of the analyte's signal.

$$(S_A)_{\text{LOI}} = (S_A)_{\text{DL}} + z\sigma_A = S_{mb} + z\sigma_{mb} + z\sigma_A$$

As shown in Figure 4.7.2 , the limit of identification provides an equal probability of a type 1 and a type 2 error at the detection limit. When the analyte's concentration is at its limit of identification, there is only a 0.135% probability that its signal is indistinguishable from that of the method blank.

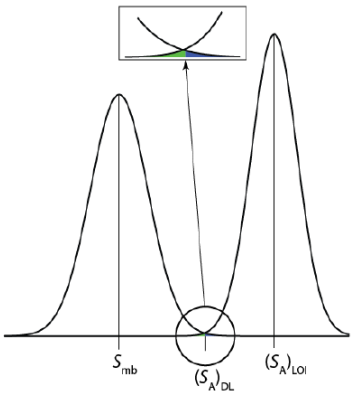


Figure 4.7.2 : Normal distribution curves for a method blank and for a sample at the limit of identification: $S_{mb} = 0$; $\sigma_{mb} = 1$; $\sigma_A = 0.8$; and $(S_A)_{\text{LOI}} = 0 + 3 \times 1 + 3 \times 0.8 = 5.4$. The inset shows that the probability of a type 1 error (0.135%) is the same as the probability of a type 2 error (0.135%).

The ability to detect the analyte with confidence is not the same as the ability to report with confidence its concentration, or to distinguish between its concentration in two samples. For this reason the American Chemical Society's Committee on Environmental Analytical Chemistry recommends the ***limit of quantitation***, $(S_A)_{\text{LOQ}}$ ["Guidelines for Data Acquisition and Data Quality Evaluation in Environmental Chemistry," *Anal. Chem.* **1980**, *52*, 2242–2249].

$$(S_A)_{\text{LOQ}} = S_{mb} + 10\sigma_{mb}$$

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5.8: USING EXCEL AND R TO ANALYZE DATA

Although the calculations in this chapter are relatively straightforward, it can be tedious to work problems using nothing more than a calculator. Both Excel and R include functions for many common statistical calculations. In addition, R provides useful functions for visualizing your data.

EXCEL

Excel has built-in functions that we can use to complete many of the statistical calculations covered in this chapter, including reporting descriptive statistics, such as means and variances, predicting the probability of obtaining a given outcome from a binomial distribution or a normal distribution, and carrying out significance tests. Table 4.8.1 provides the syntax for many of these functions; you can information on functions not included here by using Excel's Help menu.

Table 4.8.1 : Excel Functions for Statistics Calculations

Parameter	Excel Function
Descriptive Statistics	
mean	= average(data)
median	= median(data)
standard deviation for sample	= stdev.s(data)
standard deviation for populations	= stdev.p(data)
variance for sample	= var.s(data)
variance for population	= var.p(data)
maximum value	= max(data)
minimum value	= min(data)
Probability Distributions	
binomial distribution	= binom.dist(*X*, *N*, *p*, TRUE or FALSE)
normal distribution	= norm.dist(*x*, μ σ, TRUE or FALSE)
Significance Tests	
F-test	= f.test(data set 1, data set 2)
t-test	= t.test(data set 1, data set 2, tails = 1 or 2, type of *t*-test: 1 = paired; 2 = unpaired with equal variances; or 3 = unpaired with unequal variances)

DESCRIPTIVE STATISTICS

Let's use Excel to provide a statistical summary of the data in Table 4.1.1. Enter the data into a spreadsheet, as shown in Figure 4.8.1 . To calculate the sample's mean, for example, click on any empty cell, enter the formula

= **average**(b2:b8)

and press Return or Enter to replace the cell's content with Excel's calculation of the mean (3.117285714), which we round to 3.117. Excel does not have a function for the range, but we can use the functions that report the maximum value and the minimum value to calculate the range; thus

= **max**(b2:b8) – **min**(b2:b8)

returns 0.142 as an answer.

	A	B
1		mass (g)
2		3.080
3		3.094
4		3.107
5		3.056
6		3.112
7		3.174
8		3.198

Figure 4.8.1 : Portion of a spreadsheet containing data from Table 4.1.1.

PROBABILITY DISTRIBUTIONS

In Example 4.4.2 we showed that 91.10% of a manufacturer's analgesic tablets contained between 243 and 262 mg of aspirin. We arrived at this result by calculating the deviation, *z*, of each limit from the population's expected mean, μ, of 250 mg in terms of the population's

expected standard deviation, σ, of 5 mg. After we calculated values for z, we used the table in Appendix 3 to find the area under the normal distribution curve between these two limits.

We can complete this calculation in Excel using the **norm.dist** function As shown in Figure 4.8.2 , the function calculates the probability of obtaining a result less than x from a normal distribution with a mean of μ and a standard deviation of σ. To solve Example 4.4.2 using Excel enter the following formulas into separate cells

$$= \textbf{norm.dist}(243, 250, 5, \text{TRUE})$$

$$= \textbf{norm.dist}(262, 250, 5, \text{TRUE})$$

obtaining results of 0.080756659 and 0.991802464. Subtracting the smaller value from the larger value and adjusting to the correct number of significant figures gives the probability as 0.9910, or 99.10%.

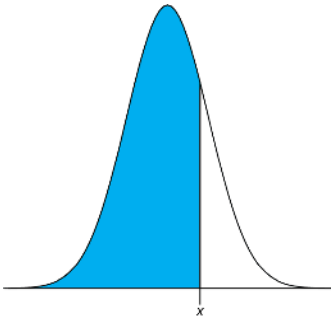


Figure 4.8.2 : Shown in blue is the area returned by the function norm.dist(x, μ σ, TRUE). The last parameter—TRUE—returns the cumulative distribution from $-\infty$ to x; entering FALSE gives the probability of obtaining a result greater than x. For our purposes, we want to use TRUE.

Excel also includes a function for working with binomial distributions. The function's syntax is

$$= \textbf{binom.dist}(X, N, p, \text{TRUE or FALSE})$$

where X is the number of times a particular outcome occurs in N trials, and p is the probability that X occurs in a single trial. Setting the function's last term to TRUE gives the total probability for any result up to X and setting it to FALSE gives the probability for X. Using Example 4.4.1 to test this function, we use the formula

$$= \textbf{binom.dist}(0, 27, 0.0111, \text{FALSE})$$

to find the probability of finding no atoms of ^{13}C atoms in a molecule of cholesterol, $C_{27}H_{44}O$, which returns a value of 0.740 after adjusting for significant figures. Using the formula

$$= \textbf{binom.dist}(2, 27, 0.0111, \text{TRUE})$$

we find that 99.7% of cholesterol molecules contain two or fewer atoms of ^{13}C.

SIGNIFICANCE TESTS

As shown in Table 4.8.1 , Excel includes functions for the following significance tests covered in this chapter:

- an *F*-test of variances
- an unpaired *t*-test of sample means assuming equal variances
- an unpaired *t*-test of sample means assuming unequal variances
- a paired *t*-test for of sample means

Let's use these functions to complete a *t*-test on the data in Table 4.4.1, which contains results for two experiments to determine the mass of a circulating U. S. penny. Enter the data from Table 4.4.1 into a spreadsheet as shown in Figure 4.8.3 .

	A	B	C
1		Set 1	Set 2
2		3.080	3.052
3		3.094	3.141
4		3.107	3.083
5		3.056	3.083
6		3.112	3.048
7		3.174	
8		3.198	

Figure 4.8.3 : Portion of a spreadsheet containing the data in Table 4.4.1.

Because the data in this case are unpaired, we will use Excel to complete an unpaired *t*-test. Before we can complete the *t*-test, we use an *F*-test to determine whether the variances for the two data sets are equal or unequal.

To complete the *F*-test, we click on any empty cell, enter the formula

= **f.test**(b2:b8, c2:c6)

and press Return or Enter, which replaces the cell's content with the value of α for which we can reject the null hypothesis of equal variances. In this case, Excel returns an α of 0.566 105 03; because this value is not less than 0.05, we retain the null hypothesis that the variances are equal. Excel's *F*-test is two-tailed; for a one-tailed *F*-test, we use the same function, but divide the result by two; thus

= **f.test**(b2:b8, c2:c6)/2

Having found no evidence to suggest unequal variances, we next complete an unpaired *t*-test assuming equal variances, entering into any empty cell the formula

= **t.test**(b2:b8, c2:c6, 2, 2)

where the first 2 indicates that this is a two-tailed *t*-test, and the second 2 indicates that this is an unpaired *t*-test with equal variances. Pressing Return or Enter replaces the cell's content with the value of α for which we can reject the null hypothesis of equal means. In this case, Excel returns an α of 0.211 627 646; because this value is not less than 0.05, we retain the null hypothesis that the means are equal.

> See Example 4.6.3 and Example 4.6.4 for our earlier solutions to this problem.

The other significance tests in Excel work in the same format. The following practice exercise provides you with an opportunity to test yourself.

? EXERCISE 4.8.1

Rework Example 4.6.5 and Example 4.6.6 using Excel.

Answer

You will find small differences between the values you obtain using Excel's built in functions and the worked solutions in the chapter. These differences arise because Excel does not round off the results of intermediate calculations.

R

R is a programming environment that provides powerful capabilities for analyzing data. There are many functions built into R's standard installation and additional packages of functions are available from the R web site (www.r-project.org). Commands in R are not available from pull down menus. Instead, you interact with R by typing in commands.

> You can download the current version of R from www.r-project.org. Click on the link for Download: CRAN and find a local mirror site. Click on the link for the mirror site and then use the link for Linux, MacOS X, or Windows under the heading "Download and Install R."

DESCRIPTIVE STATISTICS

Let's use R to provide a statistical summary of the data in Table 4.1.1. To do this we first need to create an object that contains the data, which we do by typing in the following command.

> penny1 = c(3.080, 3.094, 3.107, 3.056, 3.112, 3.174, 3.198)

> In R, the symbol '>' is a prompt, which indicates that the program is waiting for you to enter a command. When you press 'Return' or 'Enter,' R executes the command, displays the result (if there is a result to return), and returns the > prompt.

Table 4.8.2 lists some of the commands in R for calculating basic descriptive statistics. As is the case for Excel, R does not include stand alone commands for all descriptive statistics of interest to us, but we can calculate them using other commands. Using a command is easy—simply enter the appropriate code at the prompt; for example, to find the sample's variance we enter

> **var**(penny1)

[1] 0.002221918

Table 4.8.2 : R Functions for Descriptive Statistics

Parameter	Excel Function
mean	mean(object)
median	median(object)
standard deviation for sample	sd(object)
standard deviation for populations	sd(object) * ((length(object) – 1)/length(object))^0.5
variance for sample	var(object)
variance for population	var(object) * ((length(object) – 1)/length(object))
range	max(object) – min(object)

PROBABILITY DISTRIBUTIONS

In Example 4.4.2 we showed that 91.10% of a manufacturer's analgesic tablets contained between 243 and 262 mg of aspirin. We arrived at this result by calculating the deviation, *z*, of each limit from the population's expected mean, μ, of 250 mg in terms of the population's expected standard deviation, σ, of 5 mg. After we calculated values for *z*, we used the table in Appendix 3 to find the area under the normal distribution curve between these two limits.

We can complete this calculation in R using the function **pnorm**. The function's general format is

$$\textbf{pnorm}(x, \mu, \sigma)$$

where *x* is the limit of interest, μ is the distribution's expected mean, and σ is the distribution's expected standard deviation. The function returns the probability of obtaining a result of less than *x* (Figure 4.8.4).

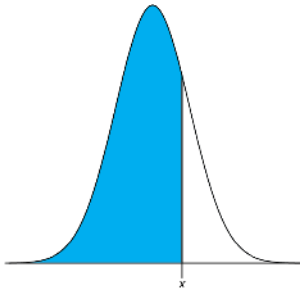


Figure 4.8.4 : Shown in blue is the area returned by the function **pnorm**(x, μ, σ).

Here is the output of an R session for solving Example 4.4.2.

> pnorm(243, 250, 5)

[1] 0.08075666

> pnorm(262, 250, 5)

[1] 0.9918025

Subtracting the smaller value from the larger value and adjusting to the correct number of significant figures gives the probability as 0.9910, or 99.10%.

R also includes functions for binomial distributions. To find the probability of obtaining a particular outcome, *X*, in *N* trials we use the **dbinom** function.

$$\textbf{dbinom}(X, N, p)$$

where *X* is the number of times a particular outcome occurs in *N* trials, and *p* is the probability that *X* occurs in a single trial. Using Example 4.4.1 to test this function, we find that the probability of finding no atoms of ^{13}C atoms in a molecule of cholesterol, $C_{27}H_{44}O$ is

> dbinom(0, 27, 0.0111)

[1] 0.7397997

0.740 after adjusting the significant figures. To find the probability of obtaining any outcome up to a maximum value of *X*, we use the **pbinom** function.

$$\textbf{pbinom}(X, N, p)$$

To find the percentage of cholesterol molecules that contain 0, 1, or 2 atoms of ^{13}C, we enter

> pbinom(2, 27, 0.0111)

[1] 0.9967226

and find that the answer is 99.7% of cholesterol molecules.

SIGNIFICANCE TESTS

R includes commands for the following significance tests covered in this chapter:

- *F*-test of variances
- unpaired *t*-test of sample means assuming equal variances
- unpaired *t*-test of sample means assuming unequal variances
- paired *t*-test for of sample means
- Dixon's *Q*-test for outliers
- Grubb's test for outliers

Let's use these functions to complete a *t*-test on the data in Table 4.4.1, which contains results for two experiments to determine the mass of a circulating U. S. penny. First, enter the data from Table 4.4.1 into two objects.

> penny1 = c(3.080, 3.094, 3.107, 3.056, 3.112, 3.174, 3.198)

> penny2 = c(3.052, 3.141, 3.083, 3.083, 3.048)

Because the data in this case are unpaired, we will use R to complete an unpaired *t*-test. Before we can complete a *t*-test we use an *F*-test to determine whether the variances for the two data sets are equal or unequal.

To complete a two-tailed *F*-test in R we use the command

var.test(*X*, *Y*)

where *X* and *Y* are the objects that contain the two data sets. Figure 4.8.5 shows the output from an R session to solve this problem.

```
> var.test(penny1, penny2)

        F test to compare two variances

data:  penny1 and penny2
F = 1.8726, num df = 6, denom df = 4, p-value = 0.5661
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.2036028 11.6609726
sample estimates:
ratio of variances
          1.872598
```

Figure 4.8.5 : Output of an R session for an *F*-test of variances. The *p*-value of 0.5661 is the probability of incorrectly rejecting the null hypothesis that the variances are equal (*note: R identifies α as a p-value*). The 95% confidence interval is the range of values for F_{exp} that are explained by random error. If this range includes the expected value for *F*, in this case 1.00, then there is insufficient evidence to reject the null hypothesis. Note that R does not adjust for significant figures.

Note that R does not provide the critical value for $F(0.05, 6, 4)$; instead it reports the 95% confidence interval for F_{exp}. Because this confidence interval of 0.204 to 11.661 includes the expected value for *F* of 1.00, we retain the null hypothesis and have no evidence for a difference between the variances. R also provides the probability of incorrectly rejecting the null hypothesis, which in this case is 0.5561.

For a one-tailed *F*-test the command is one of the following

var.test(*X*, *Y*, alternative = "greater")

var.test(*X*, *Y*, alternative = "less")

where "greater" is used when the alternative hypothesis is $s_X^2 > s_Y^2$, and "less" is used when the alternative hypothesis is $s_X^2 < s_Y^2$.

Having found no evidence suggesting unequal variances, we now complete an unpaired *t*-test assuming equal variances. The basic syntax for a two-tailed *t*-test is

t.test(*X*, *Y*, mu = 0, paired = FALSE, var.equal = FALSE)

where *X* and *Y* are the objects that contain the data sets. You can change the underlined terms to alter the nature of the *t*-test. Replacing "var.equal = FALSE" with "var.equal = TRUE" makes this a two-tailed *t*-test with equal variances, and replacing "paired = FALSE" with "paired = TRUE" makes this a paired *t*-test. The term "mu = 0" is the expected difference between the means, which for this problem is 0. You can, of course, change this to suit your needs. The underlined terms are default values; if you omit them, then R assumes you intend an unpaired two-tailed *t*-test of the null hypothesis that $X = Y$ with unequal variances. Figure 4.8.6 shows the output of an R session for this problem.

```
> t.test(penny1, penny2, var.equal=TRUE)
  Two Sample t-test
data:  penny1 and penny2
t = 1.3345, df = 10, p-value = 0.2116
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.02403040  0.09580182
sample estimates:
mean of x mean of y
 3.117286  3.081400
```

Figure 4.8.6 : Output of an R session for an unpaired *t*-test with equal variances. The *p*-value of 0.2116 is the probability of incorrectly rejecting the null hypothesis that the means are equal (*note: R identifies α as a p-value*). The 95% confidence interval is the range of values for the difference between the means that is explained by random error. If this range includes the expected value for the difference, in this case zero, then there is insufficient evidence to reject the null hypothesis. Note that R does not adjust for significant figures.

We can interpret the results of this *t*-test in two ways. First, the *p*-value of 0.2116 means there is a 21.16% probability of incorrectly rejecting the null hypothesis. Second, the 95% confidence interval of –0.024 to 0.0958 for the difference between the sample means includes the expected value of zero. Both ways of looking at the results provide no evidence for rejecting the null hypothesis; thus, we retain the null hypothesis and find no evidence for a difference between the two samples.

The other significance tests in R work in the same format. The following practice exercise provides you with an opportunity to test yourself.

? EXERCISE 4.8.2

Rework Example 4.6.5 and Example 4.6.6 using R.

Answer

Shown here are copies of R sessions for each problem. You will find small differences between the values given here for t_{exp} and for F_{exp} and those values shown with the worked solutions in the chapter. These differences arise because R does not round off the results of intermediate calculations.

Example 4.6.5

```
> AnalystA = c(86.82, 87.04, 86.93, 87.01, 86.20, 87.00)
> AnalystB = c(81.01, 86.15, 81.73, 83.19, 80.27, 83.94)
> var.test(AnalystB, AnalystA)
F test to compare two variances
data: AnalystB and AnalystA
F = 45.6358, num df = 5, denom df = 5, p-value = 0.0007148
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
6.385863 326.130970
sample estimates:
ratio of variances
45.63582
> t.test(AnalystA, AnalystB, var.equal=FALSE)
Welch Two Sample t-test
data: AnalystA and AnalystB
t = 4.6147, df = 5.219, p-value = 0.005177
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval: 1.852919 6.383748
sample estimates: mean of x mean of y
86.83333 82.71500
```

Example 4.21

```
> micro = c(129.5, 89.6, 76.6, 52.2, 110.8, 50.4, 72.4, 141.4, 75.0, 34.1, 60.3)
> elect = c(132.3, 91.0, 73.6, 58.2, 104.2, 49.9, 82.1, 154.1, 73.4, 38.1, 60.1)
```

```
> t.test(micro,elect,paired=TRUE)
Paired t-test
data: micro and elect
t = -1.3225, df = 10, p-value = 0.2155
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-6.028684 1.537775
sample estimates:
mean of the differences
–2.245455
```

Unlike Excel, R also includes functions for evaluating outliers. These functions are not part of R's standard installation. To install them enter the following command within R (*note: you will need an internet connection to download the package of functions*).

> install.packages("outliers")

After you install the package, you must load the functions into R by using the following command (*note: you need to do this step each time you begin a new R session as the package does not automatically load when you start R*).

> library("outliers")

You need to install a package once, but you need to load the package each time you plan to use it. There are ways to configure R so that it automatically loads certain packages; see *An Introduction to R* for more information (click here to view a PDF version of this document).

Let's use this package to find the outlier in Table 4.6.1 using both Dixon's *Q*-test and Grubb's test. The commands for these tests are

dixon.test(*X*, type = 10, two.sided = TRUE)

grubbs.test(*X*, type = 10, two.sided = TRUE)

where *X* is the object that contains the data, "type = 10" specifies that we are looking for one outlier, and "two.sided = TRUE" indicates that we are using the more conservative two-tailed test. Both tests have other variants that allow for the testing of outliers on both ends of the data set ("type = 11") or for more than one outlier ("type = 20"), but we will not consider these here. Figure 4.8.7 shows the output of a session for this problem. For both tests the very small *p*-value indicates that we can treat as an outlier the penny with a mass of 2.514 g.

```
> penny3=c(3.067,3.049, 3.039, 2.514, 3.048, 3.079, 3.094, 3.109, 3.102)
> dixon.test(penny3, type=10, two.sided=TRUE)

  Dixon test for outliers

data:  penny3
Q = 0.8824, p-value < 2.2e-16
alternative hypothesis: lowest value 2.514 is an outlier

> grubbs.test(penny3, type=10, two.sided=TRUE)

  Grubbs test for one outlier

data:  penny3
G = 2.6430, U = 0.0177, p-value = 1.938e-06
alternative hypothesis: lowest value 2.514 is an outlier
```

Figure 4.8.7 : Output of an R session for Dixon's *Q*-test and Grubb's test for outliers. The *p*-values for both tests show that we can treat as an outlier the penny with a mass of 2.514 g.

VISUALIZING DATA

One of R's more useful features is the ability to visualize data. Visualizing data is important because it provides us with an intuitive feel for our data that can help us in applying and evaluating statistical tests. It is tempting to believe that a statistical analysis is foolproof, particularly if the probability for incorrectly rejecting the null hypothesis is small. Looking at a visual display of our data, however, can help us determine whether our data is normally distributed—a requirement for most of the significance tests in this chapter—and can help us identify potential outliers. There are many useful ways to look at data, four of which we consider here.

Visualizing data is important, a point we will return to in Chapter 5 when we consider the mathematical modeling of data.

To plot data in R, we will use the package “lattice,” which you will need to load using the following command.

> library(“lattice”)

To demonstrate the types of plots we can generate, we will use the object “penny,” which contains the masses of the 100 pennies in Table 4.4.3.

> You do not need to use the command install.package this time because lattice was automatically installed on your computer when you downloaded R.

Our first visualization is a histogram. To construct the histogram we use mass to divide the pennies into bins and plot the number of pennies or the percent of pennies in each bin on the *y*-axis as a function of mass on the *x*-axis. Figure 4.8.8 shows the result of entering the command

> **histogram**(penny, type = “percent”, xlab = “Mass (g)”, ylab = “Percent of Pennies”, main = “Histogram of Data in Table 4.4.3”)

A histogram allows us to visualize the data’s distribution. In this example the data appear to follow a normal distribution, although the largest bin does not include the mean of 3.095 g and the distribution is not perfectly symmetric. One limitation of a histogram is that its appearance depends on how we choose to bin the data. Increasing the number of bins and centering the bins around the data’s mean gives a histogram that more closely approximates a normal distribution (Figure 4.4.5).

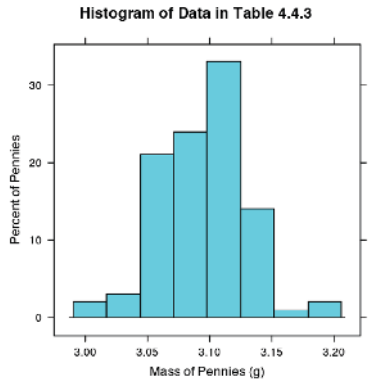


Figure 4.8.8 : Histogram of the data from Table 4.4.3.

An alternative to the histogram is a kernel density plot, which basically is a smoothed histogram. In this plot each value in the data set is replaced with a normal distribution curve whose width is a function of the data set’s standard deviation and size. The resulting curve is a summation of the individual distributions. Figure 4.8.9 shows the result of entering the command

> **densityplot**(penny, xlab = “Mass of Pennies (g)”, main = “Kernel Density Plot of Data in Table 4.4.3”)

The circles at the bottom of the plot show the mass of each penny in the data set. This display provides a more convincing picture that the data in Table 4.4.3 are normally distributed, although we see evidence of a small clustering of pennies with a mass of approximately 3.06 g.

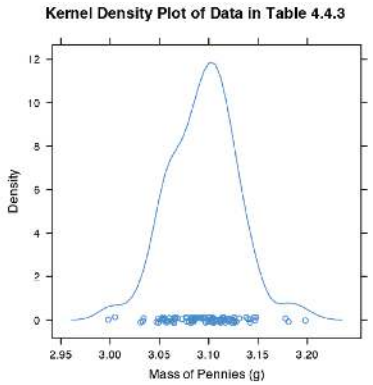


Figure 4.8.9 : Kernal plot of the data from Table 4.4.3.

We analyze samples to characterize the parent population. To reach a meaningful conclusion about a population, the samples must be representative of the population. One important requirement is that the samples are random. A dot chart provides a simple visual display that allows us to examine the data for non-random trends. Figure 4.8.10 shows the result of entering

> **dotchart**(penny, xlab = “Mass of Pennies (g)”, ylab = “Penny Number”, main = “Dotchart of Data in Table 4.4.3”)

In this plot the masses of the 100 pennies are arranged along the *y*-axis in the order in which they were sampled. If we see a pattern in the data along the *y*-axis, such as a trend toward smaller masses as we move from the first penny to the last penny, then we have clear evidence of non-random sampling. Because our data do not show a pattern, we have more confidence in the quality of our data.

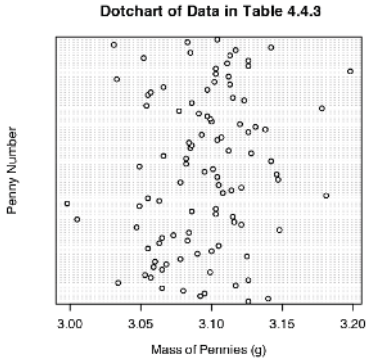


Figure 4.8.10 : Dot chart of the data from Table 4.4.3. Note that the dispersion of points along the *x*-axis is not uniform, with more points occurring near the center of the *x*-axis than at either end. This pattern is as expected for a normal distribution.

The last plot we will consider is a box plot, which is a useful way to identify potential outliers without making any assumptions about the data's distribution. A box plot contains four pieces of information about a data set: the median, the middle 50% of the data, the smallest value and the largest value within a set distance of the middle 50% of the data, and possible outliers. Figure 4.8.11 shows the result of entering

> **bwplot**(penny, xlab = "Mass of Pennies (g)", main = "Boxplot of Data in Table 4.4.3)"

The black dot (•) is the data set's median. The rectangular box shows the range of masses spanning the middle 50% of the pennies. This also is known as the interquartile range, or IQR. The dashed lines, which are called "whiskers," extend to the smallest value and the largest value that are within $\pm 1.5 \times \text{IQR}$ of the rectangular box. Potential outliers are shown as open circles (o). For normally distributed data the median is near the center of the box and the whiskers will be equidistant from the box. As is often the case in statistics, the converse is not true—finding that a boxplot is perfectly symmetric does not prove that the data are normally distributed.

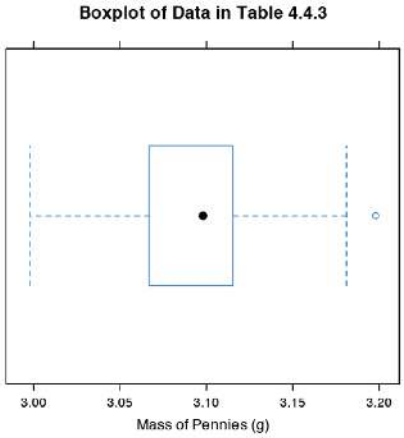


Figure 4.8.11 : Box plot of the data from Table 4.4.3.

To find the interquartile range you first find the median, which divides the data in half. The median of each half provides the limits for the box. The IQR is the median of the upper half of the data minus the median for the lower half of the data. For the data in Table 4.4.3 the median is 3.098. The median for the lower half of the data is 3.068 and the median for the upper half of the data is 3.115. The IQR is 3.115 – 3.068 = 0.047. You can use the command "summary(penny)" in R to obtain these values.

The lower "whisker" extend to the first data point with a mass larger than

$$3.068 - 1.5 \times \text{IQR} = 3.068 - 1.5 \times 0.047 = 2.9975$$

which for this data is 2.998 g. The upper "whisker" extends to the last data point with a mass smaller than

$$3.115 + 1.5 \times \text{IQR} = 3.115 + 1.5 \times 0.047 = 3.1855$$

which for this data is 3.181 g.

The box plot in Figure 4.8.11 is consistent with the histogram (Figure 4.8.8) and the kernel density plot (Figure 4.8.9). Together, the three plots provide evidence that the data in Table 4.4.3 are normally distributed. The potential outlier, whose mass of 3.198 g, is not sufficiently far away from the upper whisker to be of concern, particularly as the size of the data set (n = 100) is so large. A Grubb's test on the potential outlier does not provide evidence for treating it as an outlier.

? EXERCISE 4.8.3

Use R to create a data set consisting of 100 values from a uniform distribution by entering the command

> data = runif(100, min = 0, max = 100)

A uniform distribution is one in which every value between the minimum and the maximum is equally probable. Examine the data set by creating a histogram, a kernel density plot, a dot chart, and a box plot. Briefly comment on what the plots tell you about the your sample and its parent population.

Answer

Because we are selecting a random sample of 100 members from a uniform distribution, you will see subtle differences between your plots and the plots shown as part of this answer. Here is a record of my R session and the resulting plots.

> data = runif(100, min = 0, max = 0)

> data

[1] 18.928795 80.423589 39.399693 23.757624 30.088554

[6] 76.622174 36.487084 62.186771 81.115515 15.726404

[11] 85.765317 53.994179 7.919424 10.125832 93.153308

[16] 38.079322 70.268597 49.879331 73.115203 99.329723

[21] 48.203305 33.093579 73.410984 75.128703 98.682127

[26] 11.433861 53.337359 81.705906 95.444703 96.843476

[31] 68.251721 40.567993 32.761695 74.635385 70.914957

[36] 96.054750 28.448719 88.580214 95.059215 20.316015

[41] 9.828515 44.172774 99.648405 85.593858 82.745774

[46] 54.963426 65.563743 87.820985 17.791443 26.417481

[51] 72.832037 5.518637 58.231329 10.213343 40.581266

[56] 6.584000 81.261052 48.534478 51.830513 17.214508

[61] 31.232099 60.545307 19.197450 60.485374 50.414960

[66] 88.908862 68.939084 92.515781 72.414388 83.195206

[71] 74.783176 10.643619 41.775788 20.464247 14.547841

[76] 89.887518 56.217573 77.606742 26.956787 29.641171

[81] 97.624246 46.406271 15.906540 23.007485 17.715668

[86] 84.652814 29.379712 4.093279 46.213753 57.963604

[91] 91.160366 34.278918 88.352789 93.004412 31.055807

[96] 47.822329 24.052306 95.498610 21.089686 2.629948

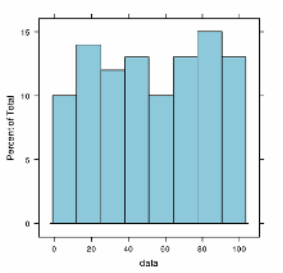
> histogram(data, type = "percent")

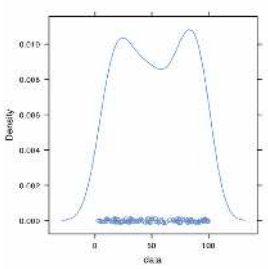
> densityplot(data)

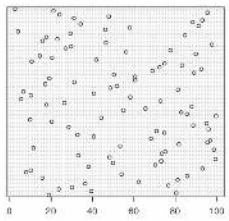
> dotchart(data)

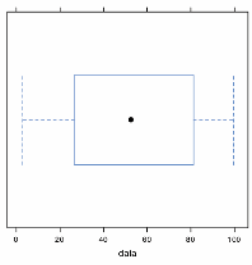
> bwplot(data)

The histogram (far left) divides the data into eight bins, each of which contains between 10 and 15 members. As we expect for a uniform distribution, the histogram's overall pattern suggests that each outcome is equally probable. In interpreting the kernel density plot (second from left), it is important to remember that it treats each data point as if it is from a normally distributed population (even though, in this case, the underlying population is uniform). Although the plot appears to suggest that there are two normally distributed populations, the individual results shown at the bottom of the plot provide further evidence for a uniform distribution. The dot chart (second from right) shows no trend along the y-axis, which indicates that the individual members of this sample were drawn at random from the population. The distribution along the x-axis also shows no pattern, as expected for a uniform distribution, Finally, the box plot (far right) shows no evidence of outliers.









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5.9: PROBLEMS

1. The following masses were recorded for 12 different U.S. quarters (all given in grams):

5.683	5.549	5.548	5.552
5.620	5.536	5.539	5.684
5.551	5.552	5.554	5.632

Report the mean, median, range, standard deviation and variance for this data.

2. A determination of acetaminophen in 10 separate tablets of Excedrin Extra Strength Pain Reliever gives the following results (in mg)

224.3	240.4	246.3	239.4	253.1
261.7	229.4	255.5	235.5	249.7

(a) Report the mean, median, range, standard deviation and variance for this data.

(b) Assuming that $\overline{X}$ and s^2 are good approximations for μ and for σ^2, and that the population is normally distributed, what percentage of tablets contain more than the standard amount of 250 mg acetaminophen per tablet?

The data in this problem are from Simonian, M. H.; Dinh, S.; Fray, L. A. *Spectroscopy* **1993**, *8(6)*, 37–47.

3. Salem and Galan developed a new method to determine the amount of morphine hydrochloride in tablets. An analysis of tablets with different nominal dosages gave the following results (in mg/tablet).

100-mg tablets	60-mg tablets	30-mg tablets	10-mg tablets
99.17	54.21	28.51	9.06
94.31	55.62	26.25	8.83
95.92	57.40	25.92	9.08
94.55	57.51	28.62	
93.83	52.59	24.93	

(a) For each dosage, calculate the mean and the standard deviation for the mg of morphine hydrochloride per tablet.

(b) For each dosage level, and assuming that $\overline{X}$ and s^2 are good approximations for μ and for σ^2, and that the population is normally distributed, what percentage of tablets contain more than the nominal amount of morphine hydro- chloride per tablet?

The data in this problem are from Salem, I. I.; Galan, A. C. Anal. Chim. Acta 1993, 283, 334–337.

4. Daskalakis and co-workers evaluated several procedures for digesting oyster and mussel tissue prior to analyzing them for silver. To evaluate the procedures they spiked samples with known amounts of silver and analyzed the samples to determine the amount of silver, reporting results as the percentage of added silver found in the analysis. A procedure was judged acceptable if its spike recoveries fell within the range 100±15%. The spike recoveries for one method are shown here.

105%	108%	92%	99%
101%	93%	93%	104%

Assuming a normal distribution for the spike recoveries, what is the probability that any single spike recovery is within the accepted range?

The data in this problem are from Daskalakis, K. D.; O'Connor, T. P.; Crecelius, E. A. *Environ. Sci. Technol.* **1997**, *31*, 2303– 2306. See Chapter 15 to learn more about using a spike recovery to evaluate an analytical method.

5. The formula weight (*FW*) of a gas can be determined using the following form of the ideal gas law

$$FW = \frac{g\mathrm{R}T}{PV}$$

where g is the mass in grams, R is the gas constant, T is the temperature in Kelvin, P is the pressure in atmospheres, and V is the volume in liters. In a typical analysis the following data are obtained (with estimated uncertainties in parentheses)

g = 0.118 g (± 0.002 g)

R = 0.082056 L atm mol^{-1} K^{-1} (± 0.000001 L atm mol^{-1} K^{-1})

T = 298.2 K (± 0.1 K)

P = 0.724 atm (± 0.005 atm)

V = 0.250 L (± 0.005 L)

(a) What is the compound's formula weight and its estimated uncertainty?

(b) To which variable(s) should you direct your attention if you wish to improve the uncertainty in the compound's molecular weight?

6. To prepare a standard solution of Mn^{2+}, a 0.250 g sample of Mn is dissolved in 10 mL of concentrated HNO_3 (measured with a graduated cylinder). The resulting solution is quantitatively transferred to a 100-mL volumetric flask and diluted to volume with distilled water. A 10-mL aliquot of the solution is pipeted into a 500-mL volumetric flask and diluted to volume.

(a) Express the concentration of Mn in mg/L, and estimate its uncertainty using a propagation of uncertainty.

(b) Can you improve the concentration's uncertainty by using a pipet to measure the HNO_3, instead of a graduated cylinder?

7. The mass of a hygroscopic compound is measured using the technique of weighing by difference. In this technique the compound is placed in a sealed container and weighed. A portion of the compound is removed and the container and the remaining material are reweighed. The difference between the two masses gives the sample's mass. A solution of a hygroscopic compound with a gram formula weight of 121.34 g/mol (±0.01 g/mol) is prepared in the following manner. A sample of the compound and its container has a mass of 23.5811 g. A portion of the compound is transferred to a 100-mL volumetric flask and diluted to volume. The mass of the compound and container after the transfer is 22.1559 g. Calculate the compound's molarity and estimate its uncertainty by a propagation of uncertainty.

8. Use a propagation of uncertainty to show that the standard error of the mean for n determinations is $\sigma/\sqrt{n}$.

9. Beginning with Equation 4.6.4 and Equation 4.6.5, use a propagation of uncertainty to derive Equation 4.6.6.

10. What is the smallest mass you can measure on an analytical balance that has a tolerance of ±0.1 mg, if the relative error must be less than 0.1%?

11. Which of the following is the best way to dispense 100.0 mL if we wish to minimize the uncertainty: (a) use a 50-mL pipet twice; (b) use a 25-mL pipet four times; or (c) use a 10-mL pipet ten times?

12. You can dilute a solution by a factor of 200 using readily available pipets (1-mL to 100-mL) and volumetric flasks (10-mL to 1000-mL) in either one step, two steps, or three steps. Limiting yourself to the glassware in Table 4.2.1, determine the proper combination of glassware to accomplish each dilution, and rank them in order of their most probable uncertainties.

13. Explain why changing all values in a data set by a constant amount will change $\overline{X}$ but has no effect on the standard deviation, s.

14. Obtain a sample of a metal, or other material, from your instructor and determine its density by one or both of the following methods:

Method A: Determine the sample's mass with a balance. Calculate the sample's volume using appropriate linear dimensions.

Method B: Determine the sample's mass with a balance. Calculate the sample's volume by measuring the amount of water it displaces by adding water to a graduated cylinder, reading the volume, adding the sample, and reading the new volume. The difference in volumes is equal to the sample's volume.

Determine the density at least five times.

(a) Report the mean, the standard deviation, and the 95% confidence interval for your results.

(b) Find the accepted value for the metal's density and determine the absolute and relative error for your determination of the metal's density.

(c) Use a propagation of uncertainty to determine the uncertainty for your method of analysis. Is the result of this calculation consistent with your experimental results? If not, suggest some possible reasons for this disagreement.

15. How many carbon atoms must a molecule have if the mean number of ^{13}C atoms per molecule is at least one? What percentage of such molecules will have no atoms of ^{13}C?

16. In Example 4.4.1 we determined the probability that a molecule of cholesterol, $C_{27}H_{44}O$, had no atoms of ^{13}C.

(a) Calculate the probability that a molecule of cholesterol, has 1 atom of ^{13}C.

(b) What is the probability that a molecule of cholesterol has two or more atoms of ^{13}C?

17. Berglund and Wichardt investigated the quantitative determination of Cr in high-alloy steels using a potentiometric titration of Cr(VI). Before the titration, samples of the steel were dissolved in acid and the chromium oxidized to Cr(VI) using peroxydisulfate. Shown here are the results (as %w/w Cr) for the analysis of a reference steel.

16.968	16.922	16.840	16.883
16.887	16.977	16.857	16.728

Calculate the mean, the standard deviation, and the 95% confidence interval about the mean. What does this confidence interval mean?

The data in this problem are from Berglund, B.; Wichardt, C. *Anal. Chim. Acta* **1990**, *236*, 399–410.

18. Ketkar and co-workers developed an analytical method to determine trace levels of atmospheric gases. An analysis of a sample that is 40.0 parts per thousand (ppt) 2-chloroethylsulfide gave the following results

43.3	34.8	31.9
37.8	34.4	31.9
42.1	33.6	35.3

(a) Determine whether there is a significant difference between the experimental mean and the expected value at $\alpha = 0.05$.

(b) As part of this study, a reagent blank was analyzed 12 times giving a mean of 0.16 ppt and a standard deviation of 1.20 ppt. What are the IUPAC detection limit, the limit of identification, and limit of quantitation for this method assuming $\alpha = 0.05$?

The data in this problem are from Ketkar, S. N.; Dulak, J. G.; Dheandhanou, S.; Fite, W. L. *Anal. Chim. Acta* **1991**, *245*, 267–270.

19. To test a spectrophotometer's accuracy a solution of 60.06 ppm $K_2Cr_2O_7$ in 5.0 mM H_2SO_4 is prepared and analyzed. This solution has an expected absorbance of 0.640 at 350.0 nm in a 1.0-cm cell when using 5.0 mM H_2SO_4 as a reagent blank. Several aliquots of the solution produce the following absorbance values.

0.639	0.638	0.640	0.639	0.640	0.639	0.638

Determine whether there is a significant difference between the experimental mean and the expected value at $\alpha = 0.01$.

20. Monna and co-workers used radioactive isotopes to date sediments from lakes and estuaries. To verify this method they analyzed a ^{208}Po standard known to have an activity of 77.5 decays/min, obtaining the following results.

77.09	75.37	72.42	76.84	77.84	76.69
78.03	74.96	77.54	76.09	81.12	75.75

Determine whether there is a significant difference between the mean and the expected value at $\alpha = 0.05$.

The data in this problem are from Monna, F.; Mathieu, D.; Marques, A. N.; Lancelot, J.; Bernat, M. *Anal. Chim. Acta* **1996**, *330*, 107–116.

21. A 2.6540-g sample of an iron ore, which is 53.51% w/w Fe, is dissolved in a small portion of concentrated HCl and diluted to volume in a 250-mL volumetric flask. A spectrophotometric determination of the concentration of Fe in this solution yields results of 5840, 5770, 5650, and 5660 ppm. Determine whether there is a significant difference between the experimental mean and the expected value at $\alpha = 0.05$.

22. Horvat and co-workers used atomic absorption spectroscopy to determine the concentration of Hg in coal fly ash. Of particular interest to the authors was developing an appropriate procedure for digesting samples and releasing the Hg for analysis. As part of their study they tested several reagents for digesting samples. Their results using HNO_3 and using a 1 + 3 mixture of HNO_3 and HCl are shown here. All concentrations are given as ppb Hg sample.

HNO_3:	161	165	160	167	166	
1 + 3 HNO_3 – HCl:	159	145	140	147	143	156

Determine whether there is a significant difference between these methods at $\alpha = 0.05$.

The data in this problem are from Horvat, M.; Lupsina, V.; Pihlar, B. *Anal. Chim. Acta* **1991**, *243*, 71–79.

23, Lord Rayleigh, John William Strutt (1842-1919), was one of the most well known scientists of the late nineteenth and early twentieth centuries, publishing over 440 papers and receiving the Nobel Prize in 1904 for the discovery of argon. An important turning point in Rayleigh's discovery of Ar was his experimental measurements of the density of N_2. Rayleigh approached this experiment in two ways: first by taking atmospheric air and removing O_2 and H_2; and second, by chemically producing N_2 by decomposing nitrogen containing compounds (NO, N_2O, and NH_4NO_3) and again removing O_2 and H_2. The following table shows his results for the density of N_2, as published in *Proc. Roy. Soc.* **1894**, *LV*, 340 (publication 210); all values are the grams of gas at an equivalent volume, pressure, and temperature.

atmospheric origin	chemical origin
2.31017	2.30143
2.30986	2.29890
2.31010	2.29816
2.31001	2.30182
2.31024	2.29869
2.31010	2.29940
2.31028	2.29849
	2.29889

Explain why this data led Rayleigh to look for and to discover Ar. You can read more about this discovery here: Larsen, R. D. *J. Chem. Educ.* **1990**, *67*, 925–928.

24. Gács and Ferraroli reported a method for monitoring the concentration of SO_2 in air. They compared their method to the standard method by analyzing urban air samples collected from a single location. Samples were collected by drawing air through a collection solution for 6 min. Shown here is a summary of their results with SO_2 concentrations reported in $\mu L/m^3$.

standard method	new method
21.62	21.54
22.20	20.51
24.27	22.31
23.54	21.30
24.25	24.62
23.09	25.72
21.02	21.54

Using an appropriate statistical test, determine whether there is any significant difference between the standard method and the new method at $\alpha = 0.05$.

The data in this problem are from Gács, I.; Ferraroli, R. *Anal. Chim. Acta* **1992**, *269*, 177–185.

25. One way to check the accuracy of a spectrophotometer is to measure absorbances for a series of standard dichromate solutions obtained from the National Institute of Standards and Technology. Absorbances are measured at 257 nm and compared to the accepted values. The results obtained when testing a newly purchased spectrophotometer are shown here. Determine if the tested spectrophotometer is accurate at $\alpha = 0.05$.

standard	measured absorbance	expected absorbance
1	0.2872	0.2871
2	0.5773	0.5760
3	0.8674	0.8677
4	1.1623	1.1608
5	1.4559	1.4565

26. Maskarinec and co-workers investigated the stability of volatile organics in environmental water samples. Of particular interest was establishing the proper conditions to maintain the sample's integrity between its collection and its analysis. Two preservatives were investigated—ascorbic acid and sodium bisulfate—and maximum holding times were determined for a number of volatile organics and water matrices. The following table shows results for the holding time (in days) of nine organic compounds in surface water.

compound	Ascorbic Acid	Sodium Bisulfate
methylene chloride	77	62
carbon disulfide	23	54
trichloroethane	52	51
benzene	62	42
1,1,2-trichlorethane	57	53
1,1,2,2-tetrachloroethane	33	85
tetrachloroethene	32	94
chlorbenzene	36	86

Determine whether there is a significant difference in the effectiveness of the two preservatives at $\alpha = 0.10$.

The data in this problem are from Maxkarinec, M. P.; Johnson, L. H.; Holladay, S. K.; Moody, R. L.; Bayne, C. K.; Jenkins, R. A. *Environ. Sci. Technol.* **1990**, *24*, 1665–1670.

27. Using X-ray diffraction, Karstang and Kvalhein reported a new method to determine the weight percent of kaolinite in complex clay minerals using X-ray diffraction. To test the method, nine samples containing known amounts of kaolinite were prepared and analyzed. The results (as % w/w kaolinite) are shown here.

actual	5.0	10.0	20.0	40.0	50.0	60.0	80.0	90.0	95.0
found	6.8	11.7	19.8	40.5	53.6	61.7	78.9	91.7	94.7

Evaluate the accuracy of the method at $\alpha = 0.05$.

The data in this problem are from Karstang, T. V.; Kvalhein, O. M. *Anal. Chem.* **1991**, *63*, 767–772.

28. Mizutani, Yabuki and Asai developed an electrochemical method for analyzing *l*-malate. As part of their study they analyzed a series of beverages using both their method and a standard spectrophotometric procedure based on a clinical kit purchased from Boerhinger Scientific. The following table summarizes their results. All values are in ppm.

Sample	Electrode	Spectrophotometric
Apple Juice 1	34.0	33.4
Apple Juice 2	22.6	28.4
Apple Juice 3	29.7	29.5
Apple Juice 4	24.9	24.8
Grape Juice 1	17.8	18.3
Grape Juice 2	14.8	15.4
Mixed Fruit Juice 1	8.6	8.5
Mixed Fruit Juice 2	31.4	31.9
White Wine 1	10.8	11.5
White Wine 2	17.3	17.6
White Wine 3	15.7	15.4
White Wine 4	18.4	18.3

The data in this problem are from Mizutani, F.; Yabuki, S.; Asai, M. *Anal. Chim. Acta* **1991**, *245*,145–150.

29. Alexiev and colleagues describe an improved photometric method for determining Fe^{3+} based on its ability to catalyze the oxidation of sulphanilic acid by KIO_4. As part of their study, the concentration of Fe^{3+} in human serum samples was determined by the improved method and the standard method. The results, with concentrations in $\mu\text{mol/L}$, are shown in the following table.

Sample	Improved Method	Standard Method
1	8.25	8.06
2	9.75	8.84
3	9.75	8.36
4	9.75	8.73
5	10.75	13.13
6	11.25	13.65
7	13.88	13.85
8	14.25	13.43

Determine whether there is a significant difference between the two methods at $\alpha = 0.05$.

The data in this problem are from Alexiev, A.; Rubino, S.; Deyanova, M.; Stoyanova, A.; Sicilia, D.; Perez Bendito, D. *Anal. Chim. Acta*, **1994**, *295*, 211–219.

30. Ten laboratories were asked to determine an analyte's concentration of in three standard test samples. Following are the results, in $\mu\text{g/ml}$.

Laboratory	Sample 1	Sample 2	Sample 3
1	22.6	13.6	16.0
2	23.0	14.2	15.9
3	21.5	13.9	16.9
4	21.9	13.9	16.9
5	21.3	13.5	16.7
6	22.1	13.5	17.4
7	23.1	13.5	17.5
8	21.7	13.5	16.8
9	22.2	12.9	17.2
10	21.7	13.8	16.7

Determine if there are any potential outliers in Sample 1, Sample 2 or Sample 3. Use all three methods—Dixon's *Q*-test, Grubb's test, and Chauvenet's criterion—and compare the results to each other. For Dixon's *Q*-test and for the Grubb's test, use a significance level of $\alpha = 0.05$.

The data in this problem are adapted from Steiner, E. H. "Planning and Analysis of Results of Collaborative Tests," in *Statistical Manual of the Association of Official Analytical Chemists*, Association of Official Analytical Chemists: Washington, D. C., 1975.

31.When copper metal and powdered sulfur are placed in a crucible and ignited, the product is a sulfide with an empirical formula of Cu_xS. The value of x is determined by weighing the Cu and the S before ignition and finding the mass of Cu_xS when the reaction is complete (any excess sulfur leaves as SO_2). The following table shows the Cu/S ratios from 62 such experiments (note that the values are organized from smallest-to-largest by rows).

1.764	1.838	1.865	1.866	1.872	1.877
1.890	1.891	1.891	1.897	1.899	1.900
1.906	1.908	1.910	1.911	1.916	1.919
1.920	1.922	1.927	1.931	1.935	1.936
1.936	1.937	1.939	1.939	1.940	1.941
1.941	1.942	1.943	1.948	1.953	1.955
1.957	1.957	1.957	1.959	1.962	1.963
1.963	1.963	1.966	1.968	1.969	1.973
1.975	1.976	1.977	1.981	1.981	1.988
1.993	1.993	1.995	1.995	1.995	2.017
2.029	2.042				

(a) Calculate the mean, the median, and the standard deviation for this data.

(b) Construct a histogram for this data. From a visual inspection of your histogram, do the data appear normally distributed?

(c) In a normally distributed population 68.26% of all members lie within the range $\mu \pm 1\sigma$. What percentage of the data lies within the range $\overline{X} \pm 1\sigma$? Does this support your answer to the previous question?

(d) Assuming that $\overline{X}$ and s^2 are good approximations for μ and for σ^2, what percentage of all experimentally determined Cu/S ratios should be greater than 2? How does this compare with the experimental data? Does this support your conclusion about whether the data is normally distributed?

(e) It has been reported that this method of preparing copper sulfide results in a non-stoichiometric compound with a Cu/S ratio of less than 2. Determine if the mean value for this data is significantly less than 2 at a significance level of $\alpha = 0.01$.

See Blanchnik, R.; Müller, A. "The Formation of Cu_2S From the Elements I. Copper Used in Form of Powders," *Thermochim. Acta*, **2000**, *361*, 31-52 for a discussion of some of the factors affecting the formation of non-stoichiometric copper sulfide. The data in this problem were collected by students at DePauw University.

32. Real-time quantitative PCR is an analytical method for determining trace amounts of DNA. During the analysis, each cycle doubles the amount of DNA. A probe species that fluoresces in the presence of DNA is added to the reaction mixture and the increase in fluorescence is monitored during the cycling. The cycle threshold, C_t, is the cycle when the fluorescence exceeds a threshold value. The data in the following table shows C_t values for three samples using real-time quantitative PCR. Each sample was analyzed 18 times.

Sample X		Sample Y		Sample Z	
24.24	25.14	24.41	28.06	22.97	23.43
23.97	24.57	27.21	27.77	22.93	23.66
24.44	24.49	27.02	28.74	22.95	28.79
24.79	24.68	26.81	28.35	23.12	23.77
23.92	24.45	26.64	28.80	23.59	23.98
24.53	24,48	27.63	27.99	23.37	23.56
24.95	24.30	28.42	28.21	24.17	22.80
24.76	24.60	25.16	28.00	23.48	23.29
25.18	24.57	28.53	28.21	23.80	23.86

Examine this data and write a brief report on your conclusions. Issues you may wish to address include the presence of outliers in the samples, a summary of the descriptive statistics for each sample, and any evidence for a difference between the samples.

The data in this problem is from Burns, M. J.; Nixon, G. J.; Foy, C. A.; Harris, N. *BMC Biotechnol.* **2005**, *5:31* (open access publication).

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5.10: ADDITIONAL RESOURCES

The following experiments provide useful introductions to the statistical analysis of data in the analytical chemistry laboratory.

- Bularzik, J. "The Penny Experiment Revisited: An Illustration of Significant Figures, Accuracy, Precision, and Data Analysis," *J. Chem. Educ.* **2007**, *84*, 1456–1458.
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- Cunningham, C. C.; Brown, G. R.; St Pierre, L. E. "Evaluation of Experimental Data," *J. Chem. Educ.* **1981**, *58*, 509–511.
- Edminston, P. L.; Williams, T. R. "An Analytical Laboratory Experiment in Error Analysis: Repeated Determination of Glucose Using Commercial Glucometers," *J. Chem. Educ.* **2000**, *77*, 377–379.
- Gordus, A. A. "Statistical Evaluation of Class Data for Two Buret Readings," *J. Chem. Educ.* **1987**, *64*, 376–377.
- Harvey, D. T. "Statistical Evaluation of Acid/Base Indicators," *J. Chem. Educ.* **1991**, *68*, 329–331.
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- Johll, M. E.; Poister, D.; Ferguson, J. "Statistical Comparison of Multiple Methods for the Determination of Dissolved Oxygen Levels in Natural Water," *Chem. Educator* **2002**, *7*, 146–148.
- Jordon, A. D. "Which Method is Most Precise; Which is Most Accurate?," *J. Chem. Educ.* **2007**, *84*, 1459–1460.
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5.11: CHAPTER SUMMARY AND KEY TERMS

SUMMARY

The data we collect are characterized by their central tendency (where the values cluster), and their spread (the variation of individual values around the central value). We report our data's central tendency by stating the mean or median, and our data's spread using the range, standard deviation or variance. Our collection of data is subject to errors, including determinate errors that affect the data's accuracy and indeterminate errors that affect its precision. A propagation of uncertainty allows us to estimate how these determinate and indeterminate errors affect our results.

When we analyze a sample several times the distribution of the results is described by a probability distribution, two examples of which are the binomial distribution and the normal distribution. Knowing the type of distribution allows us to determine the probability of obtaining a particular range of results. For a normal distribution we express this range as a confidence interval.

A statistical analysis allows us to determine whether our results are significantly different from known values, or from values obtained by other analysts, by other methods of analysis, or for other samples. We can use a *t*-test to compare mean values and an *F*-test to compare variances. To compare two sets of data you first must determine whether the data is paired or unpaired. For unpaired data you also must decide if you can pool the standard deviations. A decision about whether to retain an outlying value can be made using Dixon's *Q*-test, Grubb's test, or Chauvenet's criterion.

You should be sure to exercise caution if you decide to reject an outlier. Finally, the detection limit is a statistical statement about the smallest amount of analyte we can detect with confidence. A detection limit is not exact since its value depends on how willing we are to falsely report the analyte's presence or absence in a sample. When reporting a detection limit you should clearly indicate how you arrived at its value.

KEY TERMS

alternative hypothesis
bias
binomial distribution
box plot
central limit theorem
Chauvenet's criterion
confidence interval
constant determinate error
degrees of freedom
detection limit
determinate error
Dixon's *Q*-test
dot chart
error
F-test
Grubb's test
histogram
indeterminate error
kernel density plot
limit of identification
limit of quantitation
mean
median
measurement error
method error
normal distribution
null hypothesis
one-tailed significance test
outlier
paired data
paired t-test
personal error
population
probability distribution
propagation of uncertainty
proportional determinate error
range
repeatability
reproducibility
sample
sampling error
significance test
standard deviation
standard error of the mean
Standard Reference Material
tolerance
t-test
two-tailed significance test
type 1 error
type 2 error
uncertainty
unpaired data
variance

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CHAPTER OVERVIEW

6: STANDARDIZING ANALYTICAL METHODS

The American Chemical Society's Committee on Environmental Improvement defines standardization as the process of determining the relationship between the signal and the amount of analyte in a sample. In Chapter 3 we defined this relationship as

$$S_{total} = k_A n_A + S_{reag} \text{ or } S_{total} = k_A C_A + S_{reag}$$

where S_{total} is the signal, n_A is the moles of analyte, C_A is the analyte's concentration, k_A is the method's sensitivity for the analyte, and S_{reag} is the contribution to S_{total} from sources other than the sample. To standardize a method we must determine values for k_A and S_{reag}. Strategies for accomplishing this are the subject of this chapter.

6.1: Analytical Signals
6.2: Calibrating the Signal
6.3: Determining the Sensitivity
6.4: Linear Regression and Calibration Curves
6.5: Compensating for the Reagent Blank
6.6: Using Excel and R for a Linear Regression
6.7: Problems
6.8: Additional Resources
6.9: Chapter Summary and Key Terms

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6.1: ANALYTICAL SIGNALS

To standardize an analytical method we use standards that contain known amounts of analyte. The accuracy of a standardization, therefore, depends on the quality of the reagents and the glassware we use to prepare these standards. For example, in an acid–base titration the stoichiometry of the acid–base reaction defines the relationship between the moles of analyte and the moles of titrant. In turn, the moles of titrant is the product of the titrant's concentration and the volume of titrant used to reach the equivalence point. The accuracy of a titrimetric analysis, therefore, is never better than the accuracy with which we know the titrant's concentration.

> See Chapter 9 for a thorough discussion of titrimetric methods of analysis.

PRIMARY AND SECONDARY STANDARDS

There are two categories of analytical standards: primary standards and secondary standards. A ***primary standard*** is a reagent that we can use to dispense an accurately known amount of analyte. For example, a 0.1250-g sample of $K_2Cr_2O_7$ contains 4.249×10^{-4} moles of $K_2Cr_2O_7$. If we place this sample in a 250-mL volumetric flask and dilute to volume, the concentration of $K_2Cr_2O_7$ in the resulting solution is 1.700×10^{-3} M . A primary standard must have a known stoichiometry, a known purity (or assay), and it must be stable during long-term storage. Because it is difficult to establishing accurately the degree of hydration, even after drying, a hydrated reagent usually is not a primary standard.

Reagents that do not meet these criteria are secondary standards. The concentration of a ***secondary standard*** is determined relative to a primary standard. Lists of acceptable primary standards are available (see, for instance, Smith, B. W.; Parsons, M. L. *J. Chem. Educ.* **1973**, *50*, 679–681; or Moody, J. R.; Green- burg, P. R.; Pratt, K. W.; Rains, T. C. *Anal. Chem.* **1988**, *60*, 1203A–1218A). Appendix 8 provides examples of some common primary standards.

> NaOH is one example of a secondary standard. Commercially available NaOH contains impurities of NaCl, Na_2CO_3, and Na_2SO_4, and readily absorbs H_2O from the atmosphere. To determine the concentration of NaOH in a solution, we titrate it against a primary standard weak acid, such as potassium hydrogen phthalate, $KHC_8H_4O_4$.

OTHER REAGENTS

Preparing a standard often requires additional reagents that are not primary standards or secondary standards, such as a suitable solvent or reagents needed to adjust the standard's matrix. These solvents and reagents are potential sources of additional analyte, which, if not accounted for, produce a determinate error in the standardization. If available, reagent grade chemicals that conform to standards set by the American Chemical Society are used [Committee on Analytical Reagents, *Reagent Chemicals*, 8th ed., American Chemical Society: Washington, D. C., 1993]. The label on the bottle of a reagent grade chemical (Figure 5.1.1) lists either the limits for specific impurities or provides an assay for the impurities. We can improve the quality of a reagent grade chemical by purifying it, or by conducting a more accurate assay. As discussed later in the chapter, we can correct for contributions to S_{total} from reagents used in an analysis by including an appropriate blank determination in the analytical procedure.



Figure 5.1.1 : Two examples of packaging labels for reagent grade chemicals. The label on the bottle on the right provides the manufacturer's assay for the reagent, NaBr. Note that potassium is flagged with an asterisk (*) because its assay exceeds the limit established by the American Chemical Society (ACS). The label for the bottle on the left does not provide an assay for impurities; however it indicates that the reagent meets ACS specifications by providing the maximum limits for impurities. An assay for the reagent, $NaHCO_3$, is provided.

PREPARING A STANDARD SOLUTION

It often is necessary to prepare a series of standards, each with a different concentration of analyte. We can prepare these standards in two ways. If the range of concentrations is limited to one or two orders of magnitude, then each solution is best prepared by transferring a known mass or volume of the pure standard to a volumetric flask and diluting to volume.

When working with a larger range of concentrations, particularly a range that extends over more than three orders of magnitude, standards are best prepared by a serial dilution from a single stock solution. In a ***serial dilution*** we prepare the most concentrated standard and then dilute a portion of that solution to prepare the next most concentrated standard. Next, we dilute a portion of the second standard to prepare a third standard, continuing this process until we have prepared all of our standards. Serial dilutions must be prepared with extra care because an error in preparing one standard is passed on to all succeeding standards.

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6.2: CALIBRATING THE SIGNAL

The accuracy with which we determine k_A and S_{reag} depends on how accurately we can measure the signal, S_{total}. We measure signals using equipment, such as glassware and balances, and instrumentation, such as spectrophotometers and pH meters. To minimize determinate errors that might affect the signal, we first calibrate our equipment and instrumentation by measuring S_{total} for a standard with a known response of S_{std}, adjusting S_{total} until

$$S_{total} = S_{std}$$

Here are two examples of how we calibrate signals; other examples are provided in later chapters that focus on specific analytical methods.

When the signal is a measurement of mass, we determine S_{total} using an analytical balance. To calibrate the balance's signal we use a reference weight that meets standards established by a governing agency, such as the National Institute for Standards and Technology or the American Society for Testing and Materials. An electronic balance often includes an internal calibration weight for routine calibrations, as well as programs for calibrating with external weights. In either case, the balance automatically adjusts S_{total} to match S_{std}.

> See Chapter 2.4 to review how an electronic balance works. Calibrating a balance is important, but it does not eliminate all sources of determinate error when measuring mass. See Appendix 9 for a discussion of correcting for the buoyancy of air.

We also must calibrate our instruments. For example, we can evaluate a spectrophotometer's accuracy by measuring the absorbance of a carefully prepared solution of 60.06 mg/L $K_2Cr_2O_7$ in 0.0050 M H_2SO_4, using 0.0050 M H_2SO_4 as a reagent blank [Ebel, S. *Fresenius J. Anal. Chem.* **1992**, *342*, 769]. An absorbance of 0.640 ± 0.010 absorbance units at a wavelength of 350.0 nm indicates that the spectrometer's signal is calibrated properly.

> Be sure to read and follow carefully the calibration instructions provided with any instrument you use.

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6.3: DETERMINING THE SENSITIVITY

To standardize an analytical method we also must determine the analyte's sensitivity, k_A, in Equation 5.3.1 or Equation 5.3.2 .

$$S_{total} = k_A n_A + S_{reag} \tag{6.3.1}$$

$$S_{total} = k_A C_A + S_{reag} \tag{6.3.2}$$

In principle, it is possible to derive the value of k_A for any analytical method if we understand fully all the chemical reactions and physical processes responsible for the signal. Unfortunately, such calculations are not feasible if we lack a sufficiently developed theoretical model of the physical processes or if the chemical reaction's evince non-ideal behavior. In such situations we must determine the value of k_A by analyzing one or more standard solutions, each of which contains a known amount of analyte. In this section we consider several approaches for determining the value of k_A. For simplicity we assume that S_{reag} is accounted for by a proper reagent blank, allowing us to replace S_{total} in Equation 6.3.1 and Equation 6.3.2 with the analyte's signal, S_A.

$$S_A = k_A n_A \tag{6.3.3}$$

$$S_A = k_A C_A \tag{6.3.4}$$

> Equation 6.3.3 and Equation 6.3.4 essentially are identical, differing only in whether we choose to express the amount of analyte in moles or as a concentration. For the remainder of this chapter we will limit our treatment to Equation 6.3.4. You can extend this treatment to Equation 6.3.3 by replacing C_A with n_A.

SINGLE-POINT VERSUS MULTIPLE-POINT STANDARDIZATIONS

The simplest way to determine the value of k_A in Equation 6.3.4 is to use a single-point standardization in which we measure the signal for a standard, S_{std}, that contains a known concentration of analyte, C_{std}. Substituting these values into Equation 6.3.4

$$k_A = \frac{S_{std}}{C_{std}} \tag{6.3.5}$$

gives us the value for k_A. Having determined k_A, we can calculate the concentration of analyte in a sample by measuring its signal, S_{samp}, and calculating C_A using Equation 6.3.6.

$$C_A = \frac{S_{samp}}{k_A} \tag{6.3.6}$$

A single-point standardization is the least desirable method for standardizing a method. There are two reasons for this. First, any error in our determination of k_A carries over into our calculation of C_A. Second, our experimental value for k_A is based on a single concentration of analyte. To extend this value of k_A to other concentrations of analyte requires that we assume a linear relationship between the signal and the analyte's concentration, an assumption that often is not true [Cardone, M. J.; Palmero, P. J.; Sybrandt, L. B. *Anal. Chem.* **1980**, *52*, 1187–1191]. Figure 5.3.1 shows how assuming a constant value of k_A leads to a determinate error in C_A if k_A becomes smaller at higher concentrations of analyte. Despite these limitations, single-point standardizations find routine use when the expected range for the analyte's concentrations is small. Under these conditions it often is safe to assume that k_A is constant (although you should verify this assumption experimentally). This is the case, for example, in clinical labs where many automated analyzers use only a single standard.

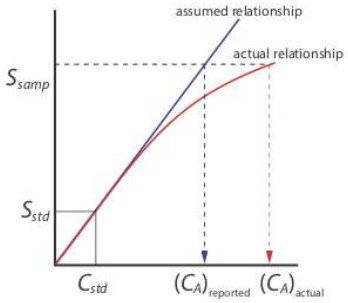


Figure 5.3.1 : Example showing how a single-point standardization leads to a determinate error in an analyte's reported concentration if we incorrectly assume that k_A is constant. The assumed relationship between S_{samp} and C_A is based on a single standard and is a straight-line; the actual relationship between S_{samp} and C_A becomes curved for larger concentrations of analyte.

The better way to standardize a method is to prepare a series of standards, each of which contains a different concentration of analyte. Standards are chosen such that they bracket the expected range for the analyte's concentration. A ***multiple-point standardization*** should

include at least three standards, although more are preferable. A plot of S_{std} versus C_{std} is called a ***calibration curve***. The exact standardization, or calibration relationship, is determined by an appropriate curve-fitting algorithm.

> Linear regression, which also is known as the method of least squares, is one such algorithm. Its use is covered in Section 5.4.

There are two advantages to a multiple-point standardization. First, although a determinate error in one standard introduces a determinate error, its effect is minimized by the remaining standards. Second, because we measure the signal for several concentrations of analyte, we no longer must assume k_A is independent of the analyte's concentration. Instead, we can construct a calibration curve similar to the "actual relationship" in Figure 5.3.1 .

EXTERNAL STANDARDS

The most common method of standardization uses one or more ***external standards***, each of which contains a known concentration of analyte. We call these standards "external" because they are prepared and analyzed separate from the samples.

> Appending the adjective "external" to the noun "standard" might strike you as odd at this point, as it seems reasonable to assume that standards and samples are analyzed separately. As we will soon learn, however, we can add standards to our samples and analyze both simultaneously.

SINGLE EXTERNAL STANDARD

With a single external standard we determine k_A using EEquation 6.3.5 and then calculate the concentration of analyte, C_A, using Equation 6.3.6.

EXAMPLE 5.3.1

A spectrophotometric method for the quantitative analysis of Pb^{2+} in blood yields an S_{std} of 0.474 for a single standard for which the concentration of lead is 1.75 ppb. What is the concentration of Pb^{2+} in a sample of blood for which S_{samp} is 0.361?

Solution

Equation 6.3.5 allows us to calculate the value of k_A using the data for the single external standard.

$$k_A = \frac{S_{std}}{C_{std}} = \frac{0.474}{1.75 \text{ ppb}} = 0.2709 \text{ ppb}^{-1}$$

Having determined the value of k_A, we calculate the concentration of Pb^{2+} in the sample of blood is calculated using Equation 6.3.6.

$$C_A = \frac{S_{samp}}{k_A} = \frac{0.361}{0.2709 \text{ ppb}^{-1}} = 1.33 \text{ ppb}$$

MULTIPLE EXTERNAL STANDARDS

Figure 5.3.2 shows a typical multiple-point external standardization. The volumetric flask on the left contains a reagent blank and the remaining volumetric flasks contain increasing concentrations of Cu^{2+}. Shown below the volumetric flasks is the resulting calibration curve. Because this is the most common method of standardization, the resulting relationship is called a ***normal calibration curve***.

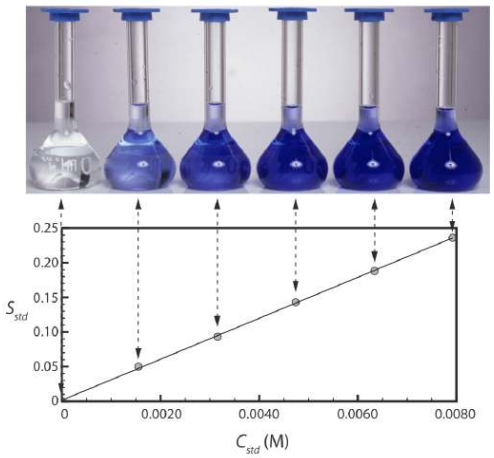


Figure 5.3.2 : The photo at the top of the figure shows a reagent blank (far left) and a set of five external standards for Cu^{2+} with concentrations that increase from left-to-right. Shown below the external standards is the resulting normal calibration curve. The absorbance of each standard, S_{std}, is shown by the filled circles.

When a calibration curve is a straight-line, as it is in Figure 5.3.2 , the slope of the line gives the value of k_A. This is the most desirable situation because the method's sensitivity remains constant throughout the analyte's concentration range. When the calibration curve is not a straight-line, the method's sensitivity is a function of the analyte's concentration. In Figure 5.3.1 , for example, the value of k_A is greatest when the analyte's concentration is small and it decreases continuously for higher concentrations of analyte. The value of k_A at any point along the calibration curve in Figure 5.3.1 is the slope at that point. In either case, a calibration curve allows to relate S_{samp} to the analyte's concentration.

EXAMPLE 5.3.2

A second spectrophotometric method for the quantitative analysis of Pb^{2+} in blood has a normal calibration curve for which

$$S_{std} = (0.296\ \text{ppb}^{-1} \times C_{std}) + 0.003$$

What is the concentration of Pb^{2+} in a sample of blood if S_{samp} is 0.397?

Solution

To determine the concentration of Pb^{2+} in the sample of blood, we replace S_{std} in the calibration equation with S_{samp} and solve for C_A.

$$C_A = \frac{S_{samp} - 0.003}{0.296\ \text{ppb}^{-1}} = \frac{0.397 - 0.003}{0.296\ \text{ppb}^{-1}} = 1.33\ \text{ppb}$$

It is worth noting that the calibration equation in this problem includes an extra term that does not appear in Equation 6.3.6. Ideally we expect our calibration curve to have a signal of zero when C_A is zero. This is the purpose of using a reagent blank to correct the measured signal. The extra term of +0.003 in our calibration equation results from the uncertainty in measuring the signal for the reagent blank and the standards.

EXERCISE 5.3.1

Figure 5.3.2 shows a normal calibration curve for the quantitative analysis of Cu^{2+}. The equation for the calibration curve is

$$S_{std} = 29.59\ \text{M}^{-1} \times C_{std} + 0.015$$

What is the concentration of Cu^{2+} in a sample whose absorbance, S_{samp}, is 0.114? Compare your answer to a one-point standardization where a standard of 3.16×10^{-3} M Cu^{2+} gives a signal of 0.0931.

Answer

Substituting the sample's absorbance into the calibration equation and solving for C_A give

$$S_{samp} = 0.114 = 29.59\ \text{M}^{-1} \times C_A + 0.015$$

$$C_A = 3.35 \times 10^{-3}\ \text{M}$$

For the one-point standardization, we first solve for k_A

$$k_A = \frac{S_{std}}{C_{std}} = \frac{0.0931}{3.16 \times 10^{-3}\ \text{M}} = 29.46\ \text{M}^{-1}$$

and then use this value of k_A to solve for C_A.

$$C_A = \frac{S_{samp}}{k_A} = \frac{0.114}{29.46\ \text{M}^{-1}} = 3.87 \times 10^{-3}\ \text{M}$$

When using multiple standards, the indeterminate errors that affect the signal for one standard are partially compensated for by the indeterminate errors that affect the other standards. The standard selected for the one-point standardization has a signal that is smaller than that predicted by the regression equation, which underestimates k_A and overestimates C_A.

An external standardization allows us to analyze a series of samples using a single calibration curve. This is an important advantage when we have many samples to analyze. Not surprisingly, many of the most common quantitative analytical methods use an external standardization.

There is a serious limitation, however, to an external standardization. When we determine the value of k_A using Equation 6.3.5, the analyte is present in the external standard's matrix, which usually is a much simpler matrix than that of our samples. When we use an external standardization we assume the matrix does not affect the value of k_A. If this is not true, then we introduce a proportional determinate error into our analysis. This is not the case in Figure 5.3.3 , for instance, where we show calibration curves for an analyte in the sample's matrix and in the standard's matrix. In this case, using the calibration curve for the external standards leads to a negative determinate error in analyte's reported concentration. If we expect that matrix effects are important, then we try to match the standard's matrix to that of the sample, a process known as ***matrix matching***. If we are unsure of the sample's matrix, then we must show that matrix effects are negligible or use an alternative method of standardization. Both approaches are discussed in the following section.

The matrix for the external standards in Figure 5.3.2 , for example, is dilute ammonia. Because the $Cu(NH_3)_4^{2+}$ complex absorbs more strongly than Cu^{2+}, adding ammonia increases the signal's magnitude. If we fail to add the same amount of ammonia to our samples, then we will introduce a proportional determinate error into our analysis.

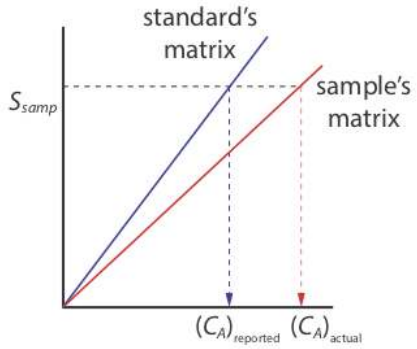


Figure 5.3.3 : Calibration curves for an analyte in the standard's matrix and in the sample's matrix. If the matrix affects the value of k_A, as is the case here, then we introduce a proportional determinate error into our analysis if we use a normal calibration curve.

STANDARD ADDITIONS

We can avoid the complication of matching the matrix of the standards to the matrix of the sample if we carry out the standardization in the sample. This is known as the ***method of standard additions***.

SINGLE STANDARD ADDITION

The simplest version of a standard addition is shown in Figure 5.3.4 . First we add a portion of the sample, V_o, to a volumetric flask, dilute it to volume, V_f, and measure its signal, S_{samp}. Next, we add a second identical portion of sample to an equivalent volumetric flask along with a spike, V_{std}, of an external standard whose concentration is C_{std}. After we dilute the spiked sample to the same final volume, we measure its signal, S_{spike}.

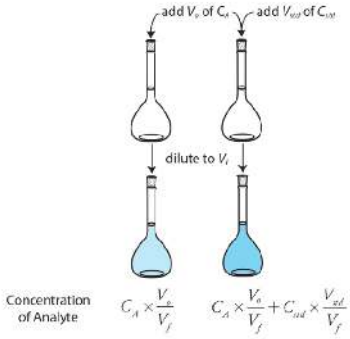


Figure 5.3.4 : Illustration showing the method of standard additions. The volumetric flask on the left contains a portion of the sample, V_o, and the volumetric flask on the right contains an identical portion of the sample and a spike, V_{std}, of a standard solution of the analyte. Both flasks are diluted to the same final volume, V_f. The concentration of analyte in each flask is shown at the bottom of the figure where C_A is the analyte's concentration in the original sample and C_{std} is the concentration of analyte in the external standard.

The following two equations relate S_{samp} and S_{spike} to the concentration of analyte, C_A, in the original sample.

$$S_{samp} = k_A C_A \frac{V_o}{V_f} \tag{6.3.7}$$

$$S_{spike} = k_A \left(C_A \frac{V_o}{V_f} + C_{std} \frac{V_{std}}{V_f} \right) \tag{6.3.8}$$

As long as V_{std} is small relative to V_o, the effect of the standard's matrix on the sample's matrix is insignificant. Under these conditions the value of k_A is the same in Equation 6.3.7 and Equation 6.3.8. Solving both equations for k_A and equating gives

$$\frac{S_{samp}}{C_A \frac{V_o}{V_f}} = \frac{S_{spike}}{C_A \frac{V_o}{V_f} + C_{std} \frac{V_{std}}{V_f}} \tag{6.3.9}$$

which we can solve for the concentration of analyte, C_A, in the original sample.

EXAMPLE 5.3.3

A third spectrophotometric method for the quantitative analysis of Pb^{2+} in blood yields an S_{samp} of 0.193 when a 1.00 mL sample of blood is diluted to 5.00 mL. A second 1.00 mL sample of blood is spiked with 1.00 mL of a 1560-ppb Pb^{2+} external standard and diluted to 5.00 mL, yielding an S_{spike} of 0.419. What is the concentration of Pb^{2+} in the original sample of blood?

Solution

We begin by making appropriate substitutions into Equation 6.3.9 and solving for C_A. Note that all volumes must be in the same units; thus, we first convert V_{std} from 1.00 mL to 1.00×10^{-3} mL.

$$\frac{0.193}{C_A \frac{1.00\text{ mL}}{5.00\text{ mL}}} = \frac{0.419}{C_A \frac{1.00\text{ mL}}{5.00\text{ mL}} + 1560\text{ ppb} \frac{1.00 \times 10^{-3}\text{ mL}}{5.00\text{ mL}}}$$

$$\frac{0.193}{0.200 C_A} = \frac{0.419}{0.200 C_A + 0.3120\text{ ppb}}$$

$$0.0386 C_A + 0.0602\text{ ppb} = 0.0838 C_A$$

$$0.0452 C_A = 0.0602\text{ ppb}$$

$$C_A = 1.33\text{ ppb}$$

The concentration of Pb^{2+} in the original sample of blood is 1.33 ppb.

It also is possible to add the standard addition directly to the sample, measuring the signal both before and after the spike (Figure 5.3.5). In this case the final volume after the standard addition is $V_o + V_{std}$ and Equation 6.3.7, Equation 6.3.8, and Equation 6.3.9 become

$$S_{samp} = k_A C_A$$

$$S_{spike} = k_A \left(C_A \frac{V_o}{V_o + V_{std}} + C_{std} \frac{V_{std}}{V_o + V_{std}} \right) \tag{6.3.10}$$

$$\frac{S_{samp}}{C_A} = \frac{S_{spike}}{C_A \frac{V_o}{V_o + V_{std}} + C_{std} \frac{V_{std}}{V_o + V_{std}}} \tag{6.3.11}$$

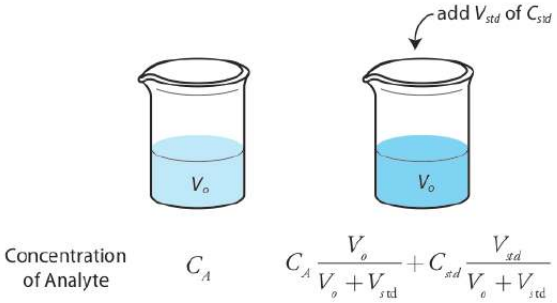


Figure 5.3.5 : Illustration showing an alternative form of the method of standard additions. In this case we add the spike of external standard directly to the sample without any further adjust in the volume.

EXAMPLE 5.3.4

A fourth spectrophotometric method for the quantitative analysis of Pb^{2+} in blood yields an S_{samp} of 0.712 for a 5.00 mL sample of blood. After spiking the blood sample with 5.00 mL of a 1560-ppb Pb^{2+} external standard, an S_{spike} of 1.546 is measured. What is the concentration of Pb^{2+} in the original sample of blood?

Solution

$$\frac{0.712}{C_A} = \frac{1.546}{C_A \frac{5.00\text{ mL}}{5.005\text{ mL}} + 1560\text{ ppb} \frac{5.00 \times 10^{-3}\text{ mL}}{5.005\text{ mL}}}$$

$$\frac{0.712}{C_A} = \frac{1.546}{0.9990 C_A + 1.558\text{ ppb}}$$

$$0.7113 C_A + 1.109\text{ ppb} = 1.546 C_A$$

$$C_A = 1.33\text{ ppb}$$

The concentration of Pb^{2+} in the original sample of blood is 1.33 ppb.

MULTIPLE STANDARD ADDITIONS

We can adapt a single-point standard addition into a multiple-point standard addition by preparing a series of samples that contain increasing amounts of the external standard. Figure 5.3.6 shows two ways to plot a standard addition calibration curve based on Equation 6.3.8. In Figure 5.3.6 a we plot S_{spike} against the volume of the spikes, V_{std}. If k_A is constant, then the calibration curve is a straight-line. It is easy to show that the *x*-intercept is equivalent to $-C_A V_o / C_{std}$.

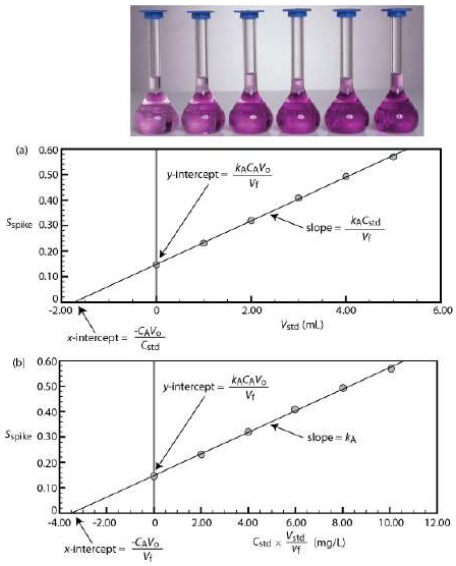


Figure 5.3.6 : Shown at the top of the figure is a set of six standard additions for the determination of Mn^{2+}. The flask on the left is a 25.00 mL sample diluted to 50.00 mL with water. The remaining flasks contain 25.00 mL of sample and, from left-to-right, 1.00, 2.00, 3.00, 4.00, and 5.00 mL spikes of an external standard that is 100.6 mg/L Mn^{2+}. Shown below are two ways to plot the standard additions calibration curve. The absorbance for each standard addition, S_{spike}, is shown by the filled circles.

EXAMPLE 5.3.5

Beginning with Equation 6.3.8 show that the equations in Figure 5.3.6 a for the slope, the *y*-intercept, and the *x*-intercept are correct.

Solution

We begin by rewriting Equation 6.3.8 as

$$S_{spike} = \frac{k_A C_A V_o}{V_f} + \frac{k_A C_{std}}{V_f} \times V_{std}$$

which is in the form of the equation for a straight-line

$$y = y\text{-intercept} + \text{slope} \times x\text{-intercept}$$

where *y* is S_{spike} and *x* is V_{std}. The slope of the line, therefore, is $k_A C_{std}/V_f$ and the *y*-intercept is $k_A C_A V_o/V_f$. The *x*-intercept is the value of *x* when *y* is zero, or

$$0 = \frac{k_A C_A V_o}{V_f} + \frac{k_A C_{std}}{V_f} \times x\text{-intercept}$$

$$x\text{-intercept} = -\frac{k_A C_A V_o / V_f}{K_A C_{std} / V_f} = -\frac{C_A V_o}{C_{std}}$$

EXERCISE 5.3.2

Beginning with Equation 6.3.8 show that the Equations in Figure 5.3.6 b for the slope, the *y*-intercept, and the *x*-intercept are correct.

Answer

We begin with Equation 6.3.8

$$S_{spike} = k_A \left(C_A \frac{V_o}{V_f} + C_{std} \frac{V_{std}}{V_f} \right)$$

rewriting it as

$$S_{spike} = \frac{k_A C_A V_o}{V_f} + k_A \left(C_{std} \frac{V_{std}}{V_f} \right)$$

which is in the form of the linear equation

$$y = y\text{-intercept} + \text{slope} \times x\text{-intercept}$$

where y is S_{spike} and x is $C_{std} \times V_{std}/V_f$. The slope of the line, therefore, is k_A, and the y-intercept is $k_A C_A V_o/V_f$. The x-intercept is the value of x when y is zero, or

$$x\text{-intercept} = -\frac{k_A C_A V_o/V_F}{k_A} = -\frac{C_A V_o}{V_f}$$

Because we know the volume of the original sample, V_o, and the concentration of the external standard, C_{std}, we can calculate the analyte's concentrations from the x-intercept of a multiple-point standard additions.

EXAMPLE 5.3.6

A fifth spectrophotometric method for the quantitative analysis of Pb^{2+} in blood uses a multiple-point standard addition based on Equation 6.3.8. The original blood sample has a volume of 1.00 mL and the standard used for spiking the sample has a concentration of 1560 ppb Pb^{2+}. All samples were diluted to 5.00 mL before measuring the signal. A calibration curve of S_{spike} versus V_{std} has the following equation

$$S_{spike} = 0.266 + 312\ \text{mL}^{-1} \times V_{std}$$

What is the concentration of Pb^{2+} in the original sample of blood?

Solution

To find the x-intercept we set S_{spike} equal to zero.

$$S_{spike} = 0.266 + 312\ \text{mL}^{-1} \times V_{std}$$

Solving for V_{std}, we obtain a value of -8.526×10^{-4} mL for the x-intercept. Substituting the x-intercept's value into the equation from Figure 5.3.6 a

$$-8.526 \times 10^{-4}\ \text{mL} = -\frac{C_A V_o}{C_{std}} = -\frac{C_A \times 1.00\ \text{mL}}{1560\ \text{ppb}}$$

and solving for C_A gives the concentration of Pb^{2+} in the blood sample as 1.33 ppb.

EXERCISE 5.3.3

Figure 5.3.6 shows a standard additions calibration curve for the quantitative analysis of Mn^{2+}. Each solution contains 25.00 mL of the original sample and either 0, 1.00, 2.00, 3.00, 4.00, or 5.00 mL of a 100.6 mg/L external standard of Mn^{2+}. All standard addition samples were diluted to 50.00 mL with water before reading the absorbance. The equation for the calibration curve in Figure 5.3.6 a is

$$S_{std} = 0.0854 \times V_{std} + 0.1478$$

What is the concentration of Mn^{2+} in this sample? Compare your answer to the data in Figure 5.3.6 b, for which the calibration curve is

$$S_{std} = 0.425 \times C_{std}(V_{std}/V_f) + 0.1478$$

Answer

Using the calibration equation from Figure 5.3.6 a, we find that the x-intercept is

$$x\text{-intercept} = -\frac{0.1478}{0.0854\ \text{mL}^{-1}} = -1.731\ \text{mL}$$

If we plug this result into the equation for the x-intercept and solve for C_A, we find that the concentration of Mn^{2+} is

$$C_A = -\frac{x\text{-intercept} \times C_{std}}{V_o} = -\frac{-1.731\ \text{mL} \times 100.6\ \text{mg/L}}{25.00\ \text{mL}} = 6.96\ \text{mg/L}$$

For Figure 5.3.6 b, the x-intercept is

$$x\text{-intercept} = -\frac{0.1478}{0.0425\ \text{mL/mg}} = -3.478\ \text{mg/mL}$$

and the concentration of Mn^{2+} is

$$C_A = -\frac{x\text{-intercept} \times V_f}{V_o} = -\frac{-3.478\ \text{mg/mL} \times 50.00\ \text{mL}}{25.00\ \text{mL}} = 6.96\ \text{mg/L}$$

Since we construct a standard additions calibration curve in the sample, we can not use the calibration equation for other samples. Each sample, therefore, requires its own standard additions calibration curve. This is a serious drawback if you have many samples. For example, suppose you need to analyze 10 samples using a five-point calibration curve. For a normal calibration curve you need to analyze only 15 solutions (five standards and ten samples). If you use the method of standard additions, however, you must analyze 50 solutions (each of the ten samples is analyzed five times, once before spiking and after each of four spikes).

USING A STANDARD ADDITION TO IDENTIFY MATRIX EFFECTS

We can use the method of standard additions to validate an external standardization when matrix matching is not feasible. First, we prepare a normal calibration curve of S_{std} versus C_{std} and determine the value of k_A from its slope. Next, we prepare a standard additions calibration curve using Equation 6.3.8, plotting the data as shown in Figure 5.3.6 b. The slope of this standard additions calibration curve provides an independent determination of k_A. If there is no significant difference between the two values of k_A, then we can ignore the difference between the sample's matrix and that of the external standards. When the values of k_A are significantly different, then using a normal calibration curve introduces a proportional determinate error.

INTERNAL STANDARDS

To use an external standardization or the method of standard additions, we must be able to treat identically all samples and standards. When this is not possible, the accuracy and precision of our standardization may suffer. For example, if our analyte is in a volatile solvent, then its concentration will increase if we lose solvent to evaporation. Suppose we have a sample and a standard with identical concentrations of analyte and identical signals. If both experience the same proportional loss of solvent, then their respective concentrations of analyte and signals remain identical. In effect, we can ignore evaporation if the samples and the standards experience an equivalent loss of solvent. If an identical standard and sample lose different amounts of solvent, however, then their respective concentrations and signals are no longer equal. In this case a simple external standardization or standard addition is not possible.

We can still complete a standardization if we reference the analyte's signal to a signal from another species that we add to all samples and standards. The species, which we call an ***internal standard***, must be different than the analyte.

Because the analyte and the internal standard receive the same treatment, the ratio of their signals is unaffected by any lack of reproducibility in the procedure. If a solution contains an analyte of concentration C_A and an internal standard of concentration C_{IS}, then the signals due to the analyte, S_A, and the internal standard, S_{IS}, are

$$S_A = k_A C_A$$

$$S_{IS} = k_{SI} C_{IS}$$

where k_A and k_{IS} are the sensitivities for the analyte and the internal standard, respectively. Taking the ratio of the two signals gives the fundamental equation for an internal standardization.

$$\frac{S_A}{S_{IS}} = \frac{k_A C_A}{k_{IS} C_{IS}} = K \times \frac{C_A}{C_{IS}} \tag{6.3.12}$$

Because K is a ratio of the analyte's sensitivity and the internal standard's sensitivity, it is not necessary to determine independently values for either k_A or k_{IS}.

SINGLE INTERNAL STANDARD

In a single-point internal standardization, we prepare a single standard that contains the analyte and the internal standard, and use it to determine the value of K in Equation 6.3.12.

$$K = \left(\frac{C_{IS}}{C_A}\right)_{std} \times \left(\frac{S_A}{S_{IS}}\right)_{std} \tag{6.3.13}$$

Having standardized the method, the analyte's concentration is given by

$$C_A = \frac{C_{IS}}{K} \times \left(\frac{S_A}{S_{IS}}\right)_{samp}$$

✔ EXAMPLE 5.3.7

A sixth spectrophotometric method for the quantitative analysis of Pb^{2+} in blood uses Cu^{2+} as an internal standard. A standard that is 1.75 ppb Pb^{2+} and 2.25 ppb Cu^{2+} yields a ratio of $(S_A/S_{IS})_{std}$ of 2.37. A sample of blood spiked with the same concentration of Cu^{2+}

gives a signal ratio, $(S_A/S_{IS})_{samp}$, of 1.80. What is the concentration of Pb^{2+} in the sample of blood?

Solution

Equation 6.3.13 allows us to calculate the value of K using the data for the standard

$$K = \left(\frac{C_{IS}}{C_A}\right)_{std} \times \left(\frac{S_A}{S_{IS}}\right)_{std} = \frac{2.25 \text{ ppb } Cu^{2+}}{1.75 \text{ ppb } Pb^{2+}} \times 2.37 = 3.05 \frac{\text{ppb } Cu^{2+}}{\text{ppb } Pb^{2+}}$$

The concentration of Pb^{2+}, therefore, is

$$C_A = \frac{C_{IS}}{K} \times \left(\frac{S_A}{S_{IS}}\right)_{samp} = \frac{2.25 \text{ ppb } Cu^{2+}}{3.05 \frac{\text{ppb } Cu^{2+}}{\text{ppb } Pb^{2+}}} \times 1.80 = 1.33 \text{ ppb } Pb^{2+}$$

MULTIPLE INTERNAL STANDARDS

A single-point internal standardization has the same limitations as a single-point normal calibration. To construct an internal standard calibration curve we prepare a series of standards, each of which contains the same concentration of internal standard and a different concentrations of analyte. Under these conditions a calibration curve of $(S_A/S_{IS})_{std}$ versus C_A is linear with a slope of K/C_{IS}.

Although the usual practice is to prepare the standards so that each contains an identical amount of the internal standard, this is not a requirement.

EXAMPLE 5.3.8

A seventh spectrophotometric method for the quantitative analysis of Pb^{2+} in blood gives a linear internal standards calibration curve for which

$$\left(\frac{S_A}{S_{IS}}\right)_{std} = (2.11 \text{ ppb}^{-1} \times C_A) - 0.006$$

What is the ppb Pb^{2+} in a sample of blood if $(S_A/S_{IS})_{samp}$ is 2.80?

Solution

To determine the concentration of Pb^{2+} in the sample of blood we replace $(S_A/S_{IS})_{std}$ in the calibration equation with $(S_A/S_{IS})_{samp}$ and solve for C_A.

$$C_A = \frac{\left(\frac{S_A}{S_{IS}}\right)_{samp} + 0.006}{2.11 \text{ ppb}^{-1}} = \frac{2.80 + 0.006}{2.11 \text{ ppb}^{-1}} = 1.33 \text{ ppb } Pb^{2+}$$

The concentration of Pb^{2+} in the sample of blood is 1.33 ppb.

In some circumstances it is not possible to prepare the standards so that each contains the same concentration of internal standard. This is the case, for example, when we prepare samples by mass instead of volume. We can still prepare a calibration curve, however, by plotting $(S_A/S_{IS})_{std}$ versus C_A/C_{IS}, giving a linear calibration curve with a slope of K.

You might wonder if it is possible to include an internal standard in the method of standard additions to correct for both matrix effects and uncontrolled variations between samples; well, the answer is yes as described in the paper "Standard Dilution Analysis," the full reference for which is Jones, W. B.; Donati, G. L.; Calloway, C. P.; Jones, B. T. *Anal. Chem.* **2015**, *87*, 2321-2327.

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6.4: LINEAR REGRESSION AND CALIBRATION CURVES

In a single-point external standardization we determine the value of k_A by measuring the signal for a single standard that contains a known concentration of analyte. Using this value of k_A and our sample's signal, we then calculate the concentration of analyte in our sample (see Example 5.3.1). With only a single determination of k_A, a quantitative analysis using a single-point external standardization is straightforward.

A multiple-point standardization presents a more difficult problem. Consider the data in Table 5.4.1 for a multiple-point external standardization. What is our best estimate of the relationship between S_{std} and C_{std}? It is tempting to treat this data as five separate single-point standardizations, determining k_A for each standard, and reporting the mean value for the five trials. Despite it simplicity, this is not an appropriate way to treat a multiple-point standardization.

Table 5.4.1 : Data for a Hypothetical Multiple-Point External Standardization

C_{std} (arbitrary units)	S_{std} (arbitrary units)	$k_A = S_{std}/C_{std}$
0.000	0.00	—
0.100	12.36	123.6
0.200	24.83	124.2
0.300	35.91	119.7
0.400	48.79	122.0
0.500	60.42	122.8
		mean k_A = 122.5

So why is it inappropriate to calculate an average value for k_A using the data in Table 5.4.1 ? In a single-point standardization we assume that the reagent blank (the first row in Table 5.4.1) corrects for all constant sources of determinate error. If this is not the case, then the value of k_A from a single-point standardization has a constant determinate error. Table 5.4.2 demonstrates how an uncorrected constant error affects our determination of k_A. The first three columns show the concentration of analyte in a set of standards, C_{std}, the signal without any source of constant error, S_{std}, and the actual value of k_A for five standards. As we expect, the value of k_A is the same for each standard. In the fourth column we add a constant determinate error of +0.50 to the signals, $(S_{std})_e$. The last column contains the corresponding apparent values of k_A. Note that we obtain a different value of k_A for each standard and that each apparent k_A is greater than the true value.

Table 5.4.2 : Effect of a Constant Determinate Error on the Value of k_A From a Single-Point Standardization

C_{std}	S_{std} (without constant error)	$k_A = S_{std}/C_{std}$ (actual)	$(S_{std})_e$ (with constant error)	$k_A = (S_{std})_e/C_{std}$ (apparent)
1.00	1.00	1.00	1.50	1.50
2.00	2.00	1.00	2.50	1.25
3.00	3.00	1.00	3.50	1.17
4.00	4.00	1.00	4.50	1.13
5.00	5.00	1.00	5.50	1.10
		mean k_A (true) = 1.00		mean k_A (apparent) = 1.23

How do we find the best estimate for the relationship between the signal and the concentration of analyte in a multiple-point standardization? Figure 5.4.1 shows the data in Table 5.4.1 plotted as a normal calibration curve. Although the data certainly appear to fall along a straight line, the actual calibration curve is not intuitively obvious. The process of determining the best equation for the calibration curve is called linear regression.

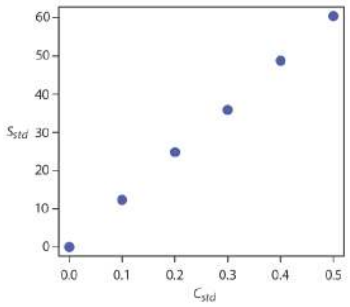


Figure 5.4.1 : Normal calibration curve data for the hypothetical multiple-point external standardization in Table 5.4.1 .

LINEAR REGRESSION OF STRAIGHT LINE CALIBRATION CURVES

When a calibration curve is a straight-line, we represent it using the following mathematical equation

$$y = \beta_0 + \beta_1 x \tag{6.4.1}$$

where y is the analyte's signal, S_{std}, and x is the analyte's concentration, C_{std}. The constants β_0 and β_1 are, respectively, the calibration curve's expected y-intercept and its expected slope. Because of uncertainty in our measurements, the best we can do is to estimate values for β_0 and β_1, which we represent as b_0 and b_1. The goal of a ***linear regression*** analysis is to determine the best estimates for b_0 and b_1. How we do this depends on the uncertainty in our measurements.

UNWEIGHTED LINEAR REGRESSION WITH ERRORS IN *Y*

The most common method for completing the linear regression for Equation 6.4.1 makes three assumptions:

1. that the difference between our experimental data and the calculated regression line is the result of indeterminate errors that affect y
2. that indeterminate errors that affect y are normally distributed
3. that the indeterminate errors in y are independent of the value of x

Because we assume that the indeterminate errors are the same for all standards, each standard contributes equally in our estimate of the slope and the y-intercept. For this reason the result is considered an ***unweighted linear regression***.

The second assumption generally is true because of the central limit theorem, which we considered in Chapter 4. The validity of the two remaining assumptions is less obvious and you should evaluate them before you accept the results of a linear regression. In particular the first assumption always is suspect because there certainly is some indeterminate error in the measurement of x. When we prepare a calibration curve, however, it is not unusual to find that the uncertainty in the signal, S_{std}, is significantly larger than the uncertainty in the analyte's concentration, C_{std}. In such circumstances the first assumption is usually reasonable.

HOW A LINEAR REGRESSION WORKS

To understand the logic of a linear regression consider the example shown in Figure 5.4.2 , which shows three data points and two possible straight-lines that might reasonably explain the data. How do we decide how well these straight-lines fit the data, and how do we determine the best straight-line?

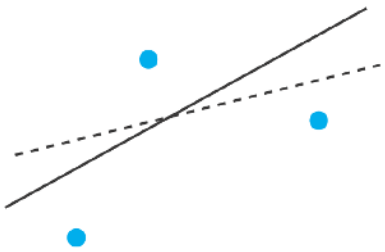


Figure 5.4.2 : Illustration showing three data points and two possible straight-lines that might explain the data. The goal of a linear regression is to find the mathematical model, in this case a straight-line, that best explains the data.

Let's focus on the solid line in Figure 5.4.2 . The equation for this line is

$$\hat{y} = b_0 + b_1 x \tag{6.4.2}$$

where b_0 and b_1 are estimates for the y-intercept and the slope, and $\hat{y}$ is the predicted value of y for any value of x. Because we assume that all uncertainty is the result of indeterminate errors in y, the difference between y and $\hat{y}$ for each value of x is the residual error, r, in our mathematical model.

$$r_i = (y_i - \hat{y}_i)$$

Figure 5.4.3 shows the residual errors for the three data points. The smaller the total residual error, R, which we define as

$$R = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2 \tag{6.4.3}$$

the better the fit between the straight-line and the data. In a linear regression analysis, we seek values of b_0 and b_1 that give the smallest total residual error.

> The reason for squaring the individual residual errors is to prevent a positive residual error from canceling out a negative residual error. You have seen this before in the equations for the sample and population standard deviations. You also can see from this equation why

a linear regression is sometimes called the method of least squares.

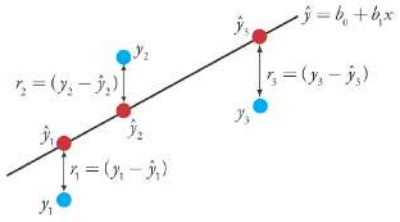


Figure 5.4.3 : Illustration showing the evaluation of a linear regression in which we assume that all uncertainty is the result of indeterminate errors in *y*. The points in blue, y , are the original data and the points in red, y_i , are the predicted values from the regression equation, $\hat{y} = b_0 + b_1 x$ .The smaller the total residual error (Equation 6.4.3), the better the fit of the straight-line to the data.

FINDING THE SLOPE AND Y-INTERCEPT

Although we will not formally develop the mathematical equations for a linear regression analysis, you can find the derivations in many standard statistical texts [See, for example, Draper, N. R.; Smith, H. Applied Regression Analysis, 3rd ed.; Wiley: New York, 1998]. The resulting equation for the slope, b_1, is

$$b_1 = \frac{n\sum_{i=1}^{n} x_i y_i - \sum_{i=1}^{n} x_i \sum_{i=1}^{n} y_i}{n\sum_{i=1}^{n} x_i^2 - \left(\sum_{i=1}^{n} x_i\right)^2} \tag{6.4.4}$$

and the equation for the *y*-intercept, b_0, is

$$b_0 = \frac{\sum_{i=1}^{n} y_i - b_1 \sum_{i=1}^{n} x_i}{n} \tag{6.4.5}$$

Although Equation 6.4.4 and Equation 6.4.5 appear formidable, it is necessary only to evaluate the following four summations

$$\sum_{i=1}^{n} x_i \quad \sum_{i=1}^{n} y_i \quad \sum_{i=1}^{n} x_i y_i \quad \sum_{i=1}^{n} x_i^2$$

Many calculators, spreadsheets, and other statistical software packages are capable of performing a linear regression analysis based on this model. To save time and to avoid tedious calculations, learn how to use one of these tools (and see Section 5.6 for details on completing a linear regression analysis using Excel and R.). For illustrative purposes the necessary calculations are shown in detail in the following example.

Equation 6.4.4 and Equation 6.4.5 are written in terms of the general variables *x* and *y*. As you work through this example, remember that *x* corresponds to C_{std}, and that *y* corresponds to S_{std}.

EXAMPLE 5.4.1

Using the data from Table 5.4.1 , determine the relationship between S_{std} and C_{std} using an unweighted linear regression.

Solution

We begin by setting up a table to help us organize the calculation.

x_i	y_i	$x_i y_i$	x_i^2
0.000	0.00	0.000	0.000
0.100	12.36	1.236	0.010
0.200	24.83	4.966	0.040
0.300	35.91	10.773	0.090
0.400	48.79	19.516	0.160
0.500	60.42	30.210	0.250

Adding the values in each column gives

$$\sum_{i=1}^{n} x_i = 1.500 \quad \sum_{i=1}^{n} y_i = 182.31 \quad \sum_{i=1}^{n} x_i y_i = 66.701 \quad \sum_{i=1}^{n} x_i^2 = 0.550$$

Substituting these values into Equation 6.4.4 and Equation 6.4.5, we find that the slope and the *y*-intercept are

$$b_1 = \frac{(6 \times 66.701) - (1.500 \times 182.31)}{(6 \times 0.550) - (1.500)^2} = 120.706 \approx 120.71$$

$$b_0 = \frac{182.31 - (120.706 \times 1.500)}{6} = 0.209 \approx 0.21$$

The relationship between the signal and the analyte, therefore, is

$$S_{std} = 120.71 \times C_{std} + 0.21$$

For now we keep two decimal places to match the number of decimal places in the signal. The resulting calibration curve is shown in Figure 5.4.4 .

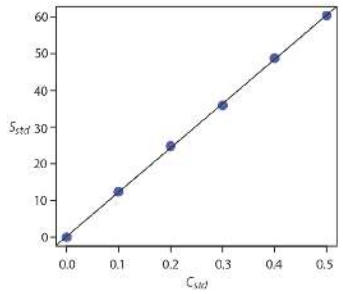


Figure 5.4.4 : Calibration curve for the data in Table 5.4.1 and Example 5.4.1 .

UNCERTAINTY IN THE REGRESSION ANALYSIS

As shown in Figure 5.4.4 , because indeterminate errors in the signal, the regression line may not pass through the exact center of each data point. The cumulative deviation of our data from the regression line—that is, the total residual error—is proportional to the uncertainty in the regression. We call this uncertainty the ***standard deviation about the regression***, s_r, which is equal to

$$s_r = \sqrt{\frac{\sum_{i=1}^{n} (y_i - \hat{y}_i)^2}{n-2}} \tag{6.4.6}$$

where y_i is the ith experimental value, and $\hat{y}_i$ is the corresponding value predicted by the regression line in Equation 6.4.2. Note that the denominator of Equation 6.4.6 indicates that our regression analysis has $n - 2$ degrees of freedom—we lose two degree of freedom because we use two parameters, the slope and the *y*-intercept, to calculate $\hat{y}_i$.

Did you notice the similarity between the standard deviation about the regression (Equation 6.4.6) and the standard deviation for a sample (Equation 4.1.1)?

A more useful representation of the uncertainty in our regression analysis is to consider the effect of indeterminate errors on the slope, b_1, and the *y*-intercept, b_0, which we express as standard deviations.

$$s_{b_1} = \sqrt{\frac{n s_r^2}{n\sum_{i=1}^{n} x_i^2 - \left(\sum_{i=1}^{n} x_i\right)^2}} = \sqrt{\frac{s_r^2}{\sum_{i=1}^{n} (x_i - \bar{x})^2}} \tag{6.4.7}$$

$$s_{b_0} = \sqrt{\frac{s_r^2 \sum_{i=1}^{n} x_i^2}{n\sum_{i=1}^{n} x_i^2 - \left(\sum_{i=1}^{n} x_i\right)^2}} = \sqrt{\frac{s_r^2 \sum_{i=1}^{n} x_i^2}{n\sum_{i=1}^{n} (x_i - \bar{x})^2}} \tag{6.4.8}$$

We use these standard deviations to establish confidence intervals for the expected slope, β_1, and the expected *y*-intercept, β_0

$$\beta_1 = b_1 \pm t s_{b_1} \tag{6.4.9}$$

$$\beta_0 = b_0 \pm t s_{b_0} \tag{6.4.10}$$

where we select *t* for a significance level of α and for $n - 2$ degrees of freedom. Note that Equation 6.4.9 and Equation 6.4.10 do not contain a factor of $(\sqrt{n})^{-1}$ because the confidence interval is based on a single regression line.

EXAMPLE 5.4.2

Calculate the 95% confidence intervals for the slope and *y*-intercept from Example 5.4.1 .

Solution

We begin by calculating the standard deviation about the regression. To do this we must calculate the predicted signals, $\hat{y}_i$, using the slope and *y*-intercept from Example 5.4.1 , and the squares of the residual error, $(y_i - \hat{y}_i)^2$. Using the last standard as an example, we find that the predicted signal is

$$\hat{y}_6 = b_0 + b_1 x_6 = 0.209 + (120.706 \times 0.500) = 60.562$$

and that the square of the residual error is

$$(y_i - \hat{y}_i)^2 = (60.42 - 60.562)^2 = 0.2016 \approx 0.202$$

The following table displays the results for all six solutions.

x_i	y_i	$\hat{y}_i$	$(y_i - \hat{y}_i)^2$
0.000	0.00	0.209	0.0437
0.100	12.36	12.280	0.0064
0.200	24.83	24.350	0.2304
0.300	35.91	36.421	0.2611
0.400	48.79	48.491	0.0894
0.500	60.42	60.562	0.0202

Adding together the data in the last column gives the numerator of Equation 6.4.6 as 0.6512; thus, the standard deviation about the regression is

$$s_r = \sqrt{\frac{0.6512}{6-2}} = 0.4035$$

Next we calculate the standard deviations for the slope and the *y*-intercept using Equation 6.4.7 and Equation 6.4.8. The values for the summation terms are from Example 5.4.1 .

$$s_{b_1} = \sqrt{\frac{6 \times (0.4035)^2}{(6 \times 0.550) - (1.500)^2}} = 0.965$$

$$s_{b_0} = \sqrt{\frac{(0.4035)^2 \times 0.550}{(6 \times 0.550) - (1.500)^2}} = 0.292$$

Finally, the 95% confidence intervals ($\alpha = 0.05$, 4 degrees of freedom) for the slope and *y*-intercept are

$$\beta_1 = b_1 \pm t s_{b_1} = 120.706 \pm (2.78 \times 0.965) = 120.7 \pm 2.7$$

$$\beta_0 = b_0 \pm t s_{b_0} = 0.209 \pm (2.78 \times 0.292) = 0.2 \pm 0.80$$

where *t*(0.05, 4) from Appendix 4 is 2.78. The standard deviation about the regression, s_r, suggests that the signal, S_{std}, is precise to one decimal place. For this reason we report the slope and the *y*-intercept to a single decimal place.

MINIMIZING UNCERTAINTY IN CALIBRATION MODEL

To minimize the uncertainty in a calibration curve's slope and *y*-intercept, we evenly space our standards over a wide range of analyte concentrations. A close examination of Equation 6.4.7 and Equation 6.4.8 help us appreciate why this is true. The denominators of both equations include the term $\sum_{i=1}^{n}(x_i - \overline{x}_i)^2$. The larger the value of this term—which we accomplish by increasing the range of *x* around its mean value—the smaller the standard deviations in the slope and the *y*-intercept. Furthermore, to minimize the uncertainty in the *y*-intercept, it helps to decrease the value of the term $\sum_{i=1}^{n} x_i$ in Equation 6.4.8, which we accomplish by including standards for lower concentrations of the analyte.

OBTAINING THE ANALYTE'S CONCENTRATION FROM A REGRESSION EQUATION

Once we have our regression equation, it is easy to determine the concentration of analyte in a sample. When we use a normal calibration curve, for example, we measure the signal for our sample, S_{samp}, and calculate the analyte's concentration, C_A, using the regression equation.

$$C_A = \frac{S_{samp} - b_0}{b_1} \tag{6.4.11}$$

What is less obvious is how to report a confidence interval for C_A that expresses the uncertainty in our analysis. To calculate a confidence interval we need to know the standard deviation in the analyte's concentration, s_{C_A}, which is given by the following equation

$$s_{C_A} = \frac{s_r}{b_1}\sqrt{\frac{1}{m} + \frac{1}{n} + \frac{\left(\overline{S}_{samp} - \overline{S}_{std}\right)^2}{(b_1)^2 \sum_{i=1}^{n}\left(C_{std_i} - \overline{C}_{std}\right)^2}} \tag{6.4.12}$$

where m is the number of replicate we use to establish the sample's average signal, S_{samp}, n is the number of calibration standards, S_{std} is the average signal for the calibration standards, and C_{std_1} and $\overline{C}_{std}$ are the individual and the mean concentrations for the calibration standards. Knowing the value of s_{C_A}, the confidence interval for the analyte's concentration is

$$\mu_{C_A} = C_A \pm t s_{C_A}$$

where μ_{C_A} is the expected value of C_A in the absence of determinate errors, and with the value of t is based on the desired level of confidence and $n - 2$ degrees of freedom.

Equation 6.4.12 is written in terms of a calibration experiment. A more general form of the equation, written in terms of x and y, is given here.

$$s_x = \frac{s_r}{b_1}\sqrt{\frac{1}{m} + \frac{1}{n} + \frac{\left(\overline{Y} - \bar{y}\right)^2}{(b_1)^2 \sum_{i=1}^{n}\left(x_i - \bar{x}\right)^2}}$$

A close examination of Equation 6.4.12 should convince you that the uncertainty in C_A is smallest when the sample's average signal, $\overline{S}_{samp}$, is equal to the average signal for the standards, $\overline{S}_{std}$. When practical, you should plan your calibration curve so that S_{samp} falls in the middle of the calibration curve. For more information about these regression equations see (a) Miller, J. N. *Analyst* **1991**, *116*, 3–14; (b) Sharaf, M. A.; Illman, D. L.; Kowalski, B. R. *Chemometrics*, Wiley-Interscience: New York, 1986, pp. 126-127; (c) Analytical Methods Committee "Uncertainties in concentrations estimated from calibration experiments," AMC Technical Brief, March 2006.

EXAMPLE 5.4.3

Three replicate analyses for a sample that contains an unknown concentration of analyte, yield values for S_{samp} of 29.32, 29.16 and 29.51 (arbitrary units). Using the results from Example 5.4.1 and Example 5.4.2 , determine the analyte's concentration, C_A, and its 95% confidence interval.

Solution

The average signal, $\overline{S}_{samp}$, is 29.33, which, using Equation 6.4.11 and the slope and the y-intercept from Example 5.4.1 , gives the analyte's concentration as

$$C_A = \frac{\overline{S}_{samp} - b_0}{b_1} = \frac{29.33 - 0.209}{120.706} = 0.241$$

To calculate the standard deviation for the analyte's concentration we must determine the values for $\overline{S}_{std}$ and for $\sum_{i=1}^{2}(C_{std_i} - \overline{C}_{std})^2$. The former is just the average signal for the calibration standards, which, using the data in Table 5.4.1 , is 30.385. Calculating $\sum_{i=1}^{2}(C_{std_i} - \overline{C}_{std})^2$ looks formidable, but we can simplify its calculation by recognizing that this sum-of-squares is the numerator in a standard deviation equation; thus,

$$\sum_{i=1}^{n}(C_{std_i} - \overline{C}_{std})^2 = (s_{C_{std}})^2 \times (n-1)$$

where $s_{C_{std}}$ is the standard deviation for the concentration of analyte in the calibration standards. Using the data in Table 5.4.1 we find that $s_{C_{std}}$ is 0.1871 and

$$\sum_{i=1}^{n}(C_{std_i} - \overline{C}_{std})^2 = (0.1872)^2 \times (6-1) = 0.175$$

Substituting known values into Equation 6.4.12 gives

$$s_{C_A} = \frac{0.4035}{120.706}\sqrt{\frac{1}{3} + \frac{1}{6} + \frac{(29.33 - 30.385)^2}{(120.706)^2 \times 0.175}} = 0.0024$$

Finally, the 95% confidence interval for 4 degrees of freedom is

$$\mu_{C_A} = C_A \pm t s_{C_A} = 0.241 \pm (2.78 \times 0.0024) = 0.241 \pm 0.007$$

Figure 5.4.5 shows the calibration curve with curves showing the 95% confidence interval for C_A.

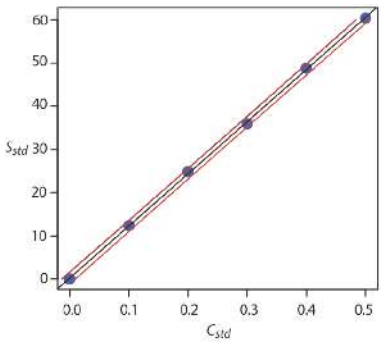


Figure 5.4.5 : Example of a normal calibration curve with a superimposed confidence interval for the analyte's concentration. The points in blue are the original data from Table 5.4.1 . The black line is the normal calibration curve as determined in Example 5.4.1 . The red lines show the 95% confidence interval for C_A assuming a single determination of S_{samp}.

In a standard addition we determine the analyte's concentration by extrapolating the calibration curve to the *x*-intercept. In this case the value of C_A is

$$C_A = x\text{-intercept} = \frac{-b_0}{b_1}$$

and the standard deviation in C_A is

$$s_{C_A} = \frac{s_r}{b_1}\sqrt{\frac{1}{n} + \frac{(\overline{S}_{std})^2}{(b_1)^2 \sum_{i=1}^{n}(C_{std_i} - \overline{C}_{std})^2}}$$

where n is the number of standard additions (including the sample with no added standard), and $\overline{S}_{std}$ is the average signal for the n standards. Because we determine the analyte's concentration by extrapolation, rather than by interpolation, s_{C_A} for the method of standard additions generally is larger than for a normal calibration curve.

? EXERCISE 5.4.1

Figure 5.4.2 shows a normal calibration curve for the quantitative analysis of Cu^{2+}. The data for the calibration curve are shown here.

$[Cu^{2+}]$ (M)	Absorbance
0	0
1.55×10^{-3}	0.050
3.16×10^{-3}	0.093
4.74×10^{-3}	0.143
6.34×10^{-3}	0.188
7.92×10^{-3}	0.236

Complete a linear regression analysis for this calibration data, reporting the calibration equation and the 95% confidence interval for the slope and the *y*-intercept. If three replicate samples give an S_{samp} of 0.114, what is the concentration of analyte in the sample and its 95% confidence interval?

Answer

We begin by setting up a table to help us organize the calculation

x_i	y_i	$x_i y_i$	x_i^2
0.000	0.000	0.000	0.000
1.55×10^{-3}	0.050	7.750×10^{-5}	2.403×10^{-6}
3.16×10^{-3}	0.093	2.939×10^{-4}	9.986×10^{-6}
4.74×10^{-3}	0.143	6.778×10^{-4}	2.247×10^{-5}
6.34×10^{-3}	0.188	1.192×10^{-3}	4.020×10^{-5}
7.92×10^{-3}	0.236	1.869×10^{-3}	6.273×10^{-5}

Adding the values in each column gives

$$\sum_{i=1}^{n} x_i = 2.371 \times 10^{-2} \quad \sum_{i=1}^{n} y_i = 0.710 \quad \sum_{i=1}^{n} x_i y_i = 4.110 \times 10^{-3} \quad \sum_{i=1}^{n} x_i^2 = 1.378 \times 10^{-4}$$

When we substitute these values into Equation 6.4.4 and Equation 6.4.5, we find that the slope and the *y*-intercept are

$$b_1 = \frac{6 \times (4.110 \times 10^{-3}) - (2.371 \times 10^{-2}) \times 0.710}{6 \times (1.378 \times 10^{-4}) - (2.371 \times 10^{-2})^2}) = 29.57$$

$$b_0 = \frac{0.710 - 29.57 \times (2.371 \times 10^{-2}}{6} = 0.0015$$

and that the regression equation is

$$S_{std} = 29.57 \times C_{std} + 0.0015$$

To calculate the 95% confidence intervals, we first need to determine the standard deviation about the regression. The following table helps us organize the calculation.

x_i	y_i	$\hat{y}_i$	$(y_i - \hat{y}_i)^2$
0.000	0.000	0.0015	2.250×10^{-6}
1.55×10^{-3}	0.050	0.0473	7.110×10^{-6}
3.16×10^{-3}	0.093	0.0949	3.768×10^{-6}
4.74×10^{-3}	0.143	0.1417	1.791×10^{-6}
6.34×10^{-3}	0.188	0.1890	9.483×10^{-6}
7.92×10^{-3}	0.236	0.2357	9.339×10^{-6}

Adding together the data in the last column gives the numerator of Equation 6.4.6 as 1.596×10^{-5}. The standard deviation about the regression, therefore, is

$$s_r = \sqrt{\frac{1.596 \times 10^{-5}}{6 - 2}} = 1.997 \times 10^{-3}$$

Next, we need to calculate the standard deviations for the slope and the *y*-intercept using Equation 6.4.7 and Equation 6.4.8.

$$s_{b_1} = \sqrt{\frac{6 \times (1.997 \times 10^{-3})^2}{6 \times (1.378 \times 10^{-4}) - (2.371 \times 10^{-2})^2}} = 0.3007$$

$$s_{b_0} = \sqrt{\frac{(1.997 \times 10^{-3})^2 \times (1.378 \times 10^{-4})}{6 \times (1.378 \times 10^{-4}) - (2.371 \times 10^{-2})^2}} = 1.441 \times 10^{-3}$$

and use them to calculate the 95% confidence intervals for the slope and the *y*-intercept

$$\beta_1 = b_1 \pm t s_{b_1} = 29.57 \pm (2.78 \times 0.3007) = 29.57\ \text{M}^{-1} \pm 0.84\ \text{M}^{-1}$$

$$\beta_0 = b_0 \pm t s_{b_0} = 0.0015 \pm (2.78 \times 1.441 \times 10^{-3}) = 0.0015 \pm 0.0040$$

With an average S_{samp} of 0.114, the concentration of analyte, C_A, is

$$C_A = \frac{S_{samp} - b_0}{b_1} = \frac{0.114 - 0.0015}{29.57\ \text{M}^{-1}} = 3.80 \times 10^{-3}\ \text{M}$$

The standard deviation in C_A is

$$s_{C_A} = \frac{1.997 \times 10^{-3}}{29.57}\sqrt{\frac{1}{3} + \frac{1}{6} + \frac{(0.114 - 0.1183)^2}{(29.57)^2 \times (4.408 \times 10^{-5})}} = 4.778 \times 10^{-5}$$

and the 95% confidence interval is

$$\mu = C_A \pm t s_{C_A} = 3.80 \times 10^{-3} \pm \{2.78 \times (4.778 \times 10^{-5})\}$$

$$\mu = 3.80 \times 10^{-3}\ \text{M} \pm 0.13 \times 10^{-3}\ \text{M}$$

EVALUATING A LINEAR REGRESSION MODEL

You should never accept the result of a linear regression analysis without evaluating the validity of the model. Perhaps the simplest way to evaluate a regression analysis is to examine the residual errors. As we saw earlier, the residual error for a single calibration standard, r_i, is

$$r_i = (y_i - \hat{y}_i)$$

If the regression model is valid, then the residual errors should be distributed randomly about an average residual error of zero, with no apparent trend toward either smaller or larger residual errors (Figure 5.4.6 a). Trends such as those in Figure 5.4.6 b and Figure 5.4.6 c provide evidence that at least one of the model's assumptions is incorrect. For example, a trend toward larger residual errors at higher concentrations, Figure 5.4.6 b, suggests that the indeterminate errors affecting the signal are not independent of the analyte's concentration. In Figure 5.4.6 c, the residual errors are not random, which suggests we cannot model the data using a straight-line relationship. Regression methods for the latter two cases are discussed in the following sections.

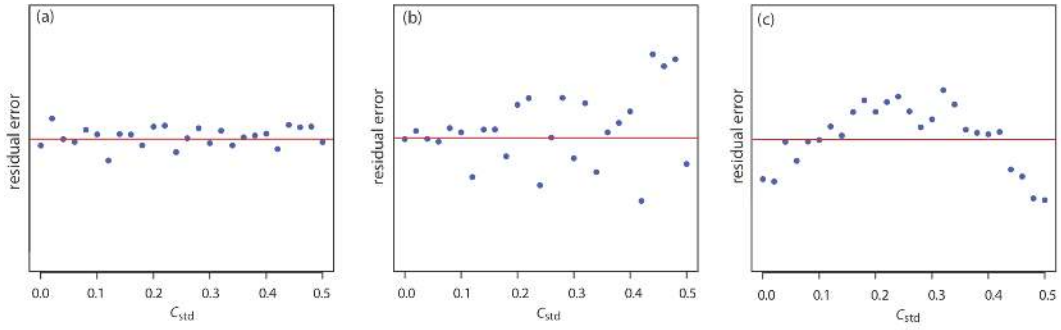


Figure 5.4.6 : Plots of the residual error in the signal, S_{std}, as a function of the concentration of analyte, C_{std}, for an unweighted straight-line regression model. The red line shows a residual error of zero. The distribution of the residual errors in (a) indicates that the unweighted linear regression model is appropriate. The increase in the residual errors in (b) for higher concentrations of analyte, suggests that a weighted straight-line regression is more appropriate. For (c), the curved pattern to the residuals suggests that a straight-line model is inappropriate; linear regression using a quadratic model might produce a better fit.

? EXERCISE 5.4.2

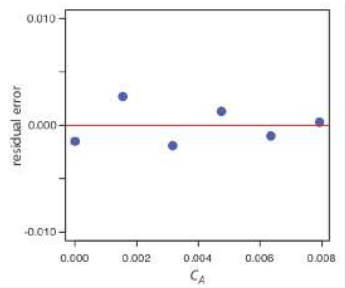
Using your results from Exercise 5.4.1 , construct a residual plot and explain its significance.

Answer

To create a residual plot, we need to calculate the residual error for each standard. The following table contains the relevant information.

x_i	y_i	$\hat{y}_i$	$y_i - \hat{y}_i$
0.000	0.000	0.0015	–0.0015
1.55×10^{-3}	0.050	0.0473	0.0027
3.16×10^{-3}	0.093	0.0949	–0.0019
4.74×10^{-3}	0.143	0.1417	0.0013
6.34×10^{-3}	0.188	0.1890	–0.0010
7.92×10^{-3}	0.236	0.2357	0.0003

The figure below shows a plot of the resulting residual errors. The residual errors appear random, although they do alternate in sign, and that do not show any significant dependence on the analyte's concentration. Taken together, these observations suggest that our regression model is appropriate.



WEIGHTED LINEAR REGRESSION WITH ERRORS IN *Y*

Our treatment of linear regression to this point assumes that indeterminate errors affecting *y* are independent of the value of *x*. If this assumption is false, as is the case for the data in Figure 5.4.6 b, then we must include the variance for each value of *y* into our determination of the *y*-intercept, b_0, and the slope, b_1; thus

$$b_0 = \frac{\sum_{i=1}^{n} w_i y_i - b_1 \sum_{i=1}^{n} w_i x_i}{n} \tag{6.4.13}$$

$$b_1 = \frac{n\sum_{i=1}^{n} w_i x_i y_i - \sum_{i=1}^{n} w_i x_i \sum_{i=1}^{n} w_i y_i}{n\sum_{i=1}^{n} w_i x_i^2 - \left(\sum_{i=1}^{n} w_i x_i\right)^2} \tag{6.4.14}$$

where w_i is a weighting factor that accounts for the variance in y_i

$$w_i = \frac{n(s_{y_i})^{-2}}{\sum_{i=1}^{n}(s_{y_i})^{-2}} \tag{6.4.15}$$

and s_{y_i} is the standard deviation for y_i. In a ***weighted linear regression***, each *xy*-pair's contribution to the regression line is inversely proportional to the precision of y_i; that is, the more precise the value of *y*, the greater its contribution to the regression.

EXAMPLE 5.4.4

Shown here are data for an external standardization in which *sstd* is the standard deviation for three replicate determination of the signal. This is the same data used in Example 5.4.1 with additional information about the standard deviations in the signal.

C_{std} (arbitrary units)	S_{std} (arbitrary units)	s_{std}
0.000	0.00	0.02
0.100	12.36	0.02
0.200	24.83	0.07
0.300	35.91	0.13
0.400	48.79	0.22
0.500	60.42	0.33

Determine the calibration curve's equation using a weighted linear regression. As you work through this example, remember that *x* corresponds to C_{std}, and that *y* corresponds to S_{std}.

Solution

We begin by setting up a table to aid in calculating the weighting factors.

C_{std} (arbitrary units)	S_{std} (arbitrary units)	s_{std}	$(s_{y_i})^{-2}$	w_i
0.000	0.00	0.02	2500.00	2.8339
0.100	12.36	0.02	250.00	2.8339
0.200	24.83	0.07	204.08	0.2313
0.300	35.91	0.13	59.17	0.0671
0.400	48.79	0.22	20.66	0.0234
0.500	60.42	0.33	9.18	0.0104

Adding together the values in the fourth column gives

$$\sum_{i=1}^{n}(s_{y_i})^{-2}$$

which we use to calculate the individual weights in the last column. As a check on your calculations, the sum of the individual weights must equal the number of calibration standards, *n*. The sum of the entries in the last column is 6.0000, so all is well. After we calculate the individual weights, we use a second table to aid in calculating the four summation terms in Equation 6.4.13 and Equation 6.4.14.

x_i	y_i	w_i	$w_i x_i$	$w_i y_i$	$w_i x_i^2$	$w_i x_i y_i$
0.000	0.00	2.8339	0.0000	0.0000	0.0000	0.0000
0.100	12.36	2.8339	0.2834	35.0270	0.0283	3.5027
0.200	24.83	0.2313	0.0463	5.7432	0.0093	1.1486
0.300	35.91	0.0671	0.0201	2.4096	0.0060	0.7229
0.400	48.79	0.0234	0.0094	1.1417	0.0037	0.4567
0.500	60.42	0.0104	0.0052	0.6284	0.0026	0.3142

Adding the values in the last four columns gives

$$\sum_{i=1}^{n} w_i x_i = 0.3644 \quad \sum_{i=1}^{n} w_i y_i = 44.9499 \quad \sum_{i=1}^{n} w_i x_i^2 = 0.0499 \quad \sum_{i=1}^{n} w_i x_i y_i = 6.1451$$

Substituting these values into the Equation 6.4.13 and Equation 6.4.14 gives the estimated slope and estimated *y*-intercept as

$$b_1 = \frac{(6 \times 6.1451) - (0.3644 \times 44.9499)}{(6 \times 0.0499) - (0.3644)^2} = 122.985$$

$$b_0 = \frac{44.9499 - (122.985 \times 0.3644)}{6} = 0.0224$$

The calibration equation is

$$S_{std} = 122.98 \times C_{std} + 0.2$$

Figure 5.4.7 shows the calibration curve for the weighted regression and the calibration curve for the unweighted regression in Example 5.4.1 . Although the two calibration curves are very similar, there are slight differences in the slope and in the *y*-intercept. Most notably, the *y*-intercept for the weighted linear regression is closer to the expected value of zero. Because the standard deviation for the signal, S_{std}, is smaller for smaller concentrations of analyte, C_{std}, a weighted linear regression gives more emphasis to these standards, allowing for a better estimate of the *y*-intercept.

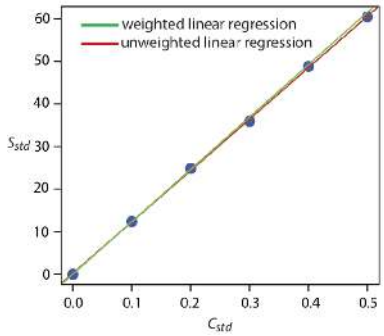


Figure 5.4.7 : A comparison of the unweighted and the weighted normal calibration curves. See Example 5.4.1 for details of the unweighted linear regression and Example 5.4.4 for details of the weighted linear regression.

Equations for calculating confidence intervals for the slope, the *y*-intercept, and the concentration of analyte when using a weighted linear regression are not as easy to define as for an unweighted linear regression [Bonate, P. J. *Anal. Chem.* **1993**, *65*, 1367–1372]. The confidence interval for the analyte's concentration, however, is at its optimum value when the analyte's signal is near the weighted centroid, y_c , of the calibration curve.

$$y_c = \frac{1}{n} \sum_{i=1}^{n} w_i x_i$$

WEIGHTED LINEAR REGRESSION WITH ERRORS IN BOTH *X* AND *Y*

If we remove our assumption that indeterminate errors affecting a calibration curve are present only in the signal (*y*), then we also must factor into the regression model the indeterminate errors that affect the analyte's concentration in the calibration standards (*x*). The solution for the resulting regression line is computationally more involved than that for either the unweighted or weighted regression lines. Although

we will not consider the details in this textbook, you should be aware that neglecting the presence of indeterminate errors in *x* can bias the results of a linear regression.

> See, for example, Analytical Methods Committee, "Fitting a linear functional relationship to data with error on both variable," AMC Technical Brief, March, 2002), as well as this chapter's Additional Resources.

CURVILINEAR AND MULTIVARIATE REGRESSION

A straight-line regression model, despite its apparent complexity, is the simplest functional relationship between two variables. What do we do if our calibration curve is curvilinear—that is, if it is a curved-line instead of a straight-line? One approach is to try transforming the data into a straight-line. Logarithms, exponentials, reciprocals, square roots, and trigonometric functions have been used in this way. A plot of log(*y*) versus *x* is a typical example. Such transformations are not without complications, of which the most obvious is that data with a uniform variance in *y* will not maintain that uniform variance after it is transformed.

> It is worth noting that the term "linear" does not mean a straight-line. A linear function may contain more than one additive term, but each such term has one and only one adjustable multiplicative parameter. The function
>
> $$y = ax + bx^2$$
>
> is an example of a linear function because the terms *x* and x^2 each include a single multiplicative parameter, *a* and *b*, respectively. The function
>
> $$y = x^b$$
>
> is nonlinear because *b* is not a multiplicative parameter; it is, instead, a power. This is why you can use linear regression to fit a polynomial equation to your data.
>
> Sometimes it is possible to transform a nonlinear function into a linear function. For example, taking the log of both sides of the nonlinear function above gives a linear function.
>
> $$\log(y) = b\log(x)$$

Another approach to developing a linear regression model is to fit a polynomial equation to the data, such as $y = a + bx + cx^2$. You can use linear regression to calculate the parameters *a*, *b*, and *c*, although the equations are different than those for the linear regression of a straight-line. If you cannot fit your data using a single polynomial equation, it may be possible to fit separate polynomial equations to short segments of the calibration curve. The result is a single continuous calibration curve known as a spline function.

> For details about curvilinear regression, see (a) Sharaf, M. A.; Illman, D. L.; Kowalski, B. R. *Chemometrics*, Wiley-Interscience: New York, 1986; (b) Deming, S. N.; Morgan, S. L. *Experimental Design: A Chemometric Approach*, Elsevier: Amsterdam, 1987.

The regression models in this chapter apply only to functions that contain a single independent variable, such as a signal that depends upon the analyte's concentration. In the presence of an interferent, however, the signal may depend on the concentrations of both the analyte and the interferent

$$S = k_A C_A + k_I CI + S_{reag}$$

where k_I is the interferent's sensitivity and C_I is the interferent's concentration. Multivariate calibration curves are prepared using standards that contain known amounts of both the analyte and the interferent, and modeled using multivariate regression.

> See Beebe, K. R.; Kowalski, B. R. *Anal. Chem.* **1987**, *59*, 1007A–1017A. for additional details, and check out this chapter's Additional Resources for more information about linear regression with errors in both variables, curvilinear regression, and multivariate regression.

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6.5: COMPENSATING FOR THE REAGENT BLANK

Thus far in our discussion of strategies for standardizing analytical methods, we have assumed that a suitable reagent blank is available to correct for signals arising from sources other than the analyte. We did not, however ask an important question: "What constitutes an appropriate reagent blank?" Surprisingly, the answer is not immediately obvious.

In one study, approximately 200 analytical chemists were asked to evaluate a data set consisting of a normal calibration curve, a separate analyte-free blank, and three samples with different sizes, but drawn from the same source [Cardone, M. J. *Anal. Chem.* **1986**, *58*, 433–438]. The first two columns in Table 5.5.1 shows a series of external standards and their corresponding signals. The normal calibration curve for the data is

$$S_{std} = 0.0750 \times W_{std} + 0.1250$$

where the *y*-intercept of 0.1250 is the calibration blank. A separate reagent blank gives the signal for an analyte-free sample.

Table 5.5.1 : Data Used to Study the Blank in an Analytical Method

W_{std}	S_{std}	Sample Number	W_{samp}	S_{samp}
1.6667	0.2500	1	62.4746	0.8000
5.0000	0.5000	2	82.7915	1.0000
8.3333	0.7500	3	103.1085	1.2000
11.6667	0.8413			
18.1600	1.4870		reagent blank	0.1000
19.9333	1.6200			
$S_{std} = 0.0750 \times W_{std} + 0.1250$				
W_{std}: weight of analyte used to prepare the external standard; diluted to a volume, V				
W_{samp}: weight of sample used to prepare sample as analyzed; diluted to a volume, V				

In working up this data, the analytical chemists used at least four different approaches to correct the signals: (a) ignoring both the calibration blank, *CB*, and the reagent blank, *RB*, which clearly is incorrect; (b) using the calibration blank only; (c) using the reagent blank only; and (d) using both the calibration blank and the reagent blank. The first four rows of Table 5.5.2 shows the equations for calculating the analyte's concentration using each approach, along with the reported concentrations for the analyte in each sample.

Table 5.5.2 : Equations and Resulting Concentrations of Analyte for Different Approaches to Correcting for the Blank

		Concentration of Analyte in...		
Approach for Correcting the Signal	Equation	Sample 1	Sample 2	Sample 3
ignore calibration and reagent blanks	$C_A = \frac{W_A}{W_{samp}} = \frac{S_{samp}}{k_A W_{samp}}$	0.1707	0.1610	0.1552
use calibration blank only	$C_A = \frac{W_A}{W_{samp}} = \frac{S_{samp} - CB}{k_A W_{samp}}$	0.1441	0.1409	0.1390
use reagent blank only	$C_A = \frac{W_A}{W_{samp}} = \frac{S_{samp} - RB}{k_A W_{samp}}$	0.1494	0.1449	0.1422
use both calibration and reagent blanks	$C_A = \frac{W_A}{W_{samp}} = \frac{S_{samp} - CB - RB}{k_A W_{samp}}$	0.1227	0.1248	0.1266
use total Youden blank	$C_A = \frac{W_A}{W_{samp}} = \frac{S_{samp} - TYB}{k_A W_{samp}}$	0.1313	0.1313	0.1313
$C_A =$ concentration of analyte; $W_A =$ weight of analyte; W_{samp} weight of sample; $k_A =$ slope of calibration curve (0.0750; slope of calibration equation); CB $=$ calibration blank (0.125; intercept of calibration equation); $RB =$ reagent blank (0.100); $TYB =$ total Youden blank (0.185; see text)				

That all four methods give a different result for the analyte's concentration underscores the importance of choosing a proper blank, but does not tell us which blank is correct. Because all four methods fail to predict the same concentration of analyte for each sample, none of these blank corrections properly accounts for an underlying constant source of determinate error.

To correct for a constant method error, a blank must account for signals from any reagents and solvents used in the analysis and any bias that results from interactions between the analyte and the sample's matrix. Both the calibration blank and the reagent blank compensate for signals from reagents and solvents. Any difference in their values is due to indeterminate errors in preparing and analyzing the standards.

> Because we are considering a matrix effect of sorts, you might think that the method of standard additions is one way to overcome this problem. Although the method of standard additions can compensate for proportional determinate errors, it cannot correct for a constant determinate error; see Ellison, S. L. R.; Thompson, M. T. "Standard additions: myth and reality," *Analyst*, **2008**, *133*, 992–997.

Unfortunately, neither a calibration blank nor a reagent blank can correct for a bias that results from an interaction between the analyte and the sample's matrix. To be effective, the blank must include both the sample's matrix and the analyte and, consequently, it must be determined using the sample itself. One approach is to measure the signal for samples of different size, and to determine the regression line for a plot of S_{samp} versus the amount of sample. The resulting *y*-intercept gives the signal in the absence of sample, and is known as the ***total Youden blank*** [Cardone, M. J. *Anal. Chem.* **1986**, *58*, 438–445]. This is the true blank correction. The regression line for the three samples in Table 5.5.1 is

$$S_{samp} = 0.009844 \times W_{samp} + 0.185$$

giving a true blank correction of 0.185. As shown in Table 5.5.2 , using this value to correct S_{samp} gives identical values for the concentration of analyte in all three samples.

The use of the total Youden blank is not common in analytical work, with most chemists relying on a calibration blank when using a calibration curve and a reagent blank when using a single-point standardization. As long we can ignore any constant bias due to interactions between the analyte and the sample's matrix, which is often the case, the accuracy of an analytical method will not suffer. It is a good idea, however, to check for constant sources of error before relying on either a calibration blank or a reagent blank.

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6.6: USING EXCEL AND R FOR A LINEAR REGRESSION

Although the calculations in this chapter are relatively straightforward—consisting, as they do, mostly of summations—it is tedious to work through problems using nothing more than a calculator. Both Excel and R include functions for completing a linear regression analysis and for visually evaluating the resulting model.

EXCEL

Let's use Excel to fit the following straight-line model to the data in Example 5.4.1.

$$y = \beta_0 + \beta_1 x$$

Enter the data into a spreadsheet, as shown in Figure 5.6.1 . Depending upon your needs, there are many ways that you can use Excel to complete a linear regression analysis. We will consider three approaches here.

	A	B
1	Cstd	Sstd
2	0.000	0.00
3	0.100	12.36
4	0.200	24.83
5	0.300	35.91
6	0.400	48.79
7	0.500	60.42

Figure 5.6.1 : Portion of a spreadsheet containing data from Example 5.4.1 (Cstd = C_{std}; Sstd = S_{std}).

USING EXCEL'S BUILT-IN FUNCTIONS

If all you need are values for the slope, β_1, and the *y*-intercept, β_0, you can use the following functions:

= intercept(*known_y's*, *known_x's*)

= slope(*known_y's*, *known_x's*)

where *known_y's* is the range of cells that contain the signals (*y*), and *known_x's* is the range of cells that contain the concentrations (*x*). For example, if you click on an empty cell and enter

= slope(B2:B7, A2:A7)

Excel returns exact calculation for the slope (120.705 714 3).

USING EXCEL'S DATA ANALYSIS TOOLS

To obtain the slope and the *y*-intercept, along with additional statistical details, you can use the data analysis tools in the Data Analysis ToolPak. The ToolPak is not a standard part of Excel's instillation. To see if you have access to the Analysis ToolPak on your computer, select **Tools** from the menu bar and look for the **Data Analysis...** option. If you do not see **Data Analysis...**, select **Add-ins...** from the **Tools** menu. Check the box for the **Analysis ToolPak** and click on **OK** to install them.

Select **Data Analysis...** from the **Tools** menu, which opens the *Data Analysis* window. Scroll through the window, select **Regression** from the available options, and press **OK**. Place the cursor in the box for *Input Y range* and then click and drag over cells B1:B7. Place the cursor in the box for *Input X range* and click and drag over cells A1:A7. Because cells A1 and B1 contain labels, check the box for *Labels*.

> Including labels is a good idea. Excel's summary output uses the *x*-axis label to identify the slope.

Select the radio button for *Output range* and click on any empty cell; this is where Excel will place the results. Clicking **OK** generates the information shown in Figure 5.6.2 .

SUMMARY OUTPUT

Regression Statistics	
Multiple R	0.99987244
R Square	0.9997449
Adjusted R Square	0.99968113
Standard Error	0.40329713
Observations	6

ANOVA

	df	SS	MS	F	Significance F
Regression	1	2549.727156	2549.72716	15676.296	2.4405E-08
Residual	4	0.650594286	0.16264857		
Total	5	2550.37775			

	Coefficients	Standard Error	t Stat	P-value	Lower 95%	Upper 95%	Lower 95.0%	Upper 95.0%
Intercept	0.20857143	0.29188503	0.71456706	0.51436267	-0.60183133	1.01897419	-0.60183133	1.01897419
Cstd	120.705714	0.964064525	125.205016	2.4405E-08	118.029042	123.382387	118.029042	123.382387

Figure 5.6.2 : Output from Excel's Regression command in the Analysis ToolPak. See the text for a discussion of how to interpret the information in these tables.

There are three parts to Excel's summary of a regression analysis. At the top of Figure 5.6.2 is a table of *Regression Statistics*. The *standard error* is the standard deviation about the regression, s_r. Also of interest is the value for *Multiple R*, which is the model's correlation coefficient, *r*, a term with which you may already be familiar. The correlation coefficient is a measure of the extent to which the regression model explains the variation in *y*. Values of *r* range from –1 to +1. The closer the correlation coefficient is to ±1, the better the model is at explaining the data. A correlation coefficient of 0 means there is no relationship between *x* and *y*. In developing the calculations for linear regression, we did not consider the correlation coefficient. There is a reason for this. For most straight-line calibration curves the correlation coefficient is very close to +1, typically 0.99 or better. There is a tendency, however, to put too much faith in the correlation coefficient's significance, and to assume that an *r* greater than 0.99 means the linear regression model is appropriate. Figure 5.6.3 provides a useful counterexample. Although the regression line has a correlation coefficient of 0.993, the data clearly is curvilinear. The take-home lesson here is simple: do not fall in love with the correlation coefficient!

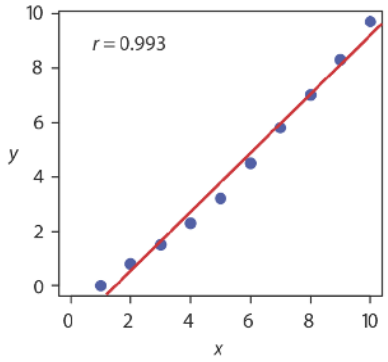


Figure 5.6.3 : Example of fitting a straight-line (in red) to curvilinear data (in blue).

The second table in Figure 5.6.2 is entitled *ANOVA*, which stands for analysis of variance. We will take a closer look at ANOVA in Chapter 14. For now, it is sufficient to understand that this part of Excel's summary provides information on whether the linear regression model explains a significant portion of the variation in the values of *y*. The value for *F* is the result of an *F*-test of the following null and alternative hypotheses.

H_0: the regression model does not explain the variation in *y*

H_A: the regression model does explain the variation in *y*

The value in the column for *Significance F* is the probability for retaining the null hypothesis. In this example, the probability is $2.5 \times 10^{-6}\%$, which is strong evidence for accepting the regression model. As is the case with the correlation coefficient, a small value for the probability is a likely outcome for any calibration curve, even when the model is inappropriate. The probability for retaining the null hypothesis for the data in Figure 5.6.3 , for example, is $9.0 \times 10^{-7}\%$.

> See Chapter 4.6 for a review of the *F*-test.

The third table in Figure 5.6.2 provides a summary of the model itself. The values for the model's coefficients—the slope, β_1, and the *y*-intercept, β_0—are identified as *intercept* and with your label for the *x*-axis data, which in this example is C_{std}. The standard deviations for the coefficients, s_{b_0} and s_{b_1}, are in the column labeled *Standard error*. The column *t Stat* and the column *P-value* are for the following *t*-tests.

$$\text{slope: } H_0\text{: } \beta_1 = 0 \quad H_A\text{: } \beta_1 \neq 0$$

y-intercept: $H_0: \beta_0 = 0 \quad H_A: \beta_0 \neq 0$

The results of these *t*-tests provide convincing evidence that the slope is not zero, but there is no evidence that the *y*-intercept differs significantly from zero. Also shown are the 95% confidence intervals for the slope and the *y*-intercept (*lower 95%* and *upper 95%*).

> See Chapter 4.6 for a review of the *t*-test.

PROGRAMMING THE FORMULAS YOURSELF

A third approach to completing a regression analysis is to program a spreadsheet using Excel's built-in formula for a summation

=sum(*first cell*:*last cell*)

and its ability to parse mathematical equations. The resulting spreadsheet is shown in Figure 5.6.4 .

	A	B	C	D	E	F
1	x	y	xy	x^2	n =	6
2	0.000	0.00	=A2*B2	=A2^2	slope =	=(F1*C8 - A8*B8)/(F1*D8-A8^2)
3	0.100	12.36	=A3*B3	=A3^2	y-int =	=(B8-F2*A8)/F1
4	0.200	24.83	=A4*B4	=A4^2		
5	0.300	35.91	=A5*B5	=A5^2		
6	0.400	48.79	=A6*B6	=A6^2		
7	0.500	60.42	=A7*B7	=A7^2		
8						
9	=sum(A2:A7)	=sum(B2:B7)	=sum(C2:C7)	=sum(D2:D7)	<--sums	

Figure 5.6.4 : Spreadsheet showing the formulas for calculating the slope and the *y*-intercept for the data in Example 5.4.1. The shaded cells contain formulas that you must enter. Enter the formulas in cells C3 to C7, and cells D3 to D7. Next, enter the formulas for cells A9 to D9. Finally, enter the formulas in cells F2 and F3. When you enter a formula, Excel replaces it with the resulting calculation. The values in these cells should agree with the results in Example 5.4.1. You can simplify the entering of formulas by copying and pasting. For example, enter the formula in cell C2. Select **Edit: Copy**, click and drag your cursor over cells C3 to C7, and select **Edit: Paste**. Excel automatically updates the cell referencing.

USING EXCEL TO VISUALIZE THE REGRESSION MODEL

You can use Excel to examine your data and the regression line. Begin by plotting the data. Organize your data in two columns, placing the *x* values in the left-most column. Click and drag over the data and select **Charts** from the ribbon. Select **Scatter**, choosing the option without lines that connect the points. To add a regression line to the chart, click on the chart's data and select **Chart: Add Trendline...** from the main men. Pick the straight-line model and click **OK** to add the line to your chart. By default, Excel displays the regression line from your first point to your last point. Figure 5.6.5 shows the result for the data in Figure 5.6.1 .

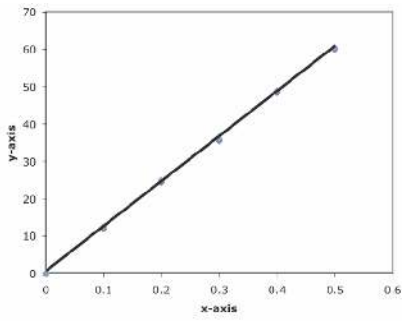


Figure 5.6.5 : Example of an Excel scatterplot showing the data and a regression line.

Excel also will create a plot of the regression model's residual errors. To create the plot, build the regression model using the Analysis ToolPak, as described earlier. Clicking on the option for *Residual plots* creates the plot shown in Figure 5.6.6 .

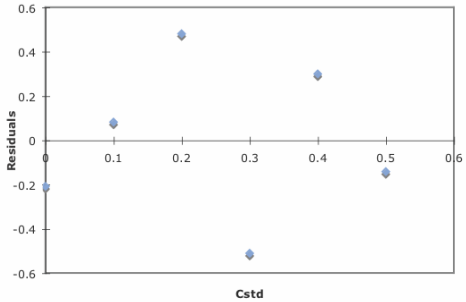


Figure 5.6.6 : Example of Excel's plot of a regression model's residual errors.

LIMITATIONS TO USING EXCEL FOR A REGRESSION ANALYSIS

Excel's biggest limitation for a regression analysis is that it does not provide a function to calculate the uncertainty when predicting values of x. In terms of this chapter, Excel can not calculate the uncertainty for the analyte's concentration, C_A, given the signal for a sample, S_{samp}. Another limitation is that Excel does not have a built-in function for a weighted linear regression. You can, however, program a spreadsheet to handle these calculations.

EXERCISE 5.6.1

Use Excel to complete the regression analysis in Exercise 5.4.1.

Answer

Begin by entering the data into an Excel spreadsheet, following the format shown in Figure 5.6.1 . Because Excel's Data Analysis tools provide most of the information we need, we will use it here. The resulting output, which is shown below, provides the slope and the y-intercept, along with their respective 95% confidence intervals.

SUMMARY OUTPUT

Regression Statistics	
Multiple R	0.99979366
R Square	0.99958737
Adjusted R Sq	0.99948421
Standard Erro	0.00199602
Observations	6

ANOVA

	df	*SS*	*MS*	*F*	*Significance F*
Regression	1	0.0386054	0.0386054	9689.9103	6.3858E-08
Residual	4	1.5936E-05	3.9841E-06		
Total	5	0.03862133			

	Coefficients	*Standard Error*	*t Stat*	*P-value*	*Lower 95%*	*Upper 95%*	*Lower 95.0%*	*Upper 95.0%*
Intercept	0.00139272	0.00144059	0.96677158	0.38840479	-0.00260699	0.00539242	-0.00260699	0.00539242
Cstd	29.5927329	0.30062507	98.437342	6.3858E-08	28.7580639	30.4274019	28.7580639	30.4274019

Excel does not provide a function for calculating the uncertainty in the analyte's concentration, C_A, given the signal for a sample, S_{samp}. You must complete these calculations by hand. With an S_{samp} of 0.114, we find that C_A is

$$C_A = \frac{S_{samp} - b_0}{b_1} = \frac{0.114 - 0.0014}{29.59\ \text{M}^{-1}} = 3.80 \times 10^{-3}\ \text{M}$$

The standard deviation in C_A is

$$s_{C_A} = \frac{1.996 \times 10^{-3}}{29.59} \sqrt{\frac{1}{3} + \frac{1}{6} + \frac{(0.114 - 0.1183)^2}{(29.59)^2 \times 4.408 \times 10^{-5})}} = 4.772 \times 10^{-5}$$

and the 95% confidence interval is

$$\mu = C_A \pm t s_{C_A} = 3.80 \times 10^{-3} \pm \{2.78 \times (4.772 \times 10^{-5})\}$$

$$\mu = 3.80 \times 10^{-3}\ \text{M} \pm 0.13 \times 10^{-3}\ \text{M}$$

R

Let's use R to fit the following straight-line model to the data in Example 5.4.1.

$$y = \beta_0 + \beta_1 x$$

ENTERING DATA AND CREATING THE REGRESSION MODEL

To begin, create objects that contain the concentration of the standards and their corresponding signals.

> conc = c(0, 0.1, 0.2, 0.3, 0.4, 0.5)

> signal = c(0, 12.36, 24.83, 35.91, 48.79, 60.42)

The command for a straight-line linear regression model is

$$\text{lm}(y \sim x)$$

where y and x are the objects the objects our data. To access the results of the regression analysis, we assign them to an object using the following command

> *model* = lm(signal ~ conc)

where *model* is the name we assign to the object.

> As you might guess, *lm* is short for linear model.
>
> You can choose any name for the object that contains the results of the regression analysis.

EVALUATING THE LINEAR REGRESSION MODEL

To evaluate the results of a linear regression we need to examine the data and the regression line, and to review a statistical summary of the model. To examine our data and the regression line, we use the **plot** command, which takes the following general form

plot(*x*, *y*, optional arguments to control style)

where *x* and *y* are the objects that contain our data, and the **abline** command

abline(*object*, optional arguments to control style)

where *object* is the object that contains the results of the linear regression. Entering the commands

> plot(conc, signal, pch = 19, col = “blue”, cex = 2)

> abline(model, col = “red”)

creates the plot shown in Figure 5.6.7 .

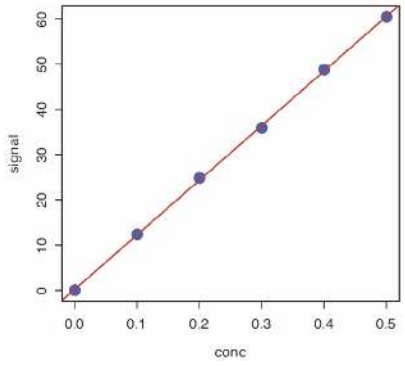


Figure 5.6.7 : Example of a regression plot in R showing the data (in blue) and the regression line (in red). You can customize your plot by adjusting the plot command’s optional arguments. For example, the argument *pch* controls the symbol used for plotting points, the argument *col* allows you to select a color for the points or the line, and the argument *cex* sets the size for the points. You can use the command *help(plot)* to learn more about the options for plotting data in R.

To review a statistical summary of the regression model, we use the **summary** command.

> summary(model)

The resulting output, shown in Figure 5.6.8 , contains three sections.

```
> model=lm(signal~conc)
> summary(model)

Call:
lm(formula = signal ~ conc)

Residuals:
     1          2         3         4         5         6
-0.20857  0.08086  0.48029 -0.51029  0.29914 -0.14143

Coefficients:
             Estimate   Std. Error   t value   Pr(>|t|)
(Intercept)  0.2086     0.2919       0.715     0.514
conc         120.7057   0.9641       125.205   2.44e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.4033 on 4 degrees of freedom
Multiple R-Squared: 0.9997,   Adjusted R-squared: 0.9997
F-statistic: 1.568e+04 on 1 and 4 DF,  p-value: 2.441e-08
```

Figure 5.6.8 : The summary of R’s regression analysis. See the text for a discussion of how to interpret the information in the output’s three sections.

The first section of R’s summary of the regression model lists the residual errors. To examine a plot of the residual errors, use the command

> plot(model, which = 1)

which produces the result shown in Figure 5.6.9 . Note that R plots the residuals against the predicted (fitted) values of *y* instead of against the known values of *x*. The choice of how to plot the residuals is not critical, as you can see by comparing Figure 5.6.9 to Figure 5.6.6 . The line in Figure 5.6.9 is a smoothed fit of the residuals.

> The reason for including the argument *which = 1* is not immediately obvious. When you use R's *plot* command on an object created by the *lm* command, the default is to create four charts summarizing the model's suitability. The first of these charts is the residual plot; thus, *which = 1* limits the output to this plot.

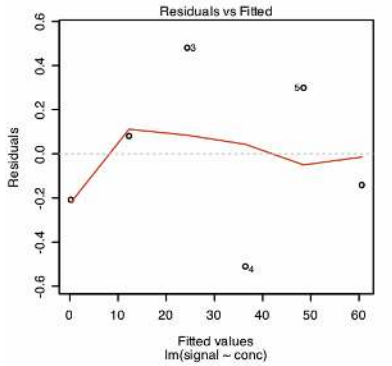


Figure 5.6.9 : Example showing R's plot of a regression model's residual error.

The second section of Figure 5.6.8 provides the model's coefficients—the slope, β_1, and the *y*-intercept, β_0—along with their respective standard deviations (*Std. Error*). The column *t value* and the column *Pr(>|t|)* are for the following *t*-tests.

$$\text{slope: } H_0\text{: } \beta_1 = 0 \quad H_A\text{: } \beta_1 \neq 0$$

$$y\text{-intercept: } H_0\text{: } \beta_0 = 0 \quad H_A\text{: } \beta_0 \neq 0$$

The results of these *t*-tests provide convincing evidence that the slope is not zero, but no evidence that the *y*-intercept differs significantly from zero.

The last section of the regression summary provides the standard deviation about the regression (*residual standard error*), the square of the correlation coefficient (*multiple R-squared*), and the result of an *F*-test on the model's ability to explain the variation in the *y* values. For a discussion of the correlation coefficient and the *F*-test of a regression model, as well as their limitations, refer to the section on using Excel's data analysis tools.

PREDICTING THE UNCERTAINTY IN C_A GIVEN S_{samp}

Unlike Excel, R includes a command for predicting the uncertainty in an analyte's concentration, C_A, given the signal for a sample, S_{samp}. This command is not part of R's standard installation. To use the command you need to install the "chemCal" package by entering the following command (*note: you will need an internet connection to download the package*).

> install.packages("chemCal")

After installing the package, you need to load the functions into R using the following command. (*note: you will need to do this step each time you begin a new R session as the package does not automatically load when you start R*).

> library("chemCal")

> You need to install a package once, but you need to load the package each time you plan to use it. There are ways to configure R so that it automatically loads certain packages; see *An Introduction to R* for more information (click here to view a PDF version of this document).

The command for predicting the uncertainty in C_A is **inverse.predict**, which takes the following form for an unweighted linear regression

inverse.predict(*object*, *newdata*, alpha = *value*)

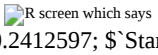
where *object* is the object that contains the regression model's results, *new-data* is an object that contains values for S_{samp}, and *value* is the numerical value for the significance level. Let's use this command to complete Example 5.4.3. First, we create an object that contains the values of S_{samp}

> sample = c(29.32, 29.16, 29.51)

and then we complete the computation using the following command

> inverse.predict(model, sample, alpha = 0.05)

producing the result shown in Figure 5.6.10 . The analyte's concentration, C_A, is given by the value *$Prediction*, and its standard deviation, s_{C_A}, is shown as *$`Standard Error`*. The value for *$Confidence* is the confidence interval, $\pm t s_{C_A}$, for the analyte's concentration, and *$`Confidence Limits`* provides the lower limit and upper limit for the confidence interval for C_A.



inverse.predict(model, sample, alpha=0.05); $Prediction; [1] 0.2412597; $`Standard Error`; [1] 0.002363588; $Confidence; [1] 0.006562373; $`Confidence Limits`; [1] 0.2346974 0.2478221." style="width: 328px; height: 243px;" width="328px" height="243px" src="/@api/deki/files/162725/Figure5.24.png">

Figure 5.6.10 : Output from R's command for predicting the analyte's concentration, C_A, from the sample's signal, S_{samp}.

USING R FOR A WEIGHTED LINEAR REGRESSION

R's command for an unweighted linear regression also allows for a weighted linear regression if we include an additional argument, *weights*, whose value is an object that contains the weights.

$$\text{lm}(y \sim x, \textit{weights} = \textit{object})$$

Let's use this command to complete Example 5.4.4. First, we need to create an object that contains the weights, which in R are the reciprocals of the standard deviations in y, $(s_{y_i})^{-2}$. Using the data from Example 5.4.4, we enter

> syi=c(0.02, 0.02, 0.07, 0.13, 0.22, 0.33)

> w=1/syi^2

to create the object that contains the weights. The commands

> modelw= lm(signal ~ conc, weights = w)

> summary(modelw)

generate the output shown in Figure 5.6.11 . Any difference between the results shown here and the results shown in Example 5.4.4 are the result of round-off errors in our earlier calculations.

> You may have noticed that this way of defining weights is different than that shown in Equation 5.4.15. In deriving equations for a weighted linear regression, you can choose to normalize the sum of the weights to equal the number of points, or you can choose not to —the algorithm in R does not normalize the weights.

```
> modelw=lm(signal~conc, weights = w)
> summary(modelw)

Call:
lm(formula = signal ~ conc, weights = w)

Residuals:
   1      2      3      4      5      6
-2.223  2.571  3.676 -7.129 -1.413 -2.864

Coefficients:
             Estimate   Std. Error  t value  Pr(>|t|)
(Intercept)  0.04446    0.08542     0.52     0.63
conc         122.64111  0.93590     131.04   2.03e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.639 on 4 degrees of freedom
Multiple R-Squared: 0.9998,   Adjusted R-squared: 0.9997
F-statistic: 1.717e+04 on 1 and 4 DF,  p-value: 2.034e-08
```

Figure 5.6.11 : The summary of R's regression analysis for a weighted linear regression. The types of information shown here is identical to that for the unweighted linear regression in Figure 5.6.8 .

? EXERCISE 5.6.2

Use R to complete the regression analysis in Exercise 5.4.1.

Answer

The figure below shows the R session for this problem, including loading the *chemCal* package, creating objects to hold the values for C_{std}, S_{std}, and S_{samp}. Note that for S_{samp}, we do not have the actual values for the three replicate measurements. In place of the actual measurements, we just enter the average signal three times. This is okay because the calculation depends on the average signal and the number of replicates, and not on the individual measurements.

```
> library("chemCal")
> conc=c(0, 1.55e-3, 3.16e-3, 4.74e-3, 6.34e-3, 7.92e-3)
> signal=c(0, 0.050, 0.093, 0.143, 0.188, 0.236)
> model=lm(signal~conc)
> summary(model)

Call:
lm(formula = signal ~ conc)

Residuals:
      1           2           3           4           5           6
-0.0013927  0.0027385 -0.0019058  0.0013377 -0.0010106  0.0002328

Coefficients:
             Estimate   Std. Error   t value   Pr(>|t|)
(Intercept)  0.001393   0.001441     0.967     0.388
conc         29.592733  0.300625     98.437    6.39e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.001996 on 4 degrees of freedom
Multiple R-Squared: 0.9996,   Adjusted R-squared: 0.9995
F-statistic:  9690 on 1 and 4 DF,  p-value: 6.386e-08

> samp=c(0.114, 0.114, 0.114)
> inverse.predict(model,samp,alpha=0.05)
$Prediction
[1] 0.003805234

$`Standard Error`
[1] 4.771723e-05

$Confidence
[1] 0.0001324843

$`Confidence Limits`
[1] 0.003672750 0.003937719
```

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6.7: PROBLEMS

1. Suppose you use a serial dilution to prepare 100 mL each of a series of standards with concentrations of 1.00×10^{-5}, 1.00×10^{-4}, 1.00×10^{-3}, and 1.00×10^{-2} M from a 0.100 M stock solution. Calculate the uncertainty for each solution using a propagation of uncertainty, and compare to the uncertainty if you prepare each solution as a single dilution of the stock solution. You will find tolerances for different types of volumetric glassware and digital pipets in Table 4.2.1 and Table 4.2.2. Assume that the uncertainty in the stock solution's molarity is ±0.0002.

2. Three replicate determinations of S_{total} for a standard solution that is 10.0 ppm in analyte give values of 0.163, 0.157, and 0.161 (arbitrary units). The signal for the reagent blank is 0.002. Calculate the concentration of analyte in a sample with a signal of 0.118.

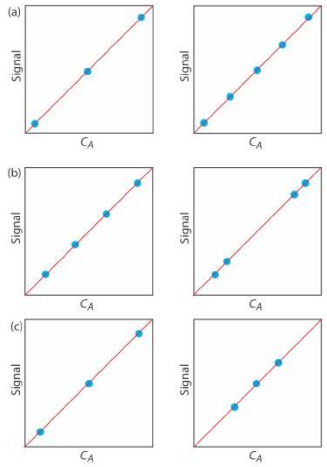
3. A 10.00-g sample that contains an analyte is transferred to a 250-mL volumetric flask and diluted to volume. When a 10.00 mL aliquot of the resulting solution is diluted to 25.00 mL it gives a signal of 0.235 (arbitrary units). A second 10.00-mL portion of the solution is spiked with 10.00 mL of a 1.00-ppm standard solution of the analyte and diluted to 25.00 mL. The signal for the spiked sample is 0.502. Calculate the weight percent of analyte in the original sample.

4. A 50.00 mL sample that contains an analyte gives a signal of 11.5 (arbitrary units). A second 50 mL aliquot of the sample, which is spiked with 1.00 mL of a 10.0-ppm standard solution of the analyte, gives a signal of 23.1. What is the analyte's concentration in the original sample?

5. A standard additions calibration curve based on Equation 5.3.10 places $S_{spike} \times (V_o + V_{std})$ on the *y*-axis and $C_{std} \times V_{std}$ on the *x*-axis. Derive equations for the slope and the *y*-intercept and explain how you can determine the amount of analyte in a sample from the calibration curve. In addition, clearly explain why you cannot plot S_{spike} on the *y*-axis and $C_{std} \times \{V_{std}/(V_o + V_{std})\}$ on the *x*-axis.

6. A standard sample contains 10.0 mg/L of analyte and 15.0 mg/L of internal standard. Analysis of the sample gives signals for the analyte and the internal standard of 0.155 and 0.233 (arbitrary units), respectively. Sufficient internal standard is added to a sample to make its concentration 15.0 mg/L. Analysis of the sample yields signals for the analyte and the internal standard of 0.274 and 0.198, respectively. Report the analyte's concentration in the sample.

7. For each of the pair of calibration curves shown ibelow, select the calibration curve that uses the more appropriate set of standards. Briefly explain the reasons for your selections. The scales for the *x*-axis and the *y*-axis are the same for each pair.



8. The following data are for a series of external standards of Cd^{2+} buffered to a pH of 4.6.

$[Cd^{2+}]$ (nM)	15.4	30.4	44.9	59.0	72.7	86.0
S_{spike} (nA)	4.8	11.4	18.2	26.6	32.3	37.7

(a) Use a linear regression analysis to determine the equation for the calibration curve and report confidence intervals for the slope and the *y*-intercept.

(b) Construct a plot of the residuals and comment on their significance.

At a pH of 3.7 the following data were recorded for the same set of external standards.

$[Cd^{2+}]$ (nM)	15.4	30.4	44.9	59.0	72.7	86.0
S_{spike} (nA)	15.0	42.7	58.5	77.0	101	118

(c) How much more or less sensitive is this method at the lower pH?

(d) A single sample is buffered to a pH of 3.7 and analyzed for cadmium, yielding a signal of 66.3 nA. Report the concentration of Cd^{2+} in the sample and its 95% confidence interval.

The data in this problem are from Wojciechowski, M.; Balcerzak, J. *Anal. Chim. Acta* **1991**, *249*, 433–445.

9. To determine the concentration of analyte in a sample, a standard addition is performed. A 5.00-mL portion of sample is analyzed and then successive 0.10-mL spikes of a 600.0 ppb standard of the analyte are added, analyzing after each spike. The following table shows the results of this analysis.

V_{spike} (mL)	0.00	0.10	0.20	0.30
S_{total} (arbitrary units)	15.0	42.7	58.5	77.0

Construct an appropriate standard additions calibration curve and use a linear regression analysis to determine the concentration of analyte in the original sample and its 95% confidence interval.

10. Troost and Olavsesn investigated the application of an internal standardization to the quantitative analysis of polynuclear aromatic hydrocarbons. The following results were obtained for the analysis of phenanthrene using isotopically labeled phenanthrene as an internal standard. Each solution was analyzed twice.

C_A/C_{IS}	0.50	1.25	2.00	3.00	4.00
S_A/S_{IS}	0.514	0.993	1.486	2.044	2.342
	0.522	1.024	1.471	2.080	2.550

(a) Determine the equation for the calibration curve using a linear regression, and report confidence intervals for the slope and the *y*-intercept. Average the replicate signals for each standard before you complete the linear regression analysis.

(b) Based on your results explain why the authors concluded that the internal standardization was inappropriate.

The data in this problem are from Troost, J. R.; Olavesen, E. Y. *Anal. Chem.* **1996**, *68*, 708–711.

11. In Chapter 4.6. we used a paired *t*-test to compare two analytical methods that were used to analyze independently a series of samples of variable composition. An alternative approach is to plot the results for one method versus the results for the other method. If the two methods yield identical results, then the plot should have an expected slope, β_1, of 1.00 and an expected *y*-intercept, β_0, of 0.0. We can use a *t*-test to compare the slope and the *y*-intercept from a linear regression to the expected values. The appropriate test statistic for the *y*-intercept is found by rearranging Equation 5.4.10.

$$t_{exp} = \frac{|\beta_0 - b_0|}{s_{b_0}} = \frac{|b_0|}{s_{b_0}}$$

Rearranging Equation 5.4.9 gives the test statistic for the slope.

$$t_{exp} = \frac{|\beta_1 - b_1}{s_{b_1}} = \frac{|b_1|}{s_{b_1}}$$

Reevaluate the data in Problem 25 from Chapter 4 using the same significance level as in the original problem.

> Although this is a common approach for comparing two analytical methods, it does violate one of the requirements for an unweighted linear regression—that indeterminate errors affect *y* only. Because indeterminate errors affect both analytical methods, the result of an unweighted linear regression is biased. More specifically, the regression underestimates the slope, b_1, and overestimates the *y*-intercept, b_0. We can minimize the effect of this bias by placing the more precise analytical method on the *x*-axis, by using more samples to increase the degrees of freedom, and by using samples that uniformly cover the range of concentrations.
>
> For more information, see Miller, J. C.; Miller, J. N. *Statistics for Analytical Chemistry*, 3rd ed. Ellis Horwood PTR Prentice-Hall: New York, 1993. Alternative approaches are found in Hartman, C.; Smeyers-Verbeke, J.; Penninckx, W.; Massart, D. L. *Anal. Chim. Acta* **1997**, *338*, 19–40, and Zwanziger, H. W.; Sârbu, C. *Anal. Chem.* **1998**, *70*, 1277–1280.

12. Consider the following three data sets, each of which gives values of *y* for the same values of *x*.

x	y_1	y_2	y_3
10.00	8.04	9.14	7.46
8.00	6.95	8.14	6.77
13.00	7.58	8.74	12.74
9.00	8.81	8.77	7.11
11.00	8.33	9.26	7.81
14.00	9.96	8.10	8.84
6.00	7.24	6.13	6.08
4.00	4.26	3.10	5.39
12.00	10.84	9.13	8.15
7.00	4.82	7.26	6.42
5.00	5.68	4.74	5.73

(a) An unweighted linear regression analysis for the three data sets gives nearly identical results. To three significant figures, each data set has a slope of 0.500 and a *y*-intercept of 3.00. The standard deviations in the slope and the *y*-intercept are 0.118 and 1.125 for each data set. All three standard deviations about the regression are 1.24. Based on these results for a linear regression analysis, comment on the similarity of the data sets.

(b) Complete a linear regression analysis for each data set and verify that the results from part (a) are correct. Construct a residual plot for each data set. Do these plots change your conclusion from part (a)? Explain.

(c) Plot each data set along with the regression line and comment on your results.

(d) Data set 3 appears to contain an outlier. Remove the apparent outlier and reanalyze the data using a linear regression. Comment on your result.

(e) Briefly comment on the importance of visually examining your data.

These three data sets are taken from Anscombe, F. J. “Graphs in Statistical Analysis,” *Amer. Statis.* **1973**, *27*, 17-21.

13. Fanke and co-workers evaluated a standard additions method for a voltammetric determination of Tl. A summary of their results is tabulated in the following table.

ppm Tl added	Instrument Response (μA)						
0.000	2.53	2.50	2.70	2.63	2.70	2.80	2.52
0.387	8.42	7.96	8.54	8.18	7.70	8.34	7.98
1.851	29.65	28.70	29.05	28.30	29.20	29.95	28.95
5.734	84.8	85.6	86.0	85.2	84.2	86.4	87.8

Use a weighted linear regression to determine the standardization relationship for this data.

The data in this problem are from Franke, J. P.; de Zeeuw, R. A.; Hakkert, R. *Anal. Chem.* **1978**, *50*, 1374–1380.

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6.8: ADDITIONAL RESOURCES

Although there are many experiments in the literature that incorporate external standards, the method of standard additions, or internal standards, the issue of choosing a method standardization is not the experiment's focus. One experiment designed to consider the issue of selecting a method of standardization is given here.

- Harvey, D. T. "External Standards or Standard Additions? Selecting and Validating a Method of Standardization," *J. Chem. Educ.* **2002**, *79*, 613–615.

In addition to the texts listed as suggested readings in Chapter 4, the following text provide additional details on linear regression.

- Draper, N. R.; Smith, H. *Applied Regression Analysis*, 2nd. ed.; Wiley: New York, 1981.

The following articles providing more details about linear regression.

- Analytical Methods Committee "Is my calibration linear?" AMC Technical Brief, December 2005.
- Analytical Methods Committee "Robust regression: an introduction, "AMCTB 50, 2012.
- Badertscher, M.; Pretsch, E. "Bad results from good data," *Trends Anal. Chem.* **2006**, *25*, 1131–1138.
- Boqué, R.; Rius, F. X.; Massart, D. L. "Straight Line Calibration: Something More Than Slopes, Intercepts, and Correlation Coefficients," *J. Chem. Educ.* **1993**, *70*, 230–232.
- Danzer, K.; Currie, L. A. "Guidelines for Calibration in Analytical Chemistry. Part 1. Fundamentals and Single Component Calibration," *Pure Appl. Chem.* **1998**, *70*, 993–1014.
- Henderson, G. "Lecture Graphic Aids for Least-Squares Analysis," *J. Chem. Educ.* **1988**, *65*, 1001–1003.
- Logan, S. R. "How to Determine the Best Straight Line," *J. Chem. Educ.* **1995**, *72*, 896–898.
- Mashkina, E.; Oldman, K. B. "Linear Regressions to Which the Standard Formulas do not Apply," *ChemTexts*, **2015**, *1*, 1–11.
- Miller, J. N. "Basic Statistical Methods for Analytical Chemistry. Part 2. Calibration and Regression Methods," *Analyst* **1991**, *116*, 3–14.
- Raposo, F. "Evaluation of analytical calibration based on least-squares linear regression for instrumental techniques: A tutorial review," *Trends Anal. Chem.* **2016**, *77*, 167–185.
- Renman, L., Jagner, D. "Asymmetric Distribution of Results in Calibration Curve and Standard Addition Evaluations," *Anal. Chim. Acta* **1997**, *357*, 157–166.
- Rodriguez, L. C.; Gamiz-Gracia; Almansa-Lopez, E. M.; Bosque-Sendra, J. M. "Calibration in chemical measurement processes. II. A methodological approach," *Trends Anal. Chem*. **2001**, *20*, 620–636.

Useful papers providing additional details on the method of standard additions are gathered here.

- Bader, M. "A Systematic Approach to Standard Addition Methods in Instrumental Analysis," *J. Chem. Educ.* **1980**, *57*, 703–706.
- Brown, R. J. C.; Roberts, M. R.; Milton, M. J. T. "Systematic error arising form 'Sequential' Standard Addition Calibrations. 2. Determination of Analyte Mass Fraction in Blank Solutions," *Anal. Chim. Acta* **2009**, *648*, 153–156.
- Brown, R. J. C.; Roberts, M. R.; Milton, M. J. T. "Systematic error arising form 'Sequential' Standard Addition Calibrations: Quantification and correction," *Anal. Chim. Acta* **2007**, *587*, 158–163.
- Bruce, G. R.; Gill, P. S. "Estimates of Precision in a Standard Additions Analysis," *J. Chem. Educ.* **1999**, *76*, 805–807.
- Kelly, W. R.; MacDonald, B. S.; Guthrie "Gravimetric Approach to the Standard Addition Method in Instrumental Analysis. 1." *Anal. Chem.* **2008**, *80*, 6154–6158.
- Meija, J.; Pagliano, E.; Mester, Z. "Coordinate Swapping in Standard Addition Graphs for Analytical Chemistry: A Simplified Path for Uncertainty Calculation in Linear and Nonlinear Plots," Anal. Chem. 2014, 86, 8563–8567.
- Nimura, Y.; Carr, M. R. "Reduction of the Relative Error in the Standard Additions Method," *Analyst* **1990**, *115*, 1589–1595.

Approaches that combine a standard addition with an internal standard are described in the following paper.

- Jones, W. B.; Donati, G. L.; Calloway, C. P.; Jones, B. T. "Standard Dilution Analysis," Anal. Chem. 2015, 87, 2321–2327.

The following papers discusses the importance of weighting experimental data when use linear regression.

- Analytical Methods Committee "Why are we weighting?" AMC Technical Brief, June 2007.
- Karolczak, M. "To Weight or Not to Weight? An Analyst's Dilemma," *Current Separations* **1995**, *13*, 98–104.

Algorithms for performing a linear regression with errors in both *X* and *Y* are discussed in the following papers. Also included here are papers that address the difficulty of using linear regression to compare two analytical methods.

- Irvin, J. A.; Quickenden, T. L. "Linear Least Squares Treatment When There are Errors in Both x and y," *J. Chem. Educ.* **1983**, *60*, 711–712.
- Kalantar, A. H. "Kerrich's Method for y = ax Data When Both y and x Are Uncertain," *J. Chem. Educ.* **1991**, *68*, 368–370.
- Macdonald, J. R.; Thompson, W. J. "Least-Squares Fitting When Both Variables Contain Errors: Pitfalls and Possibilities," *Am. J. Phys.* **1992**, *60*, 66–73.

- Martin, R. F. “General Deming Regression for Estimating Systematic Bias and Its Confidence Interval in Method-Comparison Studies,” *Clin. Chem.* **2000**, *46*, 100–104.
- Ogren, P. J.; Norton, J. R. “Applying a Simple Linear Least-Squares Algorithm to Data with Uncertain- ties in Both Variables,” *J. Chem. Educ.* **1992**, *69*, A130–A131.
- Ripley, B. D.; Thompson, M. “Regression Techniques for the Detection of Analytical Bias,” *Analyst* **1987**, *112*, 377–383.
- Tellinghuisen, J. “Least Squares in Calibration: Dealing with Uncertainty in *x*,” *Analyst*, **2010**, *135*, 1961–1969.

Outliers present a problem for a linear regression analysis. The following papers discuss the use of robust linear regression techniques.

- Glaister, P. “Robust Linear Regression Using Thiel’s Method,” *J. Chem. Educ.* **2005**, *82*, 1472–1473.
- Glasser, L. “Dealing with Outliers: Robust, Resistant Regression,” *J. Chem. Educ.* **2007**, *84*, 533–534.
- Ortiz, M. C.; Sarabia, L. A.; Herrero, A. “Robust regression techniques. A useful alternative for the detection of outlier data in chemical analysis,” *Talanta* **2006**, *70*, 499–512.

The following papers discusses some of the problems with using linear regression to analyze data that has been mathematically transformed into a linear form, as well as alternative methods of evaluating curvilinear data.

- Chong, D. P. “On the Use of Least Squares to Fit Data in Linear Form,” *J. Chem. Educ.* **1994**, *71*, 489–490.
- Hinshaw, J. V. “Nonlinear Calibration,” *LCGC* **2002**, *20*, 350–355.
- Lieb, S. G. “Simplex Method of Nonlinear Least-Squares - A Logical Complementary Method to Linear Least-Squares Analysis of Data,” *J. Chem. Educ.* **1997**, *74*, 1008–1011.
- Zielinski, T. J.; Allendoerfer, R. D. “Least Squares Fitting of Nonlinear Data in the Undergraduate Laboratory,” *J. Chem. Educ.* **1997**, *74*, 1001–1007.

More information on multivariate and multiple regression can be found in the following papers.

- Danzer, K.; Otto, M.; Currie, L. A. “Guidelines for Calibration in Analytical Chemistry. Part 2. Multispecies Calibration,” *Pure Appl. Chem.* **2004**, *76*, 1215–1225.
- Escandar, G. M.; Faber, N. M.; Goicoechea, H. C.; de la Pena, A. M.; Olivieri, A.; Poppi, R. J. “Second- and third-order multivariate calibration: data, algorithms and applications,” *Trends Anal. Chem.* **2007**, *26*, 752–765.
- Kowalski, B. R.; Seasholtz, M. B. “Recent Developments in Multivariate Calibration,” *J. Chemometrics* **1991**, *5*, 129–145.
- Lang, P. M.; Kalivas, J. H. “A Global Perspective on Multivariate Calibration Methods,” *J. Chemomet- rics* **1993**, *7*, 153–164.
- Madden, S. P.; Wilson, W.; Dong, A.; Geiger, L.; Mecklin, C. J. “Multiple Linear Regression Using a Graphing Calculator,” J. Chem. Educ. 2004, 81, 903–907.
- Olivieri, A. C.; Faber, N. M.; Ferré, J.; Boqué, R.; Kalivas, J. H.; Mark, H. “Uncertainty Estimation and Figures of Merit for Multivariate Calibration,” *Pure Appl. Chem.* **2006**, *78*, 633–661.

An additional discussion on method blanks, including the use of the total Youden blank, is found in the fol- lowing papers.

- Cardone, M. J. “Detection and Determination of Error in Analytical Methodology. Part II. Correc- tion for Corrigible Systematic Error in the Course of Real Sample Analysis,” *J. Assoc. Off. Anal. Chem.* **1983**, *66*, 1283–1294.
- Cardone, M. J. “Detection and Determination of Error in Analytical Methodology. Part IIB. Direct Calculational Technique for Making Corrigible Systematic Error Corrections,” *J. Assoc. Off. Anal. Chem.* **1985**, *68*, 199–202.
- Ferrus, R.; Torrades, F. “Bias-Free Adjustment of Analytical Methods to Laboratory Samples in Routine Analytical Procedures,” *Anal. Chem.* **1988**, *60*, 1281–1285.
- Vitha, M. F.; Carr, P. W.; Mabbott, G. A. “Appropriate Use of Blanks, Standards, and Controls in Chemical Measurements,” *J. Chem. Educ.* **2005**, *82*, 901–902.

There are a variety of computational packages for completing linear regression analyses. These papers provide details on there use in a variety of contexts.

- Espinosa-Mansilla, A.; de la Peña, A. M.; González-Gómez, D. “Using Univariate Linear Regression Calibration Software in the MATLAB Environment. Application to Chemistry Laboratory Practices,” *Chem. Educator* **2005**, *10*, 1–9.
- Harris, D. C. “Nonlinear Least-Squares Curve Fitting with Microsoft Excel Solver,” *J. Chem. Educ.* **1998**, *75*, 119–121.
- Kim, M. S.; Bukart, M.; Kim, M. H. “A Method Visual Interactive Regression,” *J. Chem. Educ.* **2006**, *83*, 1884.
- Machuca-Herrera, J. G. “Nonlinear Curve Fitting with Spreadsheets,” *J. Chem. Educ.* **1997**, *74*, 448–449.
- Smith, E. T.; Belogay, E. A.; Hõim “Linear Regression and Error Analysis for Calibration Curves and Standard Additions: An Excel Spreadsheet Exercise for Undergraduates,” Chem. Educator 2010, 15, 100–102.
- Smith, E. T.; Belogay, E. A.; Hõim “Using Multiple Linear Regression to Analyze Mixtures: An Excel Spreadsheet Exercise for Undergraduates,” *Chem. Educator* **2010**, *15*, 103–107.
- Young, S. H.; Wierzbicki, A. “Mathcad in the Chemistry Curriculum. Linear Least-Squares Regres- sion,” *J. Chem. Educ.* **2000**, *77*, 669.
- Young, S. H.; Wierzbicki, A. “Mathcad in the Chemistry Curriculum. Non-Linear Least-Squares Re- gression,” *J. Chem. Educ.* **2000**, *77*, 669.

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6.9: CHAPTER SUMMARY AND KEY TERMS

SUMMARY

In a quantitative analysis we measure a signal, S_{total}, and calculate the amount of analyte, n_A or C_A, using one of the following equations.

$$S_{total} = k_A n_A + S_{reag}$$

$$S_{total} = k_A C_A + S_{reag}$$

To obtain an accurate result we must eliminate determinate errors that affect the signal, S_{total}, the method's sensitivity, k_A, and the signal due to the reagents, S_{reag}.

To ensure that we accurately measure S_{total}, we calibrate our equipment and instruments. To calibrate a balance, for example, we use a standard weight of known mass. The manufacturer of an instrument usually suggests appropriate calibration standards and calibration methods.

To standardize an analytical method we determine its sensitivity. There are several standardization strategies available to us, including external standards, the method of standard addition, and internal standards. The most common strategy is a multiple-point external standardization and a normal calibration curve. We use the method of standard additions, in which we add known amounts of analyte to the sample, when the sample's matrix complicates the analysis. When it is difficult to reproducibly handle samples and standards, we may choose to add an internal standard.

Single-point standardizations are common, but are subject to greater uncertainty. Whenever possible, a multiple-point standardization is preferred, with results displayed as a calibration curve. A linear regression analysis provides an equation for the standardization.

A reagent blank corrects for any contribution to the signal from the reagents used in the analysis. The most common reagent blank is one in which an analyte-free sample is taken through the analysis. When a simple reagent blank does not compensate for all constant sources of determinate error, other types of blanks, such as the total Youden blank, are used.

KEY TERMS

calibration curve	external standard	internal standard
linear regression	matrix matching	method of standard additions
multiple-point standardization	normal calibration curve	primary standard
reagent grade	residual error	secondary standard
serial dilution	single-point standardization	standard deviation about the regression
total Youden blank	unweighted linear regression	weighted linear regression

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CHAPTER OVERVIEW

7: QUALITY ASSURANCE

In Chapter 14 we discussed the process of developing a standard method, including optimizing the experimental procedure, verifying that the method produces acceptable precision and accuracy in the hands of a signal analyst, and validating the method for general use by the broader analytical community. Knowing that a method meets suitable standards is important if we are to have confidence in our results. Even so, using a standard method does not guarantee that the result of an analysis is acceptable. In this chapter we introduce the quality assurance procedures used in industry and government labs for the real-time monitoring of routine chemical analyses.

7.1: The Analytical Perspective Revisited
7.2: Quality Control
7.3: Quality Assessment
7.4: Evaluating Quality Assurance Data
7.5: Problems
7.6: Additional Resources
7.7: Chapter Summary and Key Terms

Thumbnail: Examples of property control charts that show a sequence of results.

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7.1: THE ANALYTICAL PERSPECTIVE REVISITED

As we noted in Chapter 1, each area of chemistry brings a unique perspective to the broader discipline of chemistry. For analytical chemistry this perspective is as an approach to solving problems, one representation of which is shown in Figure 15.1.1 .

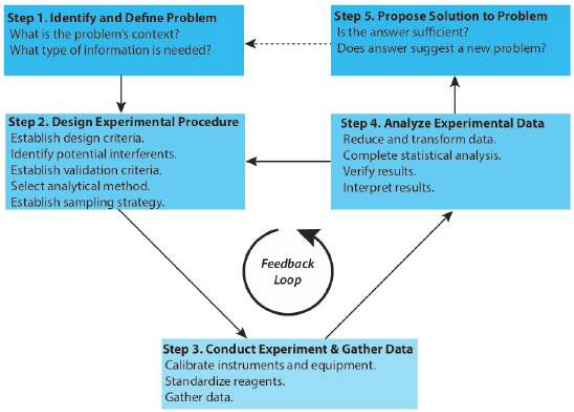


Figure 15.1.1 . Flow diagram showing one view of the analytical approach to solving problems. This diagram is modified after Atkinson, G. F. *J. Chem. Educ.* **1982**, *59*, 201–202.

> Figure 15.1.1 is the same as Figure 1.2.1. You may wish to review our earlier discussion of this figure and of the analytical approach to solving problem.

If you examine an analytical method it often seems that its development was a straightforward process of moving from a problem to its solution. Unfortunately—or, perhaps, fortunately for those who consider themselves analytical chemists!—developing an analytical method seldom is routine. Even a well-established standard analytical method, carefully followed, can yield poor data.

An important feature of the analytical approach in Figure 15.1.1 is the feedback loop that includes steps 2, 3, and 4, in which the outcome of one step may lead us to reevaluate the other steps. For example, after standardizing a spectrophotometric method for the analysis of iron (step 3), we may find that its sensitivity does not meet our original design criteria (step 2). In response, we might choose a different method, change the original design criteria, or work to improve the sensitivity.

The feedback loop in Figure 15.1.1 is maintained by a quality assurance program, whose objective is to control systematic and random sources of error [see, for example (a) Taylor, J. K. *Anal. Chem.* **1981**, *53*, 1588A–1596A; (b) Taylor, J. K. *Anal. Chem.* **1983**, *55*, 600A–608A; (c) Taylor, J. K. *Am. Lab* October 1985, *53*, 67–75; (d) Nadkarni, R. A. *Anal. Chem.* **1991**, *63*, 675A–682A; (e) Valcárcel, M.; Ríos, A. *Trends Anal. Chem.* **1994**, *13*, 17–23.] The underlying assumption of a quality assurance program is that results obtained when an analysis is under ***statistical control*** are free of bias and are characterized by well-defined confidence intervals. When used properly, a quality assurance program identifies the practices necessary to bring a system into statistical control, allows us to determine if the system remains in statistical control, and suggests a course of corrective action if the system falls out of statistical control.

> An analysis is in a state of statistical control when it is reproducible and free from bias.

The focus of this chapter is on the two principal components of a ***quality assurance program***: quality control and quality assessment. In addition, we will give considerable attention to the use of control charts for monitoring the quality of analytical data.

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7.2: QUALITY CONTROL

Quality control encompasses all activities that bring an analysis into statistical control. The most important facet of quality control is a set of written directives that describe relevant laboratory-specific, technique-specific, sample-specific, method-specific, and protocol-specific operations. ***Good laboratory practices*** (GLPs) describe the general laboratory operations that we must follow in any analysis. These practices include properly recording data and maintaining records, using chain-of-custody forms for samples, specifying and purifying chemical reagents, preparing commonly used reagents, cleaning and calibrating glassware, training laboratory personnel, and maintaining the laboratory facilities and general laboratory equipment.

> For one example of quality control, see Keith, L. H.; Crummett, W.; Deegan, J., Jr.; Libby, R. A.; Taylor, J. K.; Wentler, G. "Principles of Environmental Analysis," *Anal. Chem.* **1983**, *55*, 2210–2218. This article describes guidelines developed by the Subcommittee on Environmental Analytical Chemistry, a subcommittee of the American Chemical Society's Committee on Environmental Improvement.

Good measurement practices (GMPs) describe those operations specific to a technique. In general, GMPs provide instructions for maintaining, calibrating, and using equipment and instrumentation. For example, a GMP for a titration describes how to calibrate the buret (if required), how to fill the buret with titrant, the correct way to read the volume of titrant in the buret, and the correct way to dispense the titrant.

The directions for analyzing a specific analyte in a specific matrix are described by a ***standard operations procedure*** (SOP). The SOP indicates how we process the sample in the laboratory, how we separate the analyte from potential interferents, how we standardize the method, how we measure the analytical signal, how we transform the data into the desired result, and how we use quality assessment tools to maintain quality control. If the laboratory is responsible for sampling, then the SOP also states how we must collect, process, and preserve the sample in the field. An SOP may be developed and used by a single laboratory, or it may be a standard procedure approved by an organization such as the American Society for Testing Materials or the Federal Food and Drug Administration. A typical SOP is provided in the following example.

EXAMPLE 15.2.1

Provide an SOP for the determination of cadmium in lake sediments using atomic absorption spectroscopy and a normal calibration curve.

Solution

Collect sediment samples using a bottom grab sampler and store them at 4^oC in acid-washed polyethylene bottles during transportation to the laboratory. Dry the samples to constant weight at 105^oC and grind them to a uniform particle size. Extract the cadmium in a 1-g sample of sediment by adding the sediment and 25 mL of 0.5 M HCl to an acid-washed 100-mL polyethylene bottle and shaking for 24 h. After filtering, analyze the sample by atomic absorption spectroscopy using an air–acetylene flame, a wavelength of 228.8 nm, and a slit width of 0.5 nm. Prepare a normal calibration curve using five standards with nominal concentrations of 0.20, 0.50, 1.00, 2.00, and 3.00 ppm. Periodically check the accuracy of the calibration curve by analyzing the 1.00-ppm standard. An accuracy of $\pm$ 10% is considered acceptable.

Although an SOP provides a written procedure, it is not necessary to follow the procedure exactly as long as we are careful to identify any modifications. On the other hand, we must follow all instructions in a ***protocol for a specific purpose*** (PSP)—the most detailed of the written quality control directives—before an agency or a client will accept our results. In many cases the required elements of a PSP are established by the agency that sponsors the analysis. For example, a lab working under contract with the Environmental Protection Agency must develop a PSP that addresses such items as sampling and sample custody, frequency of calibration, schedules for the preventive maintenance of equipment and instrumentation, and management of the quality assurance program.

Two additional aspects of a quality control program deserve mention. The first is that the individuals responsible for collecting and analyzing the samples can critically examine and reject individual samples, measurements, and results. For example, when analyzing sediments for cadmium (see the SOP in Example 15.2.1) we might choose to screen sediment samples, discarding a sample that contains foreign objects—such as rocks, twigs, or trash—replacing it with an additional sample. If we observe a sudden change in the performance of the atomic absorption spectrometer, we may choose to reanalyze the affected samples. We may also decide to reanalyze a sample if the result of its analysis clearly is unreasonable. By identifying those samples, measurements, and results subject to gross systematic errors, inspection helps control the quality of an analysis.

The second additional consideration is the certification of an analyst's competence to perform the analysis for which he or she is responsible. Before an analyst is allowed to perform a new analytical method, he or she may be required to analyze successfully an

independent check sample with acceptable accuracy and precision. The check sample is similar in composition to samples that the analyst will analyze later, with a concentration that is 5 to 50 times that of the method's detection limit.

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7.3: QUALITY ASSESSMENT

The written directives of a quality control program are a necessary, but not a sufficient condition for obtaining and maintaining a state of statistical control. Although quality control directives explain how to conduct an analysis, they do not indicate whether the system is under statistical control. This is the role of ***quality assessment***, the second component of a quality assurance program.

The goals of quality assessment are to determine when an analysis has reached a state of statistical control, to detect when an analysis falls out of statistical control, and to suggest possible reasons for this loss of statistical control. For convenience, we divide quality assessment into two categories: internal methods coordinated within the laboratory, and external methods organized and maintained by an outside agency.

INTERNAL METHODS OF QUALITY ASSESSMENT

The most useful methods for quality assessment are those coordinated by the laboratory, which provide immediate feedback about the analytical method's state of statistical control. Internal methods of quality assessment include the analysis of duplicate samples, the analysis of blanks, the analysis of standard samples, and spike recoveries.

ANALYSIS OF DUPLICATE SAMPLES

An effective method for determining the precision of an analysis is to analyze ***duplicate samples***. Duplicate samples are obtained by dividing a single gross sample into two parts, although in some cases the duplicate samples are independently collected gross samples. We report the results for the duplicate samples, X_1 and X_2, by determining the difference, d, or the relative difference, $(d)_r$, between the two samples

$$d = X_1 - X_2$$

$$(d)_r = \frac{d}{(X_1 + X_2)/2} \times 100$$

and comparing to an accepted value, such as those in Table 15.3.1 for the analysis of waters and wastewaters. Alternatively, we can estimate the standard deviation using the results for a set of n duplicates

$$s = \sqrt{\frac{\sum_{i=1}^{n} d_i^2}{2n}}$$

where d_i is the difference between the ith pair of duplicates. The degrees of freedom for the standard deviation is the same as the number of duplicate samples. If we combine duplicate samples from several sources, then the precision of the measurement process must be approximately the same for each.

Table 15.3.1 : Quality Assessment Limits for the Analysis of Waters and Wastewaters

analyte	$(d)_r$: [analyte] < 20 × MDL (±%)	$(d)_r$: [analyte] > 20 × MDL (±%)	spike recovery limit (%)
acids	40	20 × MDL (±%)">20	60–140
anions	25	20 × MDL (±%)">10	80–120
bases or neutrals	40	20 × MDL (±%)">20	70–130
carbamate pesticides	40	20 × MDL (±%)">20	50–150
herbicides	40	20 × MDL (±%)">20	40–160
metals	25	20 × MDL (±%)">10	80–120
other inorganics	25	20 × MDL (±%)">10	80–120
volatile organics	40	20 × MDL (±%)">20	70–130

Abbreviation: MDL = method's detection limit

Source: Table 1020.1 in *Standard Methods for the Analysis of Water and Wastewater*, American Public Health Association: Washington, D. C., 18th Ed. 1992.

✔ EXAMPLE 15.3.1

To evaluate the precision for the determination of potassium in blood serum, duplicate analyses were performed on six samples, yielding the following results in mg K/L.

Table of potassium tests in blood serum

duplicate	X_1	X_2
1	160	147
2	196	202
3	207	196
4	185	193
5	172	188
6	133	119

Estimate the standard deviation for the analysis.

Solution

To estimate the standard deviation we first calculate the difference, d, and the squared difference, d^2, for each duplicate. The results of these calculations are summarized in the following table.

Table of potassium tests in blood serum

duplicate	$d = X_1 - X_2$	d^2
1	13	169
2	–6	36
3	11	121
4	–8	64
5	–16	256
6	14	196

Finally, we calculate the standard deviation

$$s = \sqrt{\frac{169 + 36 + 121 + 64 + 256 + 196}{2 \times 6}} = 8.4$$

EXERCISE 15.3.1

To evaluate the precision of a glucometer—a device a patient uses at home to monitor his or her blood glucose level—duplicate analyses are performed on samples drawn from five individuals, yielding the following results in mg glucose/100 mL.

duplicate	X_1	X_2
1	148.5	149.1
2	96.5	98.8
3	174.9	174.5
4	118.1	118.9
5	72.7	70.4

Estimate the standard deviation for the analysis.

Answer

To estimate the standard deviation we first calculate the difference, d, and the squared difference, d^2, for each duplicate. The results of these calculations are summarized in the following table.

duplicate	$d = X_1 - X_2$	d^2
1	–0.6	0.36
2	–2.3	5.29
3	0.4	0.16
4	–0.8	0.64
5	2.3	5.29

Finally, we calculate the standard deviation.

$$s = \sqrt{\frac{0.36 + 5.29 + 0.16 + 0.64 + 5.29}{2 \times 5}} = 1.08$$

ANALYSIS OF BLANKS

We introduced the use of a blank in Chapter 3 as a way to correct the signal for contributions from sources other than the analyte. The most common blank is a ***method blank*** in which we take an analyte free sample through the analysis using the same reagents, glassware, and instrumentation. A method blank allows us to identify and to correct systematic errors due to impurities in the reagents, contaminated glassware, and poorly calibrated instrumentation. At a minimum, a new method blank is analyzed whenever we prepare a new reagent, or after we analyze a sample with a high concentration of analyte as residual carryover of analyte may produce a positive determinate error.

When we collect samples in the field, additional blanks are needed to correct for potential sampling errors [Keith, L. H. *Environmental Sampling and Analysis: A Practical Guide*, Lewis Publishers: Chelsea, MI, 1991]. A ***field blank*** is an analyte-free sample carried from the laboratory to the sampling site. At the sampling site the blank is transferred to a clean sample container, which exposes it to the local environment. The field blank is then preserved and transported back to the laboratory for analysis. A field blank helps identify systematic errors due to sampling, transport, and analysis. A trip blank is an analyte-free sample carried from the laboratory to the sampling site and back to the laboratory without being opened. A trip blank helps to identify systematic errors due to cross-contamination of volatile organic compounds during transport, handling, storage, and analysis.

> A method blank also is called a reagent blank. The contamination of reagents over time is a significant concern. The regular use of a method blank compensates for this contamination.

ANALYSIS OF STANDARDS

Another tool for monitoring an analytical method's state of statistical control is to analyze a standard that contains a known concentration of analyte. A standard reference material (SRM) is the ideal choice, provided that the SRM's matrix is similar to that of our samples. A variety of SRMs are available from the National Institute of Standards and Technology (NIST). If a suitable SRM is not available, then we can use an independently prepared synthetic sample if it is prepared from reagents of known purity. In all cases, the analyte's experimentally determined concentration in the standard must fall within predetermined limits before the analysis is considered under statistical control.

> Table 4.2.6 in Chapter 4 provides a summary of SRM 2346, a standard sample of Gingko biloba leaves with certified values for the concentrations of flavonoids, terpene ketones, and toxic elements, such as mercury and lead.

SPIKE RECOVERIES

One of the most important quality assessment tools is the recovery of a known addition, or spike, of analyte to a method blank, a field blank, or a sample. To determine a ***spike recovery***, the blank or sample is split into two portions and a known amount of a standard solution of analyte is added to one portion. The analyte's concentration is determined for both the spiked, F, and unspiked portions, I, and the percent recovery, $\%R$, is calculated as

$$\%R = \frac{F - I}{A} \times 100$$

where A is the concentration of analyte added to the spiked portion.

✔ EXAMPLE 15.3.2

A spike recovery for the analysis of chloride in well water was performed by adding 5.00 mL of a 250.0 ppm solution of Cl^- to a 50-mL volumetric flask and diluting to volume with the sample. An unspiked sample was prepared by adding 5.00 mL of distilled water to a separate 50-mL volumetric flask and diluting to volume with the sample. Analysis of the sample and the spiked sample return chloride concentrations of 18.3 ppm and 40.9 ppm, respectively. Determine the spike recovery.

Solution

To calculate the concentration of the analyte added in the spike, we take into account the effect of dilution.

$$A = 250.0\text{ppm} \times \frac{5.00\text{mL}}{50.0\text{mL}} = 25.0\text{ppm}$$

Thus, the spike recovery is

$$\%R = \frac{40.9 - 18.3}{25.0} \times 100 = 90.4\%$$

? EXERCISE 15.3.2

To test a glucometer, a spike recovery is carried out by measuring the amount of glucose in a sample of a patient's blood before and after spiking it with a standard solution of glucose. Before spiking the sample the glucose level is 86.7 mg/100 mL and after spiking the sample it is 110.3 mg/100 mL. The spike is prepared by adding 10.0 µL of a 25 000 mg/100mL standard to a 10.0-mL portion of the blood. What is the spike recovery for this sample.

Answer

Adding a 10.0-µL spike to a 10.0-mL sample is a 1000-fold dilution; thus, the concentration of added glucose is 25.0 mg/100 mL and the spike recovery is

$$\%R = \frac{110.3 - 86.7}{25.0} \times 100 = 94.4\%$$

We can use a spike recovery on a method blank and a field blank to evaluate the general performance of an analytical procedure. A known concentration of analyte is added to each blank at a concentration that is 5 to 50 times the method's detection limit. A systematic error during sampling and transport will result in an unacceptable recovery for the field blank, but not for the method blank. A systematic error in the laboratory, however, affects the recoveries for both the field blank and the method blank.

Spike recoveries on a sample are used to detect systematic errors due to the sample's matrix, or to evaluate the stability of a sample after its collection. Ideally, samples are spiked in the field at a concentration that is 1 to 10 times the analyte's expected concentration or 5 to 50 times the method's detection limit, whichever is larger. If the recovery for a field spike is unacceptable, then a duplicate sample is spiked in the laboratory and analyzed immediately. If the laboratory spike's recovery is acceptable, then the poor recovery for the field spike likely is the result of the sample's deterioration during storage. If the recovery for the laboratory spike also is unacceptable, the most probable cause is a matrix-dependent relationship between the analytical signal and the analyte's concentration. In this case the sample is analyzed by the method of standard additions. Typical limits for spike recoveries for the analysis of waters and wastewaters are shown in Table 15.3.1 .

Figure 15.4.1, which we will discuss in the next section, illustrates the use of spike recoveries as part of a quality assessment program.

EXTERNAL METHODS OF QUALITY ASSESSMENT

Internal methods of quality assessment always carry some level of suspicion because there is a potential for bias in their execution and interpretation. For this reason, external methods of quality assessment also play an important role in a quality assurance program. One external method of quality assessment is the certification of a laboratory by a sponsoring agency. Certification of a lab is based on its successful analysis of a set of ***proficiency standards*** prepared by the sponsoring agency. For example, laboratories involved in environmental analyses may be required to analyze standard samples prepared by the Environmental Protection Agency. A second example of an external method of quality assessment is a laboratory's voluntary participation in a collaborative test sponsored by a professional organization, such as the Association of Official Analytical Chemists. Finally, an individual contracting with a laboratory can perform his or her own external quality assessment by submitting blind duplicate samples and blind standards to the laboratory for analysis. If the results for the quality assessment samples are unacceptable, then there is good reason to question the laboratory's results for other samples.

See Chapter 14 for a more detailed description of collaborative testing.

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7.4: EVALUATING QUALITY ASSURANCE DATA

In the previous section we described several internal methods of quality assessment that provide quantitative estimates of the systematic errors and the random errors in an analytical method. Now we turn our attention to how we incorporate this quality assessment data into a complete quality assurance program. There are two general approaches to developing a quality assurance program: a prescriptive approach, in which we prescribe an exact method of quality assessment, and a performance-based approach in which we can use any form of quality assessment, provided that we can demonstrate an acceptable level of statistical control [Poppiti, J. *Environ. Sci. Technol.* **1994**, *28*, 151A–152A].

PRESCRIPTIVE APPROACH

With a prescriptive approach to quality assessment, duplicate samples, blanks, standards, and spike recoveries are measured using a specific protocol. We compare the result of each analysis to a single predetermined limit, taking an appropriate corrective action if the limit is exceeded. Prescriptive approaches to quality assurance are common for programs and laboratories subject to federal regulation. For example, the Food and Drug Administration (FDA) specifies quality assurance practices that must be followed by laboratories that analyze products regulated by the FDA.

Figure 15.4.1 provides a typical example of a prescriptive approach to quality assessment. Two samples, *A* and *B*, are collected at the sample site. Sample *A* is split into two equal-volume samples, A_1 and A_2. Sample *B* is also split into two equal-volume samples, one of which, B_{SF}, is spiked in the field with a known amount of analyte. A field blank, D_F, also is spiked with the same amount of analyte. All five samples (A_1, A_2, *B*, B_{SF}, and *DF*) are preserved if necessary and transported to the laboratory for analysis.

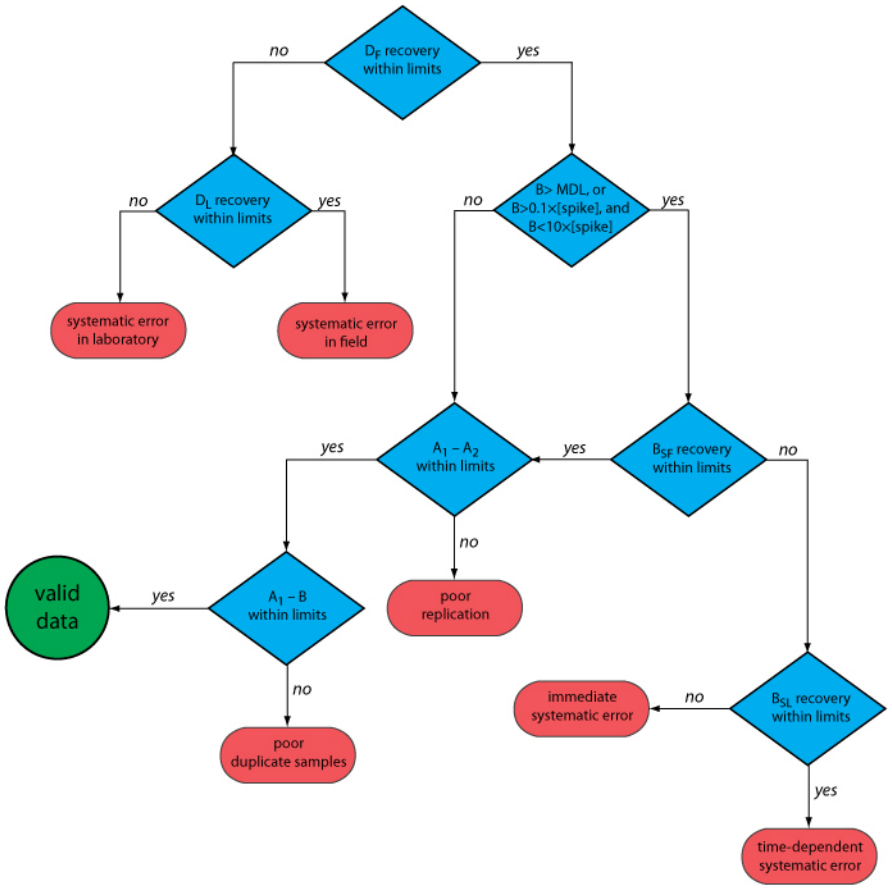


Figure 15.4.1 . Example of a prescriptive approach to quality assurance for laboratories monitoring waters and wastewaters. Adapted from Environmental Monitoring and Support Laboratory, U. S. Environmental Protection Agency, "Handbook for Analytical Quality Control in Water and Wastewater Laboratories," March 1979.

After returning to the lab, the first sample that is analyzed is the field blank. If its spike recovery is unacceptable—an indication of a systematic error in the field or in the lab—then a laboratory method blank, D_L, is prepared and analyzed. If the spike recovery for the method blank is unsatisfactory, then the systematic error originated in the laboratory; this is error the analyst can find and correct before proceeding with the analysis. An acceptable spike recovery for the method blank, however, indicates that the systematic error occurred in the field or during transport to the laboratory, casting uncertainty on the quality of the samples. The only recourse is to discard the samples and return to the field to collect new samples.

If the field blank is satisfactory, then sample B is analyzed. If the result for sample B is above the method's detection limit, or if it is within the range of 0.1 to 10 times the amount of analyte spiked into B_{SF}, then a spike recovery for B_{SF} is determined. An unacceptable spike recovery for B_{SF} indicates the presence of a systematic error that involves the sample. To determine the source of the systematic error, a laboratory spike, B_{SL}, is prepared using sample B and analyzed. If the spike recovery for B_{SL} is acceptable, then the systematic error requires a long time to have a noticeable effect on the spike recovery. One possible explanation is that the analyte has not been preserved properly or it has been held beyond the acceptable holding time. An unacceptable spike recovery for B_{SL} suggests an immediate systematic error, such as that due to the influence of the sample's matrix. In either case the systematic errors are fatal and must be corrected before the sample is reanalyzed.

If the spike recovery for B_{SF} is acceptable, or if the result for sample B is below the method's detection limit, or outside the range of 0.1 to 10 times the amount of analyte spiked in B_{SF}, then the duplicate samples A_1 and A_2 are analyzed. The results for A_1 and A_2 are discarded if the difference between their values is excessive. If the difference between the results for A_1 and A_2 is within the accepted limits, then the results for samples A_1 and B are compared. Because samples collected from the same sampling site at the same time should be identical in composition, the results are discarded if the difference between their values is unsatisfactory and the results accepted if the difference is satisfactory.

The protocol in Figure 15.4.1 requires four to five evaluations of quality assessment data before the result for a single sample is accepted, a process that we must repeat for each analyte and for each sample. Other prescriptive protocols are equally demanding. For example, Figure 3.6.1 in Chapter 3 shows a portion of a quality assurance protocol for the graphite furnace atomic absorption analysis of trace metals in aqueous solutions. This protocol involves the analysis of an initial calibration verification standard and an initial calibration blank, followed by the analysis of samples in groups of ten. Each group of samples is preceded and followed by continuing calibration verification (CCV) and continuing calibration blank (CCB) quality assessment samples. Results for each group of ten samples are accepted only if both sets of CCV and CCB quality assessment samples are acceptable.

The advantage of a prescriptive approach to quality assurance is that all laboratories use a single consistent set of guideline. A significant disadvantage is that it does not take into account a laboratory's ability to produce quality results when determining the frequency of collecting and analyzing quality assessment data. A laboratory with a record of producing high quality results is forced to spend more time and money on quality assessment than perhaps is necessary. At the same time, the frequency of quality assessment may be insufficient for a laboratory with a history of producing results of poor quality.

PERFORMANCE-BASED APPROACH

In a performance-based approach to quality assurance, a laboratory is free to use its experience to determine the best way to gather and monitor quality assessment data. The tools of quality assessment remain the same— duplicate samples, blanks, standards, and spike recoveries—because they provide the necessary information about precision and bias. What a laboratory can control is the frequency with which it analyzes quality assessment samples and the conditions it chooses to signal when an analysis no longer is in a state of statistical control.

The principal tool for performance-based quality assessment is a ***control chart***, which provides a continuous record of quality assessment data. The fundamental assumption is that if an analysis is under statistical control, individual quality assessment results are distributed randomly around a known mean with a known standard deviation. When an analysis moves out of statistical control, the quality assessment data is influenced by additional sources of error, which increases the standard deviation or changes the mean value.

Control charts were developed in the 1920s as a quality assurance tool for the control of manufactured products [Shewhart, W. A. *Economic Control of the Quality of Manufactured Products*, Macmillan: London, 1931]. Although there are many types of control charts, two are common in quality assessment programs: a property control chart, in which we record single measurements or the means for several replicate measurements, and a precision control chart, in which we record ranges or standard deviations. In either case, the control chart consists of a line that represents the experimental result and two or more boundary lines whose positions are determined by the precision of the measurement process. The position of the data points about the boundary lines determines whether the analysis is in statistical control.

CONSTRUCTING A PROPERTY CONTROL CHART

The simplest property control chart is a sequence of points, each of which represents a single determination of the property we are monitoring. To construct the control chart, we analyze a minimum of 7–15 samples while the system is under statistical control. The center line (CL) of the control chart is the average of these n samples.

$$CL = \overline{X} = \frac{\sum_{i=1}^{n} X_i}{n}$$

> The more samples in the original control chart, the easier it is to detect when an analysis is beginning to drift out of statistical control. Building a control chart with an initial run of 30 or more samples is not an unusual choice.

Boundary lines around the center line are determined by the standard deviation, *S*, of the *n* points

$$S = \sqrt{\frac{\sum_{i=1}^{n} \left(X_i - \overline{X}\right)^2}{n-1}}$$

The upper and lower warning limits (*UWL* and *LWL*) and the upper and lower control limits (*UCL* and *LCL*) are given by the following equations.

$$UWL = CL + 2S$$
$$LWL = CL - 2S$$
$$UCL = CL + 3S$$
$$LCL = CL - 3S$$

Why these limits? Examine Table 4.4.2 in Chapter 4 and consider your answer to this question. We will return to this point later in this chapter when we consider how to use a control chart.

EXAMPLE 15.4.1

Construct a property control chart using the following spike recovery data (all values are for percentage of spike recovered).

sample:	1	2	3	4	5
result:	97.3	98.1	100.3	99.5	100.9
sample:	6	7	8	9	10
result:	98.6	96.9	99.6	101.1	100.4
sample:	11	12	13	14	15
result:	100.0	95.9	98.3	99.2	102.1
sample:	16	17	18	19	20
result:	98.5	101.7	100.4	99.1	100.3

Solution

The mean and the standard deviation for the 20 data points are 99.4% and 1.6%, respectively. Using these values, we find that the *UCL* is 104.2%, the *UWL* is 102.6%, the *LWL* is 96.2%, and the *LCL* is 94.6%. To construct the control chart, we plot the data points sequentially and draw horizontal lines for the center line and the four boundary lines. The resulting property control chart is shown in Figure 15.4.2 .

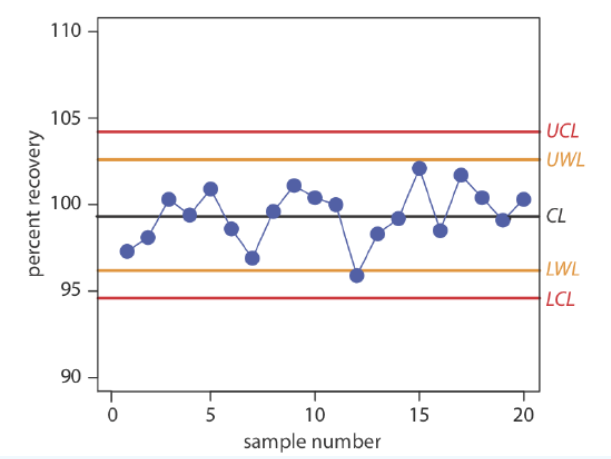


Figure 15.4.2 . Property control chart for Example 15.4.1 . The warning limits are shown in **orange** and the control limits in **red**.

EXERCISE 15.4.1

A control chart is a useful method for monitoring a glucometer's performance over time. One approach is to use the glucometer to measure the glucose level of a standard solution. An initial analysis of the standard yields a mean value of 249.4 mg/100 mL and a standard deviation of 2.5 mg/100 mL. An analysis of the standard over 20 consecutive days gives the following results.

day:	1	2	3	4	5	6	7	8	9	10
result:	248.1	246.0	247.9	249.4	250.9	249.7	250.2	250.3	247.3	245.6
day:	11	12	13	14	15	16	17	18	19	20
result:	246.2	250.8	249.0	254.3	246.1	250.8	248.1	246.7	253.5	251.0

Construct a control chart of the glucometer's performance.

Answer

The *UCL* is 256.9, the *UWL* is 254.4, the *CL* is 249.4, the *LWL* is 244.4, and the *LCL* is 241.9 mg glucose/100 mL. Figure 15.4.3 shows the resulting property control plot.

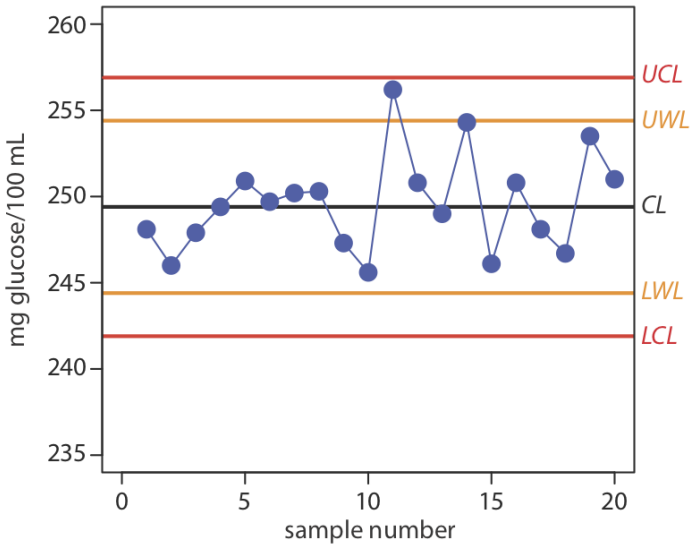


Figure 15.4.3 . Property control chart for Exercise 15.4.1 .

We also can construct a control chart using the mean for a set of replicate determinations on each sample. The mean for the *i*th sample is

$$\overline{X}_i = \frac{\sum_{j=1}^{n_{rep}} X_{ij}}{n_{rep}}$$

where X_{ij} is the *j*th replicate and n_{rep} is the number of replicate determinations for each sample. The control chart's center line is

$$CL = \frac{\sum_{i=1}^{n} \overline{X}_i}{n}$$

where *n* is the number of samples used to construct the control chart. To determine the standard deviation for the warning limits and the control limits, we first calculate the variance for each sample.

$$s_i^2 = \frac{\sum_{j=1}^{n_{rep}} \left(X_{ij} - \overline{X}_i \right)^2}{n_{rep} - 1}$$

The overall standard deviation, *S*, is the square root of the average variance for the samples used to construct the control plot.

$$S = \sqrt{\frac{\sum_{i=1}^{n} s_i^2}{n}}$$

The resulting warning and control limits are given by the following four equations.

$$UWL = CL + \frac{2S}{\sqrt{n_{rep}}}$$
$$LWL = CL - \frac{2S}{\sqrt{n_{rep}}}$$
$$UCL = CL + \frac{3S}{\sqrt{n_{rep}}}$$
$$LCL = CL - \frac{3S}{\sqrt{n_{rep}}}$$

When using means to construct a property control chart, all samples must have the same number of replicates.

CONSTRUCTING A PRECISION CONTROL CHART

A precision control chart shows how the precision of an analysis changes over time. The most common measure of precision is the range, *R*, between the largest and the smallest results for n_{rep} analyses on a sample.

$$R = X_{\text{largest}} - X_{\text{smallest}}$$

To construct the control chart, we analyze a minimum of 15–20 samples while the system is under statistical control. The center line (*CL*) of the control chart is the average range of these *n* samples.

$$\overline{R} = \frac{\sum_{i=1}^{n} R_i}{n}$$

The upper warning line and the upper control line are given by the following equations

$$UWL = f_{UWL} \times \overline{R}$$
$$UCL = f_{UCL} \times \overline{R}$$

where f_{UWL} and f_{UCL} are statistical factors determined by the number of replicates used to determine the range. Table 15.4.1 provides representative values for f_{UWL} and f_{UCL}. Because the range is greater than or equal to zero, there is no lower control limit and no lower warning limit.

Table 15.4.1 . Statistical Factors for the Upper Warning Limit and the Upper Control Limit of a Precision Control Chart

replicates	f_{UWL}	f_{UCL}
2	2.512	3.267
3	2.050	2.575
4	1.855	2.282
5	1.743	2.115
6	1.669	2.004

EXAMPLE 15.4.2

Construct a precision control chart using the following ranges, each determined from a duplicate analysis of a 10.0-ppm calibration standard.

sample:	1	2	3	4	5
result:	0.36	0.09	0.11	0.06	0.25
sample:	6	7	8	9	10
result:	0.15	0.28	0.27	0.03	0.28
sample:	11	12	13	14	15
result:	0.21	0.19	0.06	0.13	0.37
sample:	16	17	18	19	20
result:	0.01	0.19	0.39	0.05	0.05

Solution

The average range for the duplicate samples is 0.176. Because two replicates were used for each point the *UWL* and *UCL* are

$$UWL = 2.512 \times 0.176 = 0.44$$
$$UCL = 3.267 \times 0.176 = 0.57$$

The resulting property control chart is shown in Figure 15.4.4 .

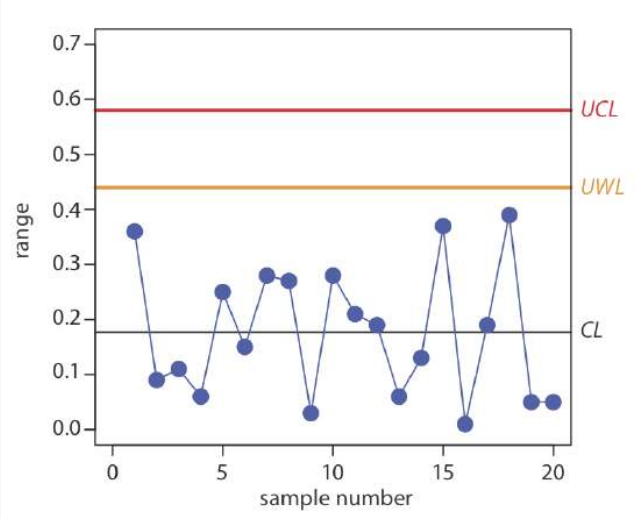


Figure 15.4.4 . Precision control chart for Example 15.4.2 . The warning limits are shown in **orange** and the control limits in **red**.

The precision control chart in Figure 15.4.4 is strictly valid only for the replicate analysis of identical samples, such as a calibration standard or a standard reference material. Its use for the analysis of nonidentical samples—as often is the case in clinical analyses and environmental analyses—is complicated by the fact that the range usually is not independent of the magnitude of the measurements. For example, Table 15.4.2 shows the relationship between the average range and the concentration of chromium in 91 water samples. The significant difference in the average range for different concentrations of chromium makes impossible a single precision control chart. As shown in Figure 15.4.5 , one solution is to prepare separate precision control charts, each of which covers a range of concentrations for which $\overline{R}$ is approximately constant.

Table 15.4.2 . Average Range for the Concentration of Chromium in Duplicate Water Samples

[Cr] (ppb)	number of duplicate samples	$\overline{R}$
5 to < 10	32	0.32
10 to < 25	15	0.57
25 to < 50	16	1.12
50 to < 150	15	3.80
150 to \(< 500)	8	5.25
> 500	5	76.0

Source: Environmental Monitoring and Support Laboratory, U. S. Environmental Protection Agency, “Handbook for Analytical Quality Control in Water and Wastewater Laboratories,” March 1979.

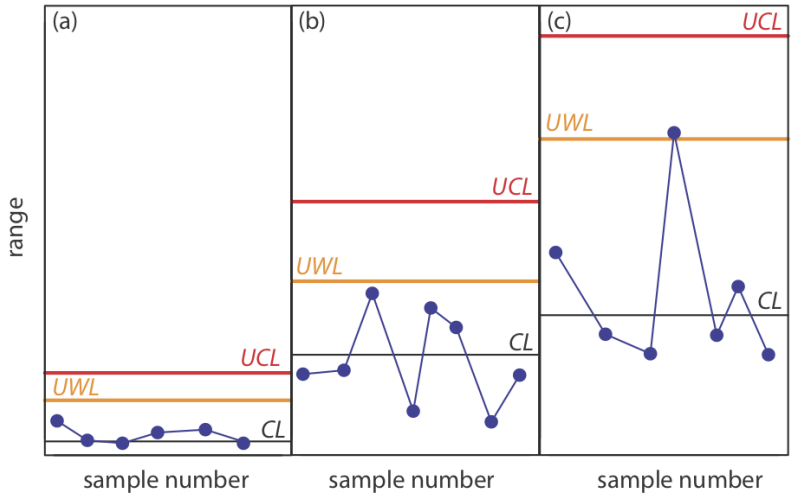


Figure 15.4.5 . Example showing the use of a precision control chart for samples that span a range of analyte concentrations. The precision control charts are for (a) low concentrations of analyte; (b) intermediate concentrations of analyte; and (c) high concentrations of analyte.

INTERPRETING CONTROL CHARTS

The purpose of a control chart is to determine if an analysis is in a state of statistical control. We make this determination by examining the location of individual results relative to the warning limits and the control limits, and by examining the distribution of results around the central line. If we assume that the individual results are normally distributed, then the probability of finding a point at any distance from the control limit is determined by the properties of a normal distribution [Mullins, E. *Analyst*, **1994**, *119*, 369–375.]. We set the upper and the lower control limits for a property control chart to $CL \pm 3S$ because 99.74% of a normally distributed population falls within three standard deviations of the population's mean. This means that there is only a 0.26% probability of obtaining a result larger than the *UCL* or smaller than the *LCL*. When a result exceeds a control limit, the most likely explanation is a systematic error in the analysis or a loss of precision. In either case, we assume that the analysis no longer is in a state of statistical control.

Rule 1. An analysis is no longer under statistical control if any single point exceeds either the *UCL* or the *LCL*.

By setting the upper and lower warning limits to $CL \pm 2S$, we expect that no more than 5% of the results will exceed one of these limits; thus

Rule 2. An analysis is no longer under statistical control if two out of three consecutive points are between the *UWL* and the *UCL* or between the *LWL* and the *LCL*.

If an analysis is under statistical control, then we expect a random distribution of results around the center line. The presence of an unlikely pattern in the data is another indication that the analysis is no longer under statistical control.

Rule 3. An analysis is no longer under statistical control if seven consecutive results are completely above or completely below the center line.

Rule 4. An analysis is no longer under statistical control if six consecutive results increase (or decrease) in value.

Rule 5. An analysis is no longer under statistical control if 14 consecutive results alternate up and down in value.

Rule 6. An analysis is no longer under statistical control if there is any obvious nonrandom pattern to the results.

Figure 15.4.6 shows three examples of control charts in which the results indicate that an analysis no longer is under statistical control. The same rules apply to precision control charts with the exception that there are no lower warning limits and lower control limits.

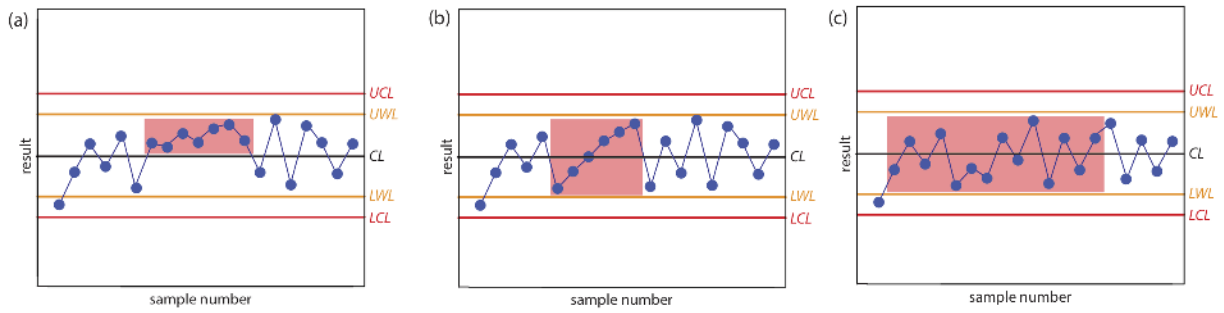


Figure 15.4.6 . Examples of property control charts that show a sequence of results—indicated by the highlighting—that violate (a) rule 3; (b) rule 4; and (c) rule 5.

? EXERCISE 15.4.2

In Exercise 15.4.1 you created a property control chart for a glucometer. Examine your property control chart and evaluate the glucometer's performance. Does your conclusion change if the next three results are 255.6, 253.9, and 255.8 mg/100 mL?

Answer

Although the variation in the results appears to be greater for the second 10 samples, the results do not violate any of the six rules. There is no evidence in Figure 15.4.3 that the analysis is out of statistical control. The next three results, in which two of the three results are between the *UWL* and the *UCL*, violates the second rule. Because the analysis is no longer under statistical control, we must stop using the glucometer until we determine the source of the problem.

USING CONTROL CHARTS FOR QUALITY ASSURANCE

Control charts play an important role in a performance-based program of quality assurance because they provide an easy to interpret picture of the statistical state of an analysis. Quality assessment samples such as blanks, standards, and spike recoveries are monitored with property control charts. A precision control chart is used to monitor duplicate samples.

The first step in using a control chart is to determine the mean value and the standard deviation (or range) for the property being measured while the analysis is under statistical control. These values are established using the same conditions that will be present during subsequent analyses. Preliminary data is collected both throughout the day and over several days to account for short-term and for long-term variability. An initial control chart is prepared using this preliminary data and discrepant points identified using the rules discussed in the previous section. After eliminating questionable points, the control chart is replotted. Once the control chart is in use, the original limits are adjusted if the number of new data points is at least equivalent to the amount of data used to construct the original control chart. For example, if the original control chart includes 15 points, new limits are calculated after collecting 15 additional points. The 30 points are pooled together to calculate the new limits. A second modification is made after collecting an additional 30 points. Another indication that a control chart needs to be modified is when points rarely exceed the warning limits. In this case the new limits are recalculated using the last 20 points.

Once a control chart is in use, new quality assessment data is added at a rate sufficient to ensure that the analysis remains in statistical control. As with prescriptive approaches to quality assurance, when the analysis falls out of statistical control, all samples analyzed since the last successful verification of statistical control are reanalyzed. The advantage of a performance-based approach to quality assurance is that a laboratory may use its experience, guided by control charts, to determine the frequency for collecting quality assessment samples. When the system is stable, quality assessment samples can be acquired less frequently.

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7.5: PROBLEMS

1. Make a list of good laboratory practices for the lab that accompanies this course, or another lab if this course does not have an associated laboratory. Explain the rationale for each item on your list.

2. Write directives outlining good measurement practices for (a) a buret, for (b) a pH meter, and for (c) a spectrophotometer.

3. A atomic absorption method for the analysis of lead in an industrial wastewater has a method detection limit of 10 ppb. The relationship between the absorbance and the concentration of lead, as determined from a calibration curve, is

$$A = 0.349 \times (\text{ppm Pb})$$

Analysis of a sample in duplicate gives absorbance values of 0.554 and 0.516. Is the precision between these two duplicates acceptable based on the limits in Table 15.3.1?

4. The following data were obtained for the duplicate analysis of a 5.00 ppm NO_3^- standard.

sample	X_1 (ppm)	X_2 (ppm)
1	5.02	4.90
2	5.10	5.18
3	5.07	4.95
4	4.96	5.01
5	4.88	4.98
6	5.04	4.97

Calculate the standard deviation for these duplicate samples. If the maximum limit for the relative standard deviation is 1.5%, are these results acceptable?

5. Gonzalez and colleagues developed a voltammetric method for the determination of *tert*-butylhydroxyanisole (BHA) in chewing gum [Gonzalez, A.; Ruiz, M. A.; Yanez-Sedeno, P.; Pingarron, J. M. *Anal. Chim. Acta* **1994**, *285*, 63–71.]. Analysis of a commercial chewing gum gave a result of 0.20 mg/g. To evaluate the accuracy of this results, the authors performed five spike recoveries, adding an amount of BHA equivalent to 0.135 mg/g to each sample. The experimentally determined concentrations of BHA in these samples were reported as 0.342, 0.340, 0.340, 0.324, and 0.322 mg/g. Determine the percent recovery for each sample and the mean percent recovery.

6. A sample is analyzed following the protocol shown in Figure 15.4.1 using a method with a detection limit of 0.05 ppm. The relationship between the analytical signal, S_{meas}, and the concentration of the analyte in parts per million, C_A, as determined from a calibration curve, is

$$S_{meas} = 0.273 \times C_A$$

Answer the following questions if the limit for a successful spike recovery is ±10%:

(a) A field blank is spiked with the analyte to a concentration of 2.00 ppm and returned to the lab. Analysis of the spiked field blank gives a signal of 0.573. Is the spike recovery for the field blank acceptable?

(b) The analysis of a spiked field blank is unacceptable. To determine the source of the problem, a spiked method blank is prepared by spiking distilled water with the analyte to a concentration of 2.00 ppm. Analysis of the spiked method blank gives a signal of 0.464. Is the source of the problem in the laboratory or in the field?

(c) The analysis for a spiked field sample, $B_{SF,}$ is unacceptable. To determine the source of the problem, the sample is spiked in the laboratory by adding sufficient analyte to increase the concentration by 2.00 ppm. Analysis of the sample before and after the spike gives signals of 0.456 for B and a signal of 1.03 for B_{SL}. Considering this data, what is the most likely source of the systematic error?

7. The following data were obtained for the repetitive analysis of a stable standard [*Standard Methods for the Analysis of Waters and Wastewaters*, American Public Health Association: Washington, D. C., 18th Ed., 1992. The data is from Table 1030:I].

sample	X_i (ppm)	sample	X_i (ppm)	sample	X_i (ppm)
1	35.1	10	35.0	18	36.4
2	33.2	11	31.4	19	32.1
3	33.7	12	35.6	20	38.2
4	35.9	13	30.2	21	33.1
5	33.5	14	32.7	22	34.9
6	34.5	15	31.1	23	36.2
7	34.4	16	34.8	24	34.0
8	34.3	17	34.3	25	33.8
9	31.8				

Construct a property control chart for these data and evaluate the state of statistical control.

8. The following data were obtained for the repetitive spike recoveries of field samples [*Standard Methods for the Analysis of Waters and Wastewaters*, American Public Health Association: Washington, D. C., 18th Ed., 1992. The data is from Table 1030:II].

sample	% recovery	sample	% recovery	sample	% recovery
1	94.6	10	104.6	18	104.6
2	93.1	11	123.8	19	91.5
3	100.0	12	93.8	20	83.1
4	122.3	13	80.0	21	100.8
5	120.8	14	99.2	22	123.1
6	93.1	15	101.5	23	96.2
7	117.7	16	74.6	24	96.9
8	96.2	17	108.5	25	102.3
9	73.8				

Construct a property control chart for these data and evaluate the state of statistical control.

9. The following data were obtained for the duplicate analysis of a stable standard [*Standard Methods for the Analysis of Waters and Wastewaters*, American Public Health Association: Washington, D. C., 18th Ed., 1992. The data is from Table 1030:I].

sample	X_1 (ppm)	X_2 (ppm)	sample	X_1 (ppm)	X_2 (ppm)
1	50	46	14	36	36
2	37	36	15	47	45
3	22	19	16	16	20
4	17	20	17	18	21
5	32	34	18	26	22
6	46	46	19	35	36
7	26	28	20	36	25
8	26	30	21	49	51
9	61	58	22	33	32
10	44	45	23	40	38
11	40	44	24	16	13
12	36	35	25	39	42
13	29	31			

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7.6: ADDITIONAL RESOURCES

The following experiments introduce aspects of quality assurance and quality control.

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- Cancilla, D. A. "Integration of Environmental Analytical Chemistry with Environmental Law: The Development of a Problem-Based Laboratory," *J. Chem. Educ.* **2001**, *78*, 1652–1660.
- Claycomb, G. D.; Venable, F. A. "Selection, Evaluation, and Modification of a Standard Operating Procedure as a Mechanism for Introducing an Undergraduate Student to Chemical Research: A Case Study," *J. Chem. Educ.* **2015**, *92*, 256–262.
- Laquer, F. C. "Quality Control Charts in the Quantitative Analysis Laboratory Using Conductance Measurement," *J. Chem. Educ.* **1990**, *67*, 900–902.
- Marcos, J.; Ríos, A.; Valcárcel, M. "Practicing Quality Control in a Bioanalytical Experiment," *J. Chem. Educ.* **1995**, *72*, 947–949.

The following texts and articles may be consulted for an additional discussion of quality assurance and quality control.

- Amore, F. "Good Analytical Practices," *Anal. Chem.* **1979**, *51*, 1105A–1110A.
- Anderson, J. E. T. "On the development of quality assurance," *TRAC-Trend. Anal. Chem.* **2014**, *60*, 16–24.
- Barnard, Jr. A. J.; Mitchell, R. M.; Wolf, G. E. "Good Analytical Practices in Quality Control," *Anal. Chem.* **1978**, *50*, 1079A–1086A.
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- Taylor, J. K. *Quality Assurance of Chemical Measurements*, Lewis Publishers: Chelsa, MI, 1987.
- Wedlich, R. C.; Libera, A. E.; Pires, A.; Therrien, M. T. "Good Laboratory Practice. Part 1. An Introduction," *J. Chem. Educ.* **2013**, *90*, 854–857.
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- Wedlich, R. C.; Libera, A. E.; Fazzino, L.; Fransen, J. M. "Good Laboratory Practice. Part 1. Imple- menting Good Laboratory Practice in the Analytical Lab," *J. Chem. Educ.* **2013**, *90*, 862–865.

Additional information about the construction and use of control charts may be found in the following sources.

- Miller, J. C.; Miller, J. N. Statistics for Analytical Chemistry, 2nd Ed., Ellis Horwood Limited: Chich-ester, 1988.
- Ouchi, G. I. "Creating Control Charts with a Spreadsheet Program," *LC•GC* **1993**, *11*, 416–423.
- Ouchi, G. I. "Creating Control Charts with a Spreadsheet Program," *LC•GC* **1997**, *15*, 336–344.
- Simpson, J. M. "Spreadsheet Statistics," *J. Chem. Educ.* **1994**, *71*, A88–A89.

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7.7: CHAPTER SUMMARY AND KEY TERMS

SUMMARY

Few analyses are so straightforward that high quality results are obtained with ease. Good analytical work requires careful planning and an attention to detail. Creating and maintaining a quality assurance program is one way to help ensure the quality of analytical results. Quality assurance programs usually include elements of quality control and quality assessment.

Quality control encompasses all activities used to bring a system into statistical control. The most important facet of quality control is written documentation, including statements of good laboratory practices, good measurement practices, standard operating procedures, and protocols for a specific purpose.

Quality assessment includes the statistical tools used to determine whether an analysis is in a state of statistical control, and, if possible, to suggest why an analysis has drifted out of statistical control. Among the tools included in quality assessment are the analysis of duplicate samples, the analysis of blanks, the analysis of standards, and the analysis of spike recoveries.

Another important quality assessment tool, which provides an ongoing evaluation of an analysis, is a control chart. A control chart plots a property, such as a spike recovery, as a function of time. Results that exceed warning and control limits, or unusual patterns of results indicate that an analysis is no longer under statistical control.

KEY TERMS

control chart
duplicate samples
field blank
good laboratory practices
good measurement practices
method blank
proficiency standard
protocol for a specific purpose
quality assessment
quality assurance program
quality control
reagent blank
spike recovery
standard operations procedure
statistical control
trip blank

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CHAPTER OVERVIEW

8: EQUILIBRIUM CHEMISTRY

Regardless of the problem on which an analytical chemist is working, its solution requires a knowledge of chemistry and the ability to apply that knowledge to solve a problem. For example, an analytical chemist who is studying the effect of pollution on spruce trees needs to know, or know where to find, the chemical differences between *p*-hydroxybenzoic acid and *p*-hydroxyacetophenone, two common phenols found in the needles of spruce trees.

The ability to "think as a chemist" is a product of your experience in the classroom and in the laboratory. For the most part, the material in this text assumes you are familiar with topics covered in earlier courses; however, because of its importance to analytical chemistry, this chapter provides a review of equilibrium chemistry. Much of the material in this chapter should be familiar to you, although some topics—ladder diagrams and activity, for example—likely afford you with new ways to look at equilibrium chemistry.

8.1: Reversible Reactions and Chemical Equilibria
8.2: Thermodynamics and Equilibrium Chemistry
8.3: Manipulating Equilibrium Constants
8.4: Equilibrium Constants for Chemical Reactions
8.5: Le Châtelier's Principle
8.6: Ladder Diagrams
8.7: Solving Equilibrium Problems
8.8: Activity Effects
8.9: Using Excel and R to Solve Equilibrium Problems
8.10: Some Final Thoughts on Equilibrium Calculations
8.11: Problems
8.12: Additional Resources
8.13: Chapter Summary and Key Terms

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8.1: REVERSIBLE REACTIONS AND CHEMICAL EQUILIBRIA

In 1798, the chemist Claude Berthollet accompanied Napoleon's military expedition to Egypt. While visiting the Natron Lakes, a series of salt water lakes carved from limestone, Berthollet made an observation that led him to an important discovery. When exploring the lake's shore, Berthollet found deposits of Na_2CO_3, a result he found surprising. Why did Berthollet find this result surprising and how did it contribute to an important discovery? Answering these questions provides us with an example of chemical reasoning and introduces us to the topic of this chapter.

> Napoleon's expedition to Egypt was the first to include a significant scientific presence. The Commission of Sciences and Arts, which included Claude Berthollet, began with 151 members, and operated in Egypt for three years. In addition to Berthollet's work, other results included a publication on mirages and a detailed catalogs of plant and animal life, mineralogy, and archeology. For a review of the Commission's contributions, see Gillispie, C. G. "Scientific Aspects of the French Egyptian Expedition, 1798-1801," *Proc. Am. Phil. Soc.* **1989**, *133*, 447–474.

At the end of the 18th century, chemical reactivity was explained in terms of elective affinities [Quilez, J. *Chem. Educ. Res. Pract.* **2004**, *5*, 69–87]. If, for example, substance A reacts with substance BC to form AB

$$\mathrm{A + BC \rightarrow AB + C}$$

then A and B were said to have an elective affinity for each other. With elective affinity as the driving force for chemical reactivity, reactions were understood to proceed to completion and to proceed in one direction. Once formed, the compound AB could not revert to A and BC.

$$\mathrm{A + BC \nrightarrow AB + C}$$

From his experience in the laboratory, Berthollet knew that adding solid Na_2CO_3 to a solution of $CaCl_2$ produces a precipitate of $CaCO_3$.

$$\mathrm{Na_2CO_3}(s) + \mathrm{CaCl_2}(aq) \rightarrow 2\mathrm{NaCl}(aq) + \mathrm{CaCO_3}(s)$$

Understanding this, Berthollet was surprised to find solid Na_2CO_3 forming on the edges of the lake, particularly since the deposits formed only when the lake's salt water, NaCl(*aq*), was in contact with solid limestone, $CaCO_3$(*s*). Where the lake was in contact with clay soils, there was little or no Na_2CO_3.

> Natron is another name for the mineral sodium carbonate, Na_2CO_3•$10H_2O$. In nature, it usually contains impurities of $NaHCO_3$ and NaCl. In ancient Egypt, natron was mined and used for a variety of purposes, including as a cleaning agent and in mummification.

Berthollet's important insight was recognizing that the chemistry leading to the formation of Na_2CO_3 is the reverse of that seen in the laboratory.

$$2\mathrm{NaCl}(aq) + \mathrm{CaCO_3}(s) \rightarrow \mathrm{Na_2CO_3}(s) + \mathrm{CaCl_2}(aq)$$

Using this insight Berthollet reasoned that the reaction is reversible, and that the relative amounts of NaCl, $CaCO_3$, Na_2CO_3, and $CaCl_2$ determine the direction in which the reaction occurs and the final composition of the reaction mixture. We recognize a reaction's ability to move in both directions by using a double arrow when we write the reaction.

$$\mathrm{Na_2CO_3}(s) + \mathrm{CaCl_2}(aq) \rightleftharpoons 2\mathrm{NaCl}(aq) + \mathrm{CaCO_3}(s)$$

> For obvious reasons, we call the double arrow, $\rightleftharpoons$, an equilibrium arrow.

Berthollet's reasoning that reactions are reversible was an important step in understanding chemical reactivity. When we mix together solutions of Na_2CO_3 and $CaCl_2$ they react to produce NaCl and $CaCO_3$. As the reaction takes place, if we monitor the mass of Ca^{2+} that remains in solution and the mass of $CaCO_3$ that precipitates, the result looks something like Figure 6.1.1 . At the start of the reaction the mass of Ca^{2+} decreases and the mass of $CaCO_3$ increases. Eventually the reaction reaches a point after which there is no further change in the amounts of these species. Such a condition is called a state of ***equilibrium***.

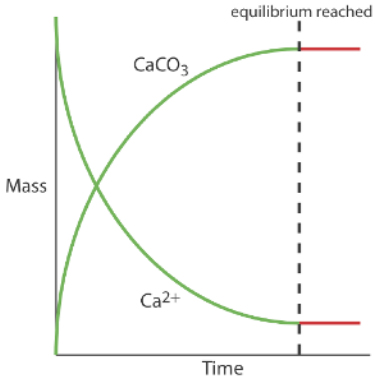


Figure 6.1.1 . Graph showing how the masses of Ca^{2+} and $CaCO_3$ change as a function of time during the precipitation of $CaCO_3$. The dashed line indicates when the reaction reaches equilibrium. Prior to equilibrium the masses of Ca^{2+} and $CaCO_3$ are changing; after equilibrium is reached, their masses remain constant.

Although a system at equilibrium appears static on a macroscopic level, it is important to remember that the forward and the reverse reactions continue to occur. A reaction at equilibrium exists in a ***steady-state***, in which the rate at which a species forms equals the rate at which it is consumed.

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8.2: THERMODYNAMICS AND EQUILIBRIUM CHEMISTRY

Thermodynamics is the study of thermal, electrical, chemical, and mechanical forms of energy. The study of thermodynamics crosses many disciplines, including physics, engineering, and chemistry. Of the various branches of thermodynamics, the most important to chemistry is the study of how energy changes during a chemical reaction.

Consider, for example, the general equilibrium reaction shown in Equation 8.2.1, which involves the species A, B, C, and D, with stoichiometric coefficients of *a*, *b*, *c*, and *d*.

$$aA + bB \rightleftharpoons cC + dD \tag{8.2.1}$$

By convention, we identify the species on the left side of the equilibrium arrow as reactants and those on the right side of the equilibrium arrow as products. As Berthollet discovered, writing a reaction in this fashion does not guarantee that the reaction of A and B to produce C and D is favorable. Depending on initial conditions the reaction may move to the left, it may move to the right, or it may exist in a state of equilibrium. Understanding the factors that determine the reaction's final equilibrium position is one of the goals of chemical thermodynamics.

The direction of a reaction is that which lowers the overall free energy. At a constant temperature and pressure, which is typical of many benchtop chemical reactions, a reaction's free energy is given by the ***Gibb's free energy*** function

$$\Delta G = \Delta H - T\Delta S \tag{8.2.2}$$

where T is the temperature in kelvin, and ΔG, ΔH, and ΔS are the differences in the Gibb's free energy, the enthalpy, and the entropy between the products and the reactants.

Enthalpy is a measure of the flow of energy, as heat, during a chemical reaction. A reaction that releases heat has a negative ΔH and is called exothermic. An endothermic reaction absorbs heat from its surroundings and has a positive ΔH. ***Entropy*** is a measure of energy that is unavailable for useful, chemical work. The entropy of an individual species is always positive and generally is larger for gases than for solids, and for more complex molecules than for simpler molecules. Reactions that produce a large number of simple, gaseous products usually have a positive ΔS.

> For many students, entropy is the most difficult topic in thermodynamics to understand. For a rich resource on entropy, visit the following web site: http://entropysite.oxy.edu/.

The sign of ΔG indicates the direction in which a reaction moves to reach its equilibrium position. A reaction is thermodynamically favorable when its enthalpy, ΔH, decreases and its entropy, ΔS, increases. Substituting the inequalities $\Delta H < 0$ and $\Delta S > 0$ into Equation 8.2.2 shows that a reaction is thermodynamically favorable when ΔG is negative. When ΔG is positive the reaction is unfavorable as written (although the reverse reaction is favorable). A reaction at equilibrium has a ΔG of zero.

> Equation 8.2.2 shows that the sign of ΔG depends on the signs of ΔH and of ΔS, and the temperature, T. The following table summarizes the possibilities.
>
ΔH	ΔS	ΔG
−	+	$\Delta G < 0$ at all temperatures
−	−	$\Delta G < 0$ at low temperatures only
+	+	$\Delta G < 0$ at high temperatures only
+	−	$\Delta G > 0$ at all temperatures
>
> Note that the what constitutes "low temperatures" or "high temperatures" depends on the reaction.

As a reaction moves from its initial, non-equilibrium condition to its equilibrium position, its value of ΔG approaches zero. At the same time, the chemical species in the reaction experience a change in their concentrations. The Gibb's free energy, therefore, must be a function of the concentrations of reactants and products.

As shown in Equation 8.2.3, we can divide the Gibb's free energy, ΔG, into two terms.

$$\triangle G = \Delta G^{\circ} + RT \ln Q_r \tag{8.2.3}$$

The first term, ΔG^{o}, is the change in the Gibb's free energy when each species in the reaction is in its ***standard state***, which we define as follows: gases with unit partial pressures, solutes with unit concentrations, and pure solids and pure liquids. The second term includes the reaction quotient, Q_r, which accounts for non-standard state pressures and concentrations. For reaction 8.2.1 the reaction quotient is

$$Q_r = \frac{[\mathrm{C}]^c[\mathrm{D}]^d}{[\mathrm{A}]^a[\mathrm{B}]^b} \tag{8.2.4}$$

where the terms in brackets are the concentrations of the reactants and products. Note that we define the reaction quotient with the products in the numerator and the reactants in the denominator. In addition, we raise the concentration of each species to a power equivalent to its stoichiometry in the balanced chemical reaction. For a gas, we use partial pressure in place of concentration. Pure solids and pure liquids do not appear in the reaction quotient.

> Although not shown here, each concentration term in Equation 8.2.4 is divided by the corresponding standard state concentration; thus, the term $[\mathrm{C}]^c$ really means
>
> $$\left\{\frac{[\mathrm{C}]}{[\mathrm{C}]^\circ}\right\}$$
>
> where $[\mathrm{C}]^o$ is the standard state concentration for C. There are two important consequences of this: (1) the value of Q is unitless; and (2) the ratio has a value of 1 for a pure solid or a pure liquid. This is the reason that pure solids and pure liquids do not appear in the reaction quotient.

At equilibrium the Gibb's free energy is zero, and Equation 8.2.3 simplifies to

$$\triangle G^\circ = -RT \ln K$$

where K is an ***equilibrium constant*** that defines the reaction's equilibrium position. The equilibrium constant is just the reaction quotient's numerical value when we substitute equilibrium concentrations into Equation 8.2.4.

$$K = \frac{[\mathrm{C}]^c_{\mathrm{eq}}[\mathrm{D}]^d_{\mathrm{eq}}}{[\mathrm{A}]^a_{\mathrm{eq}}[\mathrm{B}]^b_{\mathrm{eq}}} \tag{8.2.5}$$

Here we include the subscript "eq" to indicate a concentration at equilibrium. Although generally we will omit the "eq" when we write an equilibrium constant expressions, it is important to remember that the value of K is determined by equilibrium concentrations.

> As written, Equation 8.2.5 is a limiting law that applies only to infinitely dilute solutions where the chemical behavior of one species is unaffected by the presence of other species. Strictly speaking, Equation 8.2.5 is written in terms of activities instead of concentrations. We will return to this point in Chapter 6.9. For now, we will stick with concentrations as this convention already is familiar to you.

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8.3: MANIPULATING EQUILIBRIUM CONSTANTS

We will take advantage of two useful relationships when we work with equilibrium constants. First, if we reverse a reaction's direction, the equilibrium constant for the new reaction is the inverse of that for the original reaction. For example, the equilibrium constant for the reaction

$$\mathrm{A} + 2\mathrm{B} \rightleftharpoons \mathrm{AB_2} \qquad K_1 = \frac{[\mathrm{AB_2}]}{[\mathrm{A}][\mathrm{B}]^2}$$

is the inverse of that for the reaction

$$\mathrm{AB_2} \rightleftharpoons \mathrm{A} + 2\mathrm{B} \qquad K_2 = (K_1)^{-1} = \frac{[\mathrm{A}][\mathrm{B}]^2}{[\mathrm{AB_2}]}$$

Second, if we add together two reactions to form a new reaction, the equilibrium constant for the new reaction is the product of the equilibrium constants for the original reactions.

$$A + C \rightleftharpoons AC \qquad K_3 = \frac{[AC]}{[A][C]}$$

$$\mathrm{AC} + \mathrm{C} \rightleftharpoons \mathrm{AC_2} \qquad K_4 = \frac{[\mathrm{AC_2}]}{[\mathrm{AC}][\mathrm{C}]}$$

$$\mathrm{A} + 2\mathrm{C} \rightleftharpoons \mathrm{AC_2} \qquad K_5 = K_3 \times K_4 = \frac{[\mathrm{AC}]}{[\mathrm{A}][\mathrm{C}]} \times \frac{[\mathrm{AC_2}]}{[\mathrm{AC}][\mathrm{C}]} = \frac{[\mathrm{AC_2}]}{[\mathrm{A}][\mathrm{C}]^2}$$

EXAMPLE 6.3.1

Calculate the equilibrium constant for the reaction

$$2\mathrm{A} + \mathrm{B} \rightleftharpoons \mathrm{C} + 3\mathrm{D}$$

given the following information

$$\begin{aligned} &\mathrm{Rxn\ 1}: A + B \rightleftharpoons D && K_1 = 0.40 \\ &\mathrm{Rxn\ 2}: A + E \rightleftharpoons C + D + F && K_2 = 0.10 \\ &\mathrm{Rxn\ 3}: C + E \rightleftharpoons B && K_3 = 2.0 \\ &\mathrm{Rxn\ 4}: F + C \rightleftharpoons D + B && K_4 = 5.0 \end{aligned}$$

Solution

The overall reaction is equivalent to

$$\mathrm{Rxn\ 1} + \mathrm{Rxn\ 2} - \mathrm{Rxn\ 3} + \mathrm{Rxn\ 4}$$

Subtracting a reaction is equivalent to adding the reverse reaction; thus, the overall equilibrium constant is

$$K = \frac{K_1 \times K_2 \times K_4}{K_3} = \frac{0.40 \times 0.10 \times 5.0}{2.0} = 0.10$$

EXERCISE 6.3.1

Calculate the equilibrium constant for the reaction

$$C + D + F \rightleftharpoons 2A + 3B$$

using the equilibrium constants from Example 6.3.1 .

Answer

The overall reaction is equivalent to

$$\mathrm{Rxn\ 4} - 2 \times \mathrm{Rxn\ 1}$$

Subtracting a reaction is equivalent to adding the reverse reaction; thus, the overall equilibrium constant is

$$K = \frac{K_4}{(K_1)^2} = \frac{(5.0)}{(0.40)^2} = 31.25 \approx 31$$

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8.4: EQUILIBRIUM CONSTANTS FOR CHEMICAL REACTIONS

Several types of chemical reactions are important in analytical chemistry, either in preparing a sample for analysis or during the analysis. The most significant of these are precipitation reactions, acid–base reactions, complexation reactions, and oxidation–reduction reactions. In this section we review these reactions and their equilibrium constant expressions.

> Another common name for an oxidation–reduction reaction is a redox reaction, where "red" is short for reduction and "ox" is short for oxidation.

PRECIPITATION REACTIONS

In a precipitation reaction, two or more soluble species combine to form an insoluble ***precipitate***. The most common precipitation reaction is a metathesis reaction in which two soluble ionic compounds exchange parts. For example, if we add a solution of lead nitrate, $Pb(NO_3)_2$, to a solution of potassium chloride, KCl, a precipitate of lead chloride, $PbCl_2$, forms. We usually write a precipitation reaction as a net ionic equation, which shows only the precipitate and those ions that form the precipitate; thus, the precipitation reaction for $PbCl_2$ is

$$Pb^{2+}(aq) + 2Cl^-(aq) \rightleftharpoons PbCl_2(s)$$

When we write the equilibrium constant for a precipitation reaction, we focus on the precipitate's solubility; thus, for $PbCl_2$, the solubility reaction is

$$PbCl_2(s) \rightleftharpoons Pb^{2+}(aq) + 2Cl^-(aq)$$

and its equilibrium constant, or ***solubility product***, K_{sp}, is

$$K_{sp} = \left[Pb^{2+}\right]\left[Cl^-\right]^2 \tag{8.4.1}$$

Even though it does not appear in the K_{sp} expression, it is important to remember that Equation 8.4.1 is valid only if $PbCl_2(s)$ is present and in equilibrium with Pb^{2+} and Cl^-. You will find values for selected solubility products in Appendix 10.

ACID–BASE REACTIONS

A useful definition of acids and bases is that independently introduced in 1923 by Johannes Brønsted and Thomas Lowry. In the Brønsted-Lowry definition, an ***acid*** is a proton donor and a ***base*** is a proton acceptor. Note the connection between these definitions—defining a base as a proton acceptor implies there is an acid available to donate the proton. For example, in reaction 8.4.2 acetic acid, CH_3COOH, donates a proton to ammonia, NH_3, which serves as the base.

$$CH_3COOH(aq) + NH_3(aq) \rightleftharpoons NH_4^+(aq) + CH_3COO^-(aq) \tag{8.4.2}$$

When an acid and a base react, the products are a new acid and a new base. For example, the acetate ion, CH_3COO^-, in reaction 8.4.2 is a base that can accept a proton from the acidic ammonium ion, NH_4^+, forming acetic acid and ammonia. We call the acetate ion the conjugate base of acetic acid, and we call the ammonium ion the conjugate acid of ammonia.

STRONG AND WEAK ACIDS

The reaction of an acid with its solvent (typically water) is an acid dissociation reaction. We divide acids into two categories—strong and weak—based on their ability to donate a proton to the solvent. A strong acid, such as HCl, almost completely transfers its proton to the solvent, which acts as the base.

$$HCl(aq) + H_2O(l) \rightarrow H_3O^+(aq) + Cl^-(aq)$$

We use a single arrow ($\rightarrow$) in place of the equilibrium arrow ($\rightleftharpoons$) because we treat HCl as if it dissociates completely in an aqueous solution. In water, the common strong acids are hydrochloric acid (HCl), hydroiodic acid (HI), hydrobromic acid (HBr), nitric acid (HNO_3), perchloric acid ($HClO_4$), and the first proton of sulfuric acid (H_2SO_4).

> The strength of an acid is a function of the acid and the solvent. For example, HCl does not act as a strong acid in methanol. In this case we use the equilibrium arrow when writing the acid–base reaction.
>
> $$HCl + CH_3OH \rightleftharpoons CH_3OH_2^+ + Cl^-$$

A weak acid, of which aqueous acetic acid is one example, does not completely donate its acidic proton to the solvent. Instead, most of the acid remains undissociated with only a small fraction present as the conjugate base.

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq)$$

The equilibrium constant for this reaction is an ***acid dissociation constant***, K_a, which we write as

$$K_a = \frac{\left[CH_3COO^-\right]\left[H_3O^+\right]}{\left[CH_3COOH\right]} = 1.75 \times 10^{-5}$$

The magnitude of K provides information about a weak acid's relative strength, with a smaller K_a corresponding to a weaker acid. The ammonium ion, NH_4^+, for example, has a K_a of 5.702×10^{-10} and is a weaker acid than acetic acid.

> Earlier we noted that we omit pure solids and pure liquids from equilibrium constant expressions. Because the solvent, H_2O, is not pure, you might wonder why we have not included it in acetic acid's K_a expression. Recall that we divide each term in an equilibrium constant expression by its standard state value. Because the concentration of H_2O is so large—it is approximately 55.5 mol/L—its concentration as a pure liquid and as a solvent are virtually identical. The ratio
>
> $$\frac{[H_2O]}{[H_2O]^\circ}$$
>
> is essentially 1.00.

A ***monoprotic*** weak acid, such as acetic acid, has only a single acidic proton and a single acid dissociation constant. Other acids, such as phosphoric acid, have multiple acidic protons, each characterized by an acid dissociation constant. We call such acids ***polyprotic***. Phosphoric acid, for example, has three acid dissociation reactions and three acid dissociation constants.

$$H_3PO_4(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + H_2PO_4^-(aq)$$

$$K_{a1} = \frac{\left[H_2PO_4^-\right]\left[H_3O^+\right]}{\left[H_3PO_4\right]} = 7.11 \times 10^{-3}$$

$$H_2PO_4^-(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + HPO_4^{2-}(aq)$$

$$K_{a2} = \frac{\left[HPO_4^{2-}\right]\left[H_3O^+\right]}{\left[H_2PO_4^-\right]} = 6.32 \times 10^{-8}$$

$$HPO_4^{2-}(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + PO_4^{3-}(aq)$$

$$K_{a3} = \frac{\left[PO_4^{3-}\right]\left[H_3O^+\right]}{\left[HPO_4^{2-}\right]} = 4.5 \times 10^{-13}$$

The decrease in the acid dissociation constants from K_{a1} to K_{a3} tells us that each successive proton is harder to remove. Consequently, H_3PO_4 is a stronger acid than $H_2PO_4^-$, and $H_2PO_4^-$ is a stronger acid than HPO_4^{2-}.

STRONG AND WEAK BASES

The most common example of a strong base is an alkali metal hydroxide, such as sodium hydroxide, NaOH, which completely dissociates to produce hydroxide ion.

$$NaOH(s) \rightarrow Na^+(aq) + OH^-(aq)$$

A weak base, such as the acetate ion, CH_3COO^-, only partially accepts a proton from the solvent, and is characterized by a ***base dissociation constant***, K_b. For example, the base dissociation reaction and the base dissociation constant for the acetate ion are

$$CH_3COO^-(aq) + H_2O(l) \rightleftharpoons OH^-(aq) + CH_3COOH(aq)$$

$$K_b = \frac{\left[CH_3COOH\right]\left[OH^-\right]}{\left[CH_3COO^-\right]} = 5.71 \times 10^{-10}$$

A polyprotic weak base, like a polyprotic acid, has more than one base dissociation reaction and more than one base dissociation constant.

AMPHIPROTIC SPECIES

Some species can behave as either a weak acid or as a weak base. For example, the following two reactions show the chemical reactivity of the bicarbonate ion, HCO_3^-, in water.

$$HCO_3^-(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CO_3^{2-}(aq) \tag{8.4.3}$$

$$HCO_3^-(aq) + H_2O(l) \rightleftharpoons OH^-(aq) + H_2CO_3(aq) \tag{8.4.4}$$

A species that is both a proton donor and a proton acceptor is called ***amphiprotic***. Whether an amphiprotic species behaves as an acid or as a base depends on the equilibrium constants for the competing reactions. For bicarbonate, the acid dissociation constant for reaction 8.4.3

$$K_{a2} = \frac{\left[CO_3^{2-}\right]\left[H_3O^+\right]}{\left[HCO_3^-\right]} = 4.69 \times 10^{-11}$$

is smaller than the base dissociation constant for reaction 8.4.4.

$$K_{b2} = \frac{\left[H_2CO_3\right]\left[OH^-\right]}{\left[HCO_3^-\right]} = 2.25 \times 10^{-8}$$

Because bicarbonate is a stronger base than it is an acid, we expect that an aqueous solution of HCO_3^- is basic.

DISSOCIATION OF WATER

Water is an amphiprotic solvent because it can serve as an acid or as a base. An interesting feature of an amphiprotic solvent is that it is capable of reacting with itself in an acid–base reaction.

$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq) \tag{8.4.5}$$

We identify the equilibrium constant for this reaction as water's dissociation constant, K_w,

$$K_w = \left[H_3O^+\right]\left[OH^-\right] = 1.00 \times 10^{-14} \tag{8.4.6}$$

at a temperature of 24°C. The value of K_w varies substantially with temperature. For example, at 20°C K_w is 6.809×10^{-15}, while at 30°C K_w is 1.469×10^{-14}. At 25°C, K_w is 1.008×10^{-14}, which is sufficiently close to 1.00×10^{-14} that we can use the latter value with negligible error.

An important consequence of Equation 8.4.6 is that the concentration of H_3O^+ and the concentration of OH^- are related. If we know $[H_3O^+]$ for a solution, then we can calculate $[OH^-]$ using Equation 8.4.6.

EXAMPLE 6.4.1

What is the $[OH^-]$ if the $[H_3O^+]$ is 6.12×10^{-5} M?

Solution

$$\left[OH^-\right] = \frac{K_w}{\left[H_3O^+\right]} = \frac{1.00 \times 10^{-14}}{6.12 \times 10^{-5}} = 1.63 \times 10^{-10}$$

THE PH SCALE

Equation 8.4.6 allows us to develop a ***pH scale*** ($pH = -\log[H_3O^+]$) that indicates a solution's acidity. When the concentrations of H_3O^+ and OH^- are equal a solution is neither acidic nor basic; that is, the solution is neutral. Letting

$$\left[H_3O^+\right] = \left[OH^-\right]$$

substituting into Equation 8.4.6

$$K_w = \left[H_3O^+\right]^2 = 1.00 \times 10^{-14}$$

and solving for $[H_3O^+]$ gives

$$\left[H_3O^+\right] = \sqrt{1.00 \times 10^{-14}} = 1.00 \times 10^{-7}$$

A neutral solution of water at 25°C has a hydronium ion concentration of 1.00×10^{-7} M and a pH of 7.00. In an acidic solution the concentration of H_3O^+ is greater than that for OH^-, which means that

$$\left[H_3O^+\right] > 1.00 \times 10^{-7}\text{M}$$

The pH of an acidic solution, therefore, is less than 7.00. A basic solution, on the other hand, has a pH greater than 7.00. Figure 6.4.1 shows the pH scale and pH values for some representative solutions.

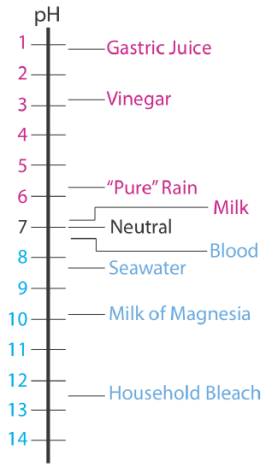


Figure 6.4.1 . Scale showing the pH value for representative solutions. Milk of Magnesia is a saturated solution of $Mg(OH)_2$.

TABULATING VALUES FOR K_A AND K_B

A useful observation about weak acids and weak bases is that the strength of a weak base is inversely proportional to the strength of its conjugate weak acid. Consider, for example, the dissociation reactions of acetic acid and acetate.

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq) \tag{8.4.7}$$

$$CH_3COO^-(aq) + H_2O(l) \rightleftharpoons OH^-(aq) + CH_3COOH(aq) \tag{8.4.8}$$

Adding together these two reactions gives the reaction

$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq)$$

for which the equilibrium constant is K_w. Because adding together two reactions is equivalent to multiplying their respective equilibrium constants, we may express K_w as the product of K_a for CH3COOH and K_b for $CH3COO^-$.

$$K_w = K_{a,CH_3COOH} \times K_{b,CH_3COO^-}$$

For any weak acid, HA, and its conjugate weak base, A^-, we can generalize this to the following equation

$$K_w = K_{a,HA} \times K_{b,A^-} \tag{8.4.9}$$

where HA and A^- are a conjugate acid–base pair. The relationship between K_a and K_b for a conjugate acid–base pair simplifies our tabulation of acid and base dissociation constants. Appendix 11 includes acid dissociation constants for a variety of weak acids. To find the value of K_b for a weak base, use Equation 8.4.9 and the K_a value for its corresponding weak acid.

A common mistake when using Equation 8.4.9 is to forget that it applies to a conjugate acid–base pair only.

EXAMPLE 6.4.2

Using Appendix 11, calculate values for the following equilibrium constants.

a. K_b for pyridine, C_5H_5N
b. K_b for dihydrogen phosphate, $H_2PO_4^-$

Solution

$$\text{(a) } K_{b,C_5H_5N} = \frac{K_w}{K_{a,C_5H_5NH^+}} = \frac{1.00 \times 10^{-14}}{5.90 \times 10^{-6}} = 1.69 \times 10^{-9}$$

$$\text{(b) } K_{b,H_2PO_4^-} = \frac{K_w}{K_{a,H_3PO_4}} = \frac{1.00 \times 10^{-14}}{7.11 \times 10^{-3}} = 1.41 \times 10^{-12}$$

When finding the K_b value for a polyprotic weak base, be careful to choose the correct K_a value. Remember that Equation 8.4.9 applies to a conjugate acid–base pair only. The conjugate acid of $H_2PO_4^-$ is H_3PO_4, not HPO_4^{2-}.

EXERCISE 6.4.1

Using Appendix 11, calculate K_b values for hydrogen oxalate, $HC_2O_4^-$, and for oxalate, $C_2O_4^{2-}$.

Answer

The K_b for hydrogen oxalate is

$$K_{b,HC_2O_4^-} = \frac{K_w}{K_{a,H_2C_2O_4}} = \frac{1.00 \times 10^{-14}}{5.60 \times 10^{-2}} = 1.79 \times 10^{-13}$$

and the K_b for oxalate is

$$K_{b,C_2O_4^{2-}} = \frac{K_w}{K_{a,HC_2O_4^-}} = \frac{1.00 \times 10^{-14}}{5.42 \times 10^{-5}} = 1.85 \times 10^{-10}$$

As we expect, the K_b value for $C_2O_4^{2-}$ is larger than that for $HC_2O_4^-$.

COMPLEXATION REACTIONS

A more general definition of acids and bases was proposed in 1923 by G. N. Lewis. The Brønsted-Lowry definition of acids and bases focuses on an acid's proton-donating ability and a base's proton-accepting ability. Lewis theory, on the other hand, uses the breaking and the forming of covalent bonds to describe acids and bases. In this treatment, an acid is an electron pair acceptor and a base in an electron pair donor. Although we can apply Lewis theory to the treatment of acid–base reactions, it is more useful for treating complexation reactions between metal ions and ligands.

The following reaction between the metal ion Cd^{2+} and the ***ligand*** NH_3 is typical of a complexation reaction.

$$Cd^{2+}(aq) + 4:NH_3(aq) \rightleftharpoons Cd(:NH_3)_4^{2+}(aq) \tag{8.4.10}$$

The product of this reaction is a ***metal–ligand complex***. In writing this reaction we show ammonia as $:NH_3$, using a pair of dots to emphasize the pair of electrons that it donates to Cd^{2+}. In subsequent reactions we will omit this notation.

METAL-LIGAND FORMATION CONSTANTS

We characterize the formation of a metal–ligand complex by a ***formation constant***, K_f. For example, the complexation reaction between Cd^{2+} and NH_3, reaction 8.4.10, has the following equilibrium constant.

$$K_f = \frac{\left[Cd(NH_3)_4^{2+}\right]}{\left[Cd^{2+}\right]\left[NH_3\right]^4} = 5.5 \times 10^7 \tag{8.4.11}$$

The reverse of reaction 8.4.10 is a dissociation reaction, which we characterize by a ***dissociation constant***, K_d, that is the reciprocal of K_f.

Many complexation reactions occur in a stepwise fashion. For example, the reaction between Cd^{2+} and NH_3 involves four successive reactions.

$$Cd^{2+}(aq) + NH_3(aq) \rightleftharpoons Cd(NH_3)^{2+}(aq) \tag{8.4.12}$$

$$Cd(NH_3)^{2+}(aq) + NH_3(aq) \rightleftharpoons Cd(NH_3)_2^{2+}(aq) \tag{8.4.13}$$

$$Cd(NH_3)_2^{2+}(aq) + NH_3(aq) \rightleftharpoons Cd(NH_3)_3^{2+}(aq) \tag{8.4.14}$$

$$Cd(NH_3)_3^{2+}(aq) + NH_3(aq) \rightleftharpoons Cd(NH_3)_4^{2+}(aq) \tag{8.4.15}$$

To avoid ambiguity, we divide formation constants into two categories. A ***stepwise formation constant***, which we designate as K_i for the ith step, describes the successive addition of one ligand to the metal–ligand complex from the previous step. Thus, the equilibrium constants for reactions 8.4.12–8.4.15 are, respectively, K_1, K_2, K_3, and K_4. An overall, or ***cumulative formation constant***, which we designate as β_i, describes the addition of i ligands to the free metal ion. The equilibrium constant in Equation 8.4.11 is correctly identified as β_4, where

$$\beta_4 = K_1 \times K_2 \times K_3 \times K_4$$

In general

$$\beta_n = K_1 \times K_2 \times \cdots \times K_n = \prod_{i=1}^{n} K_i$$

Stepwise and overall formation constants for selected metal–ligand complexes are in Appendix 12.

METAL-LIGAND COMPLEXATION AND SOLUBILITY

A formation constant describes the addition of one or more ligands to a free metal ion. To find the equilibrium constant for a complexation reaction that includes a solid, we combine appropriate K_{sp} and K_f expressions. For example, the solubility of AgCl increases in the presence of excess chloride ions as the result of the following complexation reaction.

$$\mathrm{AgCl}(s) + \mathrm{Cl}^-(aq) \rightleftharpoons \mathrm{Ag(Cl)}_2^-(aq) \tag{8.4.16}$$

We can write this reaction as the sum of three other equilibrium reactions with known equilibrium constants—the solubility of AgCl, which is described by its K_{sp} reaction

$$\mathrm{AgCl}(s) \rightleftharpoons \mathrm{Ag}^+(aq) + \mathrm{Cl}^-(aq)$$

and the stepwise formation of AgCl_2^-, which is described by $K_1$and K_2 reactions.

$$\mathrm{Ag}^+(aq) + \mathrm{Cl}^-(aq) \rightleftharpoons \mathrm{AgCl}(aq)$$

$$\mathrm{AgCl}(aq) + \mathrm{Cl}^-(aq) \rightleftharpoons \mathrm{AgCl}_2^-(aq)$$

The equilibrium constant for reaction 8.4.16, therefore, is $K_{sp} \times K_1 \times K_2$.

EXAMPLE 6.4.3

Determine the value of the equilibrium constant for the reaction

$$\mathrm{PbCl_2}(s) \rightleftharpoons \mathrm{PbCl_2}(aq)$$

Solution

We can write this reaction as the sum of three other reactions. The first of these reactions is the solubility of $PbCl_2$*(s)*, which is described by its K_{sp} reaction.

$$\mathrm{PbCl_2}(s) \rightleftharpoons \mathrm{Pb}^{2+}(aq) + 2\mathrm{Cl}^-(aq)$$

The remaining two reactions are the stepwise formation of $PbCl_2$*(aq)*, which are described by K_1 and K_2.

$$\mathrm{Pb}^{2+}(aq) + \mathrm{Cl}^-(aq) \rightleftharpoons \mathrm{PbCl}^+(aq)$$

$$\mathrm{PbCl}^+(aq) + \mathrm{Cl}^-(aq) \rightleftharpoons \mathrm{PbCl_2}(aq)$$

Using values for K_{sp}, K_1, and K_2 from Appendix 10 and Appendix 12, we find that the equilibrium constant is

$$K = K_{sp} \times K_1 \times K_2 = \left(1.7 \times 10^{-5}\right) \times 38.9 \times 1.62 = 1.1 \times 10^{-3}$$

EXERCISE 6.4.2

What is the equilibrium constant for the following reaction? You will find appropriate equilibrium constants in Appendix 10 and Appendix 12.

$$\mathrm{AgBr}(s) + 2\mathrm{S_2O_3^{2-}}(aq) \rightleftharpoons \mathrm{Ag\,(S_2O_3)_2^{3-}}(aq) + \mathrm{Br}^-(aq)$$

Answer

We can write the reaction as a sum of three other reactions. The first reaction is the solubility of AgBr(s), which we characterize by its K_{sp}.

$$\mathrm{AgBr}(s) \rightleftharpoons \mathrm{Ag}^+(aq) + \mathrm{Br}^-(aq)$$

The remaining two reactions are the stepwise formation of $\mathrm{Ag(S_2O_3)_2^{3-}}$, which we characterize by K_1 and K_2.

$$\mathrm{Ag}^+(aq) + \mathrm{S_2O_3^{2-}}(aq) \rightleftharpoons \mathrm{Ag\,(S_2O_3)^-}(aq)$$

$$\mathrm{Ag\,(S_2O_3)^-}(aq) + \mathrm{S_2O_3^{2-}}(aq) \rightleftharpoons \mathrm{Ag\,(S_2O_3)_2^{3-}}(aq)$$

Using values for K_{sp}, K_1, and K_2 from Appendix 10 and Appendix 12, we find that the equilibrium constant for our reaction is

$$K = K_{sp} \times K_1 \times K_2 = \left(5.0 \times 10^{-13}\right)\left(6.6 \times 10^{8}\right)\left(7.1 \times 10^{4}\right) = 23$$

OXIDATION–REDUCTION (REDOX) REACTIONS

An oxidation–reduction reaction occurs when electrons move from one reactant to another reactant. As a result of this transfer of electrons, the reactants undergo a change in oxidation state. Those reactant that increases its oxidation state undergoes ***oxidation***, and the reactant that decreases its oxidation state undergoes ***reduction***. For example, in the following redox reaction between Fe^{3+} and oxalic acid, $H_2C_2O_4$, iron is reduced because its oxidation state changes from +3 to +2.

$$2Fe^{3+}(aq) + H_2C_2O_4(aq) + 2H_2O(l) \rightleftharpoons 2Fe^{2+}(aq) + 2CO_2(g) + 2H_3O^+(aq) \tag{8.4.17}$$

Oxalic acid, on the other hand, is oxidized because the oxidation state for carbon increases from +3 in $H_2C_2O_4$ to +4 in CO_2.

We can divide a redox reaction, such as reaction 8.4.17, into separate ***half-reactions*** that show the oxidation and the reduction processes.

$$H_2C_2O_4(aq) + 2H_2O(l) \rightleftharpoons 2CO_2(g) + 2H_3O^+(aq) + 2e^-$$

$$Fe^{3+}(aq) + e^- \rightleftharpoons Fe^{2+}(aq)$$

It is important to remember, however, that an oxidation reaction and a reduction reaction always occur as a pair. We formalize this relationship by identifying as a ***reducing agent*** the reactant that is oxidized, because it provides the electrons for the reduction half-reaction. Conversely, the reactant that is reduced is an ***oxidizing agent***. In reaction 8.4.17, Fe^{3+} is the oxidizing agent and $H_2C_2O_4$ is the reducing agent.

The products of a redox reaction also have redox properties. For example, the Fe^{2+} in reaction 8.4.17 is oxidized to Fe^{3+} when CO_2 is reduced to $H_2C_2O_4$. Borrowing some terminology from acid–base chemistry, Fe^{2+} is the conjugate reducing agent of the oxidizing agent Fe^{3+}, and CO_2 is the conjugate oxidizing agent of the reducing agent $H_2C_2O_4$.

THERMODYNAMICS OF REDOX REACTIONS

Unlike precipitation reactions, acid–base reactions, and complexation reactions, we rarely express the equilibrium position of a redox reaction with an equilibrium constant. Because a redox reaction involves a transfer of electrons from a reducing agent to an oxidizing agent, it is convenient to consider the reaction's thermodynamics in terms of the electron.

For a reaction in which one mole of a reactant undergoes oxidation or reduction, the net transfer of charge, *Q*, in coulombs is

$$Q = nF$$

where *n* is the moles of electrons per mole of reactant, and *F* is Faraday's constant (96485 C/mol). The free energy, Δ*G*, to move this charge, *Q*, over a change in ***potential***, *E*, is

$$\triangle G = EQ$$

The change in free energy (in kJ/mole) for a redox reaction, therefore, is

$$\Delta G = -nFE \tag{8.4.18}$$

where Δ*G* has units of kJ/mol. The minus sign in Equation 8.4.18 is the result of a different convention for assigning a reaction's favorable direction. In thermodynamics, a reaction is favored when Δ*G* is negative, but an oxidation-reduction reaction is favored when *E* is positive. Substituting Equation 8.4.18 into equation 6.2.3

$$-nFE = -nFE^\circ + RT \ln Q_r$$

and dividing by –*nF*, leads to the well-known ***Nernst equation***

$$E = E^\circ - \frac{RT}{nF} \ln Q_r$$

where E^o is the potential under standard-state conditions. Substituting appropriate values for *R* and *F*, assuming a temperature of 25 °C (298 K), and switching from *ln* to *log* gives the potential in volts as

$$E = E^o - \frac{0.05916}{n} \log Q_r \tag{8.4.19}$$

STANDARD POTENTIALS

A redox reaction's ***standard potential***, E^o, provides an alternative way of expressing its equilibrium constant and, therefore, its equilibrium position. Because a reaction at equilibrium has a Δ*G* of zero, the potential, *E*, also is zero at equilibrium. Substituting these values into Equation 8.4.19 and rearranging provides a relationship between E^o and *K*

$$E^\circ = \frac{0.05916}{n} \log K \tag{8.4.20}$$

A standard potential is the potential when all species are in their standard states. You may recall that we define standard state conditions as follows: all gases have unit partial pressures, all solutes have unit concentrations, and all solids and liquids are pure.

We generally do not tabulate standard potentials for redox reactions. Instead, we calculate E^o using the standard potentials for the corresponding oxidation half-reaction and reduction half-reaction. By convention, standard potentials are provided for reduction half-reactions. The standard potential for a redox reaction, E^o, is

$$E^\circ = E^\circ_{red} - E^\circ_{ox}$$

where E°_{red} and E°_{ox} are the standard reduction potentials for the reduction half-reaction and the oxidation half-reaction.

Because we cannot measure the potential for a single half-reaction, we arbitrarily assign a standard reduction potential of zero to a reference half-reaction

$$2H_3O^+(aq) + 2e^- \rightleftharpoons 2H_2O(l) + H_2(g)$$

and report all other reduction potentials relative to this reference. Appendix 13 contains a list of selected standard reduction potentials. The more positive the standard reduction potential, the more favorable the reduction reaction is under standard state conditions. For example, under standard state conditions the reduction of Cu^{2+} to Cu (E^o = +0.3419 V) is more favorable than the reduction of Zn^{2+} to Zn (E^o = –0.7618 V).

EXAMPLE 6.4.4

Calculate (a) the standard potential, (b) the equilibrium constant, and (c) the potential when $[Ag^+]$ = 0.020 M and $[Cd^{2+}]$ = 0.050 M, for the following reaction at 25°C.

$$Cd(s) + 2Ag^+(aq) \rightleftharpoons 2Ag(s) + Cd^{2+}(aq)$$

Solution

(a) In this reaction Cd is oxidized and Ag^+ is reduced. The standard cell potential, therefore, is

$$E^\circ = E^\circ_{Ag^+/Ag} - E^\circ_{Cd^{2+}/Cd} = 0.7996 - (-0.4030) = 1.2026 \text{ V}$$

(b) To calculate the equilibrium constant we substitute appropriate values into Equation 8.4.20.

$$E^\circ = 1.2026 \text{ V} = \frac{0.05916 \text{ V}}{2} \log K$$

Solving for K gives the equilibrium constant as

$$\log K = 40.6558$$
$$K = 4.527 \times 10^{40}$$

(c) To calculate the potential when $[Ag^+]$ is 0.020 M and $[Cd^{2+}]$ is 0.050M, we use the appropriate relationship for the reaction quotient, Q_r, in Equation 8.4.19.

$$E = E^\circ - \frac{0.05916 \text{ V}}{n} \log \frac{[Cd^{2+}]}{[Ag^+]^2}$$
$$E = 1.2026 \text{ V} - \frac{0.05916 \text{ V}}{2} \log \frac{0.050}{(0.020)^2} = 1.14 \text{ V}$$

EXERCISE 6.4.3

For the following reaction at 25°C

$$5Fe^{2+}(aq) + MnO_4^-(aq) + 8H^+(aq) \rightleftharpoons 5Fe^{3+}(aq) + Mn^{2+}(aq) + 4H_2O(l)$$

calculate (a) the standard potential, (b) the equilibrium constant, and (c) the potential under these conditions: $[Fe^{2+}]$ = 0.50 M, $[Fe^{3+}]$ = 0.10 M, $[MnO_4^-]$ = 0.025 M, $[Mn^{2+}]$ = 0.015 M, and a pH of 7.00. See Appendix 13 for standard state reduction potentials.

Answer

The two half-reactions are the oxidation of Fe^{2+} and the reduction of MnO_4^-.

$$Fe^{2+}(aq) \rightleftharpoons Fe^{3+}(aq) + e^-$$

$$MnO_4^-(aq) + 8H^+(aq) + 5e^- \rightleftharpoons Mn^{2+}(aq) + 4H_2O(l)$$

From Appendix 13, the standard state reduction potentials for these half-reactions are

$$E^\circ_{Fe^{3+}/Fe^{2+}} = 0.771 \text{ V and } E^\circ_{MnO_4^-/Mn^{2+}} = 1.51 \text{ V}$$

(a) The standard state potential for the reaction is

$$E^\circ = E^\circ_{MnO_4^-/Mn^{2+}} - E^\circ_{Fe^{3+}/Fe^{2+}} = 1.51 \text{ V} - 0.771 \text{ V} = 0.74 \text{ V}$$

(b) To calculate the equilibrium constant we substitute appropriate values into Equation 8.4.20.

$$E^\circ = 0.74 \text{ V} = \frac{0.05916}{5} \log K$$

Solving for *K* gives its value as 3.5×10^{62}.

(c) To calculate the potential under these non-standard state conditions, we make appropriate substitutions into the Nernst equation.

$$E = E^\circ - \frac{RT}{nF} \ln \frac{\left[Mn^{2+}\right]\left[Fe^{3+}\right]^5}{\left[MnO_4^-\right]\left[Fe^{2+}\right]^5\left[H^+\right]^8}$$

$$E = 0.74 - \frac{0.05916}{5} \log \frac{(0.015)(0.10)^5}{(0.025)(0.50)^5\left(1 \times 10^{-7}\right)^8} = 0.12 \text{ V}$$

When writing precipitation, acid–base, and metal–ligand complexation reactions, we represent acidity as H_3O^+. Redox reactions more commonly are written using H^+ instead of H_3O^+. For the reaction in Exercise 6.4.3 , we could replace H^+ with H_3O^+ and increase the stoichiometric coefficient for H_2O from 4 to 12.

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8.5: LE CHÂTELIER'S PRINCIPLE

At a temperature of 25°C, acetic acid's dissociation reaction

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq)$$

has an equilibrium constant of

$$K_a = \frac{\left[CH_3COO^-\right]\left[H_3O^+\right]}{[CH_3COOH]} = 1.75 \times 10^{-5} \tag{8.5.1}$$

Because Equation 8.5.1 has three variables—[CH_3COOH], [CH_3COO^-], and [H_3O^+]—it does not have a unique mathematical solution. Nevertheless, although two solutions of acetic acid may have different values for [CH_3COOH], [CH_3COO^-], and [H_3O^+], each solution has the same value of K_a.

If we add sodium acetate to a solution of acetic acid, the concentration of CH_3COO^- increases, which suggests there is an increase in the value of K_a; however, because K_a must remain constant, the concentration of all three species in Equation 8.5.1 must change to restore K_a to its original value. In this case, a partial reaction of CH_3COO^- and H_3O^+ decreases their concentrations, increases the concentration of CH_3COOH, and reestablishes the equilibrium.

The observation that a system at equilibrium responds to an external action by reequilibrating itself in a manner that diminishes that action, is formalized as ***Le Châtelier's principle***. One common action is to change the concentration of a reactant or product for a system at equilibrium. As noted above for a solution of acetic acid, if we add a product to a reaction at equilibrium the system responds by converting some of the products into reactants. Adding a reactant has the opposite effect, resulting in the conversion of reactants to products.

When we add sodium acetate to a solution of acetic acid, we directly apply the action to the system. It is also possible to apply a change concentration indirectly. Consider, for example, the solubility of AgCl.

$$AgCl(s) \rightleftharpoons Ag^+(aq) + Cl^-(aq) \tag{8.5.2}$$

The effect on the solubility of AgCl of adding $AgNO_3$ is obvious, but what is the effect if we add a ligand that forms a stable, soluble complex with Ag^+? Ammonia, for example, reacts with Ag^+ as shown here

$$Ag^+(aq) + 2NH_3(aq) \rightleftharpoons Ag(NH_3)_2^+(aq) \tag{8.5.3}$$

Adding ammonia decreases the concentration of Ag^+ as the $Ag(NH_3)_2^+$ complex forms. In turn, a decrease in the concentration of Ag^+ increases the solubility of AgCl as reaction 8.5.2 reestablishes its equilibrium position. Adding together reaction 8.5.2 and reaction 8.5.3 clarifies the effect of ammonia on the solubility of AgCl, by showing ammonia as a reactant.

$$AgCl(s) + 2NH_3(aq) \rightleftharpoons Ag(NH_3)_2^+(aq) + Cl^-(aq) \tag{8.5.4}$$

So what is the effect on the solubility of AgCl of adding $AgNO_3$? Adding $AgNO_3$ increases the concentration of Ag^+ in solution. To reestablish equilibrium, some of the Ag^+ and Cl^- react to form additional AgCl; thus, the solubility of AgCl decreases. The solubility product, K_{sp}, of course, remains unchanged.

✔ EXAMPLE 6.5.1

What happens to the solubility of AgCl if we add HNO_3 to the equilibrium solution defined by reaction 8.5.4?

Solution

Nitric acid is a strong acid, which reacts with ammonia as shown here

$$HNO_3(aq) + NH_3(aq) \rightleftharpoons NH_4^+(aq) + NO_3^-(aq)$$

Adding nitric acid lowers the concentration of ammonia. Decreasing ammonia's concentration causes reaction 8.5.4 to move from products to reactants, decreasing the solubility of AgCl.

Increasing or decreasing the partial pressure of a gas is the same as increasing or decreasing its concentration. Because the concentration of a gas depends on its partial pressure, and not on the total pressure of the system, adding or removing an inert gas has no effect on a reaction's equilibrium position.

We can use the ideal gas law to deduce the relationship between pressure and concentration. Starting with $PV = nRT$, we solve for the molar concentration

$$M = \frac{n}{V} = \frac{P}{RT}$$

Of course, this assumes that the gas is behaving ideally, which usually is a reasonable assumption under normal laboratory conditions.

Most reactions involve reactants and products dispersed in a solvent. If we change the amount of solvent by diluting the solution, then the concentrations of all reactants and products must increase; conversely, if we allow the solvent to evaporate partially, then the concentration of the solutes must increase. The effect of simultaneously changing the concentrations of all reactants and products is not intuitively as obvious as when we change the concentration of a single reactant or product. As an example, let's consider how diluting a solution affects the equilibrium position for the formation of the aqueous silver-amine complex (reaction 8.5.3). The equilibrium constant for this reaction is

$$\beta_2 = \frac{\left[\mathrm{Ag(NH_3)_2^+}\right]_{\mathrm{eq}}}{\left[\mathrm{Ag^+}\right]_{\mathrm{eq}}[\mathrm{NH_3}]^2_{\mathrm{eq}}} \tag{8.5.5}$$

where we include the subscript "eq" for clarification. If we dilute a portion of this solution with an equal volume of water, each of the concentration terms in Equation 8.5.5 is cut in half. The reaction quotient, Q_r, becomes

$$Q_r = \frac{0.5\left[\mathrm{Ag(NH_3)_2^+}\right]_{\mathrm{eq}}}{0.5\left[\mathrm{Ag^+}\right]_{\mathrm{eq}}(0.5)^2[\mathrm{NH_3}]^2_{\mathrm{eq}}} = \frac{0.5}{(0.5)^3} \times \frac{\left[\mathrm{Ag(NH_3)_2^+}\right]_{\mathrm{eq}}}{\left[\mathrm{Ag^+}\right]_{\mathrm{eq}}[\mathrm{NH_3}]^2_{\mathrm{eq}}} = 4\beta_2 \tag{8.5.6}$$

Because Q_r is greater than β_2, equilibrium is reestablished by shifting the reaction to the left, decreasing the concentration of $\mathrm{Ag(NH_3)_2^+}$. Note that the new equilibrium position lies toward the side of the equilibrium reaction that has the greatest number of solute particles (one $\mathrm{Ag^+}$ ion and two molecules of $\mathrm{NH_3}$ versus a single metal-ligand complex). If we concentrate the solution of $\mathrm{Ag(NH_3)_2^+}$ by evaporating some of the solvent, equilibrium is reestablished in the opposite direction. This is a general conclusion that we can apply to any reaction. Increasing volume always favors the direction that produces the greatest number of particles, and decreasing volume always favors the direction that produces the fewest particles. If the number of particles is the same on both sides of the reaction, then the equilibrium position is unaffected by a change in volume.

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8.6: LADDER DIAGRAMS

When we develop or evaluate an analytical method, we often need to understand how the chemistry that takes place affects our results. Suppose we wish to isolate Ag^+ by precipitating it as AgCl. If we also need to control pH, then we must use a reagent that does not adversely affect the solubility of AgCl. It is a mistake to use NH_3 to adjust the pH, for example, because it increases the solubility of AgCl (see reaction 6.5.4). One of the primary sources of determinate errors in many analytical methods is failing to account for potential chemical interferences.

In this section we introduce the ladder diagram as a simple graphical tool for visualizing equilibrium chemistry. We will use ladder diagrams to determine what reactions occur when we combine several reagents, to estimate the approximate composition of a system at equilibrium, and to evaluate how a change to solution conditions might affect an analytical method.

> Although not specifically on the topic of ladder diagrams as developed in this section, the following papers provide appropriate background information: (a) Runo, J. R.; Peters, D. G. *J. Chem. Educ.* **1993**, *70*, 708–713; (b) Vale, J.; Fernández-Pereira, C.; Alcalde, M. *J. Chem. Educ.* **1993**, *70*, 790–795; (c) Fernández-Pereira, C.; Vale, J. *Chem. Educator* **1996**, *6*, 1–18; (d) Fernández- Pereira, C.; Vale, J.; Alcalde, M. *Chem. Educator* **2003**, *8*, 15–21; (e) Fernández-Pereira, C.; Alcalde, M.; Villegas, R.; Vale, J. *J. Chem. Educ.* **2007**, *84*, 520–525. Ladder diagrams are a great tool for helping you to think intuitively about analytical chemistry. We will make frequent use of them in the chapters to follow.

LADDER DIAGRAMS FOR ACID–BASE EQUILIBRIA

Let's use acetic acid, CH_3COOH, to illustrate the process we will use to draw and to interpret an acid–base ladder diagram. Before we draw the diagram, however, let's consider the equilibrium reaction in more detail. Acetic acid's acid dissociation reaction and equilibrium constant expression are

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq)$$

$$K_a = \frac{[CH_3COO^-]\,[H_3O^+]}{[CH_3COOH]} = 1.75 \times 10^{-5}$$

First, let's take the logarithm of each term in this equation and multiply through by –1

$$-\log K_a = 4.76 = -\log[H_3O^+] - \log \frac{[CH_3COO^-]}{[CH_3COOH]}$$

Now, let's replace $-\log[H_3O^+]$ with pH and rearrange the equation to obtain the result shown here.

$$pH = 4.76 + \log \frac{[CH_3COO^-]}{[CH_3COOH]} \tag{8.6.1}$$

Equation 8.6.1 tells us a great deal about the relationship between pH and the relative amounts of acetic acid and acetate at equilibrium. If the concentrations of CH_3COOH and CH_3COO^- are equal, then Equation 8.6.1 reduces to

$$pH = 4.76 + \log(1) = 4.76 + 0 = 4.76$$

If the concentration of CH_3COO^- is greater than that of CH_3COOH, then the log term in Equation 8.6.1 is positive and the pH is greater than 4.76. This is a reasonable result because we expect the concentration of the conjugate base, CH_3COO^-, to increase as the pH increases. Similar reasoning will convince you that the pH is less than 4.76 when the concentration of CH_3COOH exceeds that of CH_3COO^-.

Now we are ready to construct acetic acid's ladder diagram (Figure 6.6.1). First, we draw a vertical arrow that represents the solution's pH, with smaller (more acidic) pH levels at the bottom and larger (more basic) pH levels at the top. Second, we draw a horizontal line at a pH equal to acetic acid's pK_a value. This line, or step on the ladder, divides the pH axis into regions where either CH_3COOH or CH_3COO^- is the predominate species. This completes the ladder diagram.

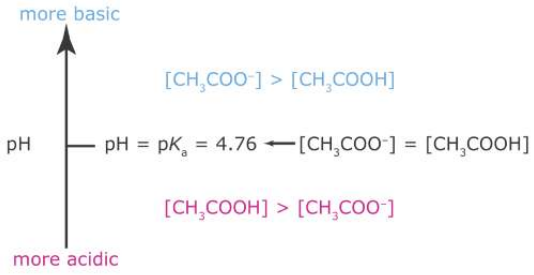


Figure 6.6.1 . Acid–base ladder diagram for acetic acid showing the relative concentrations of CH_3COOH and CH_3COO^-. A simpler version of this ladder diagram dispenses with the equalities and inequalities and shows only the predominate species in each region.

Using the ladder diagram, it is easy to identify the predominate form of acetic acid at any pH. At a pH of 3.5, for example, acetic acid exists primarily as CH_3COOH. If we add sufficient base to the solution such that the pH increases to 6.5, the predominate form of acetic acid is CH_3COO^-.

EXAMPLE 6.6.1

Draw a ladder diagram for the weak base *p*-nitrophenolate and identify its predominate form at a pH of 6.00.

Solution

To draw a ladder diagram for a weak base, we simply draw the ladder diagram for its conjugate weak acid. From Appendix 11, the pK_a for *p*-nitrophenol is 7.15. The resulting ladder diagram is shown in Figure 6.6.2 . At a pH of 6.00, *p*-nitrophenolate is present primarily in its weak acid form.

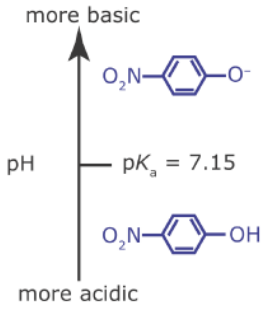


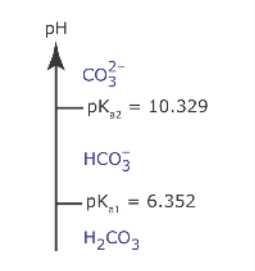
Figure 6.6.2 . Acid–base ladder diagram for *p*-nitrophenolate.

EXERCISE 6.6.1

Draw a ladder diagram for carbonic acid, H_2CO_3. Because H_2CO_3 is a diprotic weak acid, your ladder diagram will have two steps. What is the predominate form of carbonic acid when the pH is 7.00? Relevant equilibrium constants are in Appendix 11.

Answer

From Appendix 11, the pK_a values for H_2CO_3 are 6.352 and 10.329. The ladder diagram for H_2CO_3 is shown below. The predominate form at a pH of 7.00 is HCO_3^-.



https://chem.libretexts.org/@go/page/540040

A ladder diagram is particularly useful for evaluating the reactivity between a weak acid and a weak base. Figure 6.6.3 , for example, shows a single ladder diagram for acetic acid/acetate and for *p*-nitrophenol/*p*-nitrophenolate. An acid and a base can not co-exist if their respective areas of predominance do not overlap. If we mix together solutions of acetic acid and sodium *p*-nitrophenolate, the reaction

$$C_6H_4NO_2^-(aq) + CH_3COOH(aq) \rightleftharpoons CH_3COO^-(aq) + C_6H_4NO_2H(aq) \tag{8.6.2}$$

occurs because the areas of predominance for acetic acid and *p*-nitrophenolate do not overlap. The solution's final composition depends on which species is the limiting reagent. The following example shows how we can use the ladder diagram in Figure 6.6.3 to evaluate the result of mixing together solutions of acetic acid and *p*-nitrophenolate.

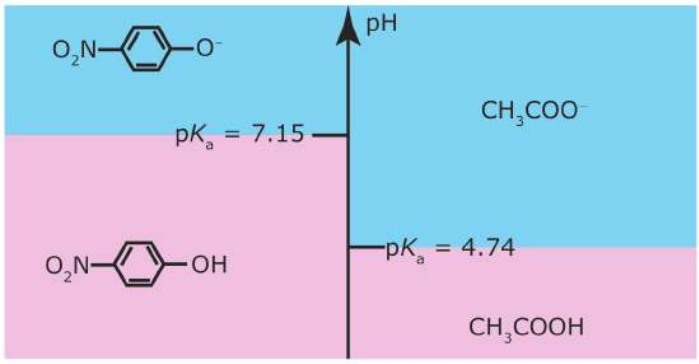


Figure 6.6.3 . Acid–base ladder diagram showing the areas of predominance for acetic acid/acetate and for *p*-nitrophenol/*p*-nitrophenolate. The areas shaded in blue shows the pH range where the weak bases are the predominate species; the weak acid forms are the predominate species in the areas shaded in pink.

EXAMPLE 6.6.2

Predict the approximate pH and the final composition after mixing together 0.090 moles of acetic acid and 0.040 moles of *p*-nitrophenolate.

Solution

The ladder diagram in Figure 6.6.3 indicates that the reaction between acetic acid and *p*-nitrophenolate is favorable. Because acetic acid is in excess, we assume the reaction of *p*-nitrophenolate to *p*-nitrophenol is complete. At equilibrium essentially no *p*-nitrophenolate remains and there are 0.040 mol of *p*-nitrophenol. Converting *p*-nitrophenolate to *p*-nitrophenol consumes 0.040 moles of acetic acid; thus

$$\text{moles } CH_3COOH = 0.090 - 0.040 = 0.050 \text{ mol}$$
$$\text{moles } CH_3COO^- = 0.040 \text{ mol}$$

According to the ladder diagram, the pH is 4.74 when there are equal amounts of CH_3COOH and CH_3COO^-. Because we have slightly more CH_3COOH than CH_3COO^-, the pH is slightly less than 4.74.

EXERCISE 6.6.2

Using Figure 6.6.3 , predict the approximate pH and the composition of the solution formed by mixing together 0.090 moles of *p*-nitrophenolate and 0.040 moles of acetic acid.

Answer

The ladder diagram in Figure 6.6.3 indicates that the reaction between acetic acid and *p*-nitrophenolate is favorable. Because *p*-nitrophenolate is in excess, we assume the reaction of acetic acid to acetate is complete. At equilibrium essentially no acetic acid remains and there are 0.040 moles of acetate. Converting acetic acid to acetate consumes 0.040 moles of *p*-nitrophenolate; thus

$$\text{moles } p\text{-nitrophenolate} = 0.090 - 0.040 = 0.050 \text{ mol}$$

$$\text{moles } p\text{-nitrophenol} = 0.040 \text{ mol}$$

According to the ladder diagram for this system, the pH is 7.15 when there are equal concentrations of *p*-nitrophenol and *p*-nitrophenolate. Because we have slightly more *p*-nitrophenolate than we have *p*-nitrophenol, the pH is slightly greater than 7.15.

If the areas of predominance for an acid and a base overlap, then we do not expect that much of a reaction will occur. For example, if we mix together solutions of CH_3COO^- and *p*-nitrophenol, we do not expect a significant change in the moles of either reagent. Furthermore,

the pH of the mixture must be between 4.76 and 7.15, with the exact pH depending upon the relative amounts of CH_3COO^- and *p*-nitrophenol.

We also can use an acid–base ladder diagram to evaluate the effect of pH on other equilibria. For example, the solubility of CaF_2

$$CaF_2(s) \rightleftharpoons Ca^{2+}(aq) + 2F^-(aq)$$

is affected by pH because F^- is a weak base. From Le Châtelier's principle, we know that converting F^- to HF will increase the solubility of CaF_2. To minimize the solubility of CaF_2 we need to maintain the solution's pH so that F^- is the predominate species. The ladder diagram for HF (Figure 6.6.4) shows us that maintaining a pH of more than 3.17 will minimize solubility losses.

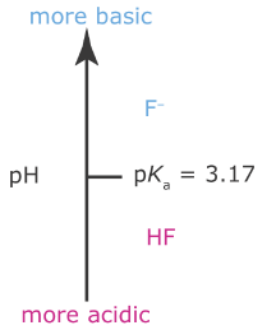


Figure 6.6.4 . Acid–base ladder diagram for HF. To minimize the solubility of CaF_2, we need to keep the pH above 3.17, with more basic pH levels leading to smaller solubility losses. See Chapter 8 for a more detailed discussion.

LADDER DIAGRAMS FOR COMPLEXATION EQUILIBRIA

We can apply the same principles for constructing and interpreting an acid–base ladder diagram to equilibria that involve metal–ligand complexes. For a complexation reaction we define the ladder diagram's scale using the concentration of uncomplexed, or free ligand, pL. Using the formation of $Cd(NH_3)^{2+}$ as an example

$$Cd^{2+}(aq) + NH_3(aq) \rightleftharpoons Cd(NH_3)^{2+}(aq)$$

we can show that $\log K_1$ is the dividing line between the areas of predominance for Cd^{2+} and for $Cd(NH_3)^{2+}$.

$$K_1 = 3.55 \times 10^2 = \frac{\left[Cd(NH_3)^{2+}\right]}{\left[Cd^{2+}\right]\left[NH_3\right]}$$

$$\log K_1 = \log\left(3.55 \times 10^2\right) = \log \frac{\left[Cd(NH_3)^{2+}\right]}{\left[Cd^{2+}\right]} - \log[NH_3]$$

$$\log K_1 = 2.55 = \log \frac{\left[Cd(NH_3)^{2+}\right]}{\left[Cd^{2+}\right]} + pNH_3$$

$$pNH_3 = \log K_1 + \log \frac{\left[Cd^{2+}\right]}{\left[Cd(NH_3)^{2+}\right]} = 2.55 + \log \frac{\left[Cd^{2+}\right]}{\left[Cd(NH_3)^{2+}\right]}$$

Thus, Cd^{2+} is the predominate species when pNH_3 is greater than 2.55 (a concentration of NH_3 smaller than 2.82×10^{-3} M) and for a pNH_3 value less than 2.55, $Cd(NH_3)^{2+}$ is the predominate species. Figure 6.6.5 shows a complete metal–ligand ladder diagram for Cd^{2+} and NH_3 that includes additional Cd–NH_3 complexes.

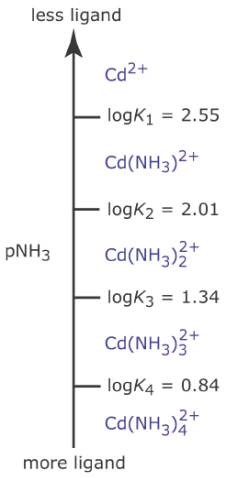


Figure 6.6.5 . Metal–ligand ladder diagram for Cd^{2+}–NH_3 complexation reactions. Note that higher-order complexes form when pNH_3 is smaller (which corresponds to larger concentrations of NH_3).

EXAMPLE 6.6.3

Draw a single ladder diagram for the $Ca(EDTA)^{2-}$ and the $Mg(EDTA)^{2-}$ metal–ligand complexes. Use your ladder diagram to predict the result of adding 0.080 moles of Ca^{2+} to 0.060 moles of $Mg(EDTA)^{2-}$. EDTA is an abbreviation for the ligand ethylenediaminetetraacetic acid.

Solution

Figure 6.6.6 shows the ladder diagram for this system of metal–ligand complexes. Because the predominance regions for Ca^{2+} and $Mg(EDTA)^{2-}$ do not overlap, the reaction

$$Ca^{2+}(aq) + Mg(EDTA)^{2-}(aq) \rightleftharpoons Ca(EDTA)^{2-}(aq) + Mg^{2+}(aq)$$

proceeds essentially to completion. Because Ca^{2+} is the excess reagent, the composition of the final solution is approximately

$$\text{moles } Ca^{2+} = 0.080 - 0.060 = 0.020 \text{ mol}$$

$$\text{moles } Ca(EDTA)^{2-} = 0.060 \text{ mol}$$

$$\text{moles } Mg^{2+} = 0.060 \text{ mol}$$

$$\text{moles } Mg(EDTA)^{2-} = 0 \text{ mol}$$

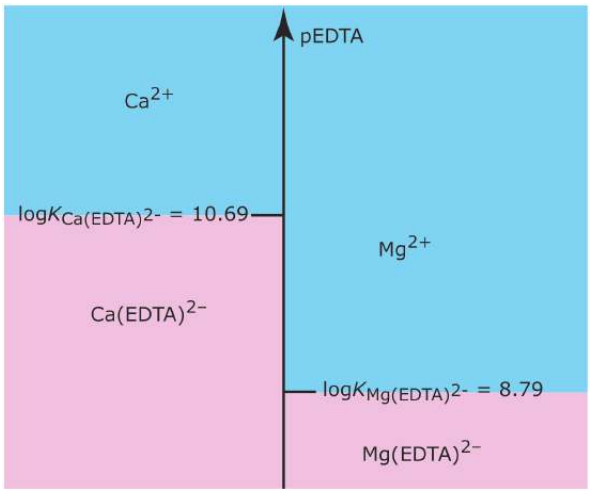


Figure 6.6.6 . Metal–ligand ladder diagram for $Ca(EDTA)^{2-}$ and for $Mg(EDTA)^{2-}$. The areas shaded in blue show the pEDTA range where the free metal ions are the predominate species; the metal–ligand complexes are the predominate species in the areas shaded in pink.

The metal–ligand ladder diagram in Figure 6.6.5 uses stepwise formation constants. We also can construct a ladder diagram using cumulative formation constants. For example, the first three stepwise formation constants for the reaction of Zn^{2+} with NH_3

$$Zn^{2+}(aq) + NH_3(aq) \rightleftharpoons Zn(NH_3)^{2+}(aq) \quad K_1 = 1.6 \times 10^2$$

$$Zn(NH_3)^{2+}(aq) + NH_3(aq) \rightleftharpoons Zn(NH_3)_2^{2+}(aq) \quad K_2 = 1.95 \times 10^2$$

$$Zn(NH_3)_2^{2+}(aq) + NH_3(aq) = Zn(NH_3)_3^{2+}(aq) \quad K_3 = 2.3 \times 10^2$$

suggests that the formation of $Zn(NH_3)_3^{2+}$ is more favorable than the formation of $Zn(NH_3)^{2+}$ or $Zn(NH_3)_2^{2+}$. For this reason, the equilibrium is best represented by the cumulative formation reaction shown here.

$$Zn^{2+}(aq) + 3NH_3(aq) \rightleftharpoons Zn(NH_3)_3^{2+}(aq) \quad \beta_3 = 7.2 \times 10^6$$

Because K_3 is greater than K_2, which is greater than K_1, the formation of the metal-ligand complex $Zn(NH_3)_3^{2+}$ is more favorable than the formation of the other metal ligand complexes. For this reason, at lower values of pNH_3 the concentration of $Zn(NH_3)_3^{2+}$ is larger than the concentrations of $Zn(NH_3)^{2+}$ or $Zn(NH_3)_2^{2+}$. The value of β_3 is

$$\beta_3 = K_1 \times K_2 \times K_3$$

To see how we incorporate this cumulative formation constant into a ladder diagram, we begin with the reaction's equilibrium constant expression.

$$\beta_3 = \frac{\left[Zn(NH_3)_3^{2+}\right]}{\left[Zn^{2+}\right]\left[NH_3\right]^3}$$

Taking the log of each side

$$\log \beta_3 = \log \frac{\left[Zn(NH_3)_3^{2+}\right]}{\left[Zn^{2+}\right]} - 3\log[NH_3]$$

and rearranging gives

$$pNH_3 = \frac{1}{3}\log \beta_3 + \frac{1}{3}\log \frac{\left[Zn^{2+}\right]}{\left[Zn(NH_3)_3^{2+}\right]}$$

When the concentrations of Zn and $Zn(NH_3)_3^{2+}$ are equal, then

$$pNH_3 = \frac{1}{3}\log \beta_3 = 2.29$$

In general, for the metal–ligand complex ML_n, the step for a cumulative formation constant is

$$pL = \frac{1}{n}\log \beta_n$$

Figure 6.6.7 shows the complete ladder diagram for the Zn^{2+}–NH_3 system.

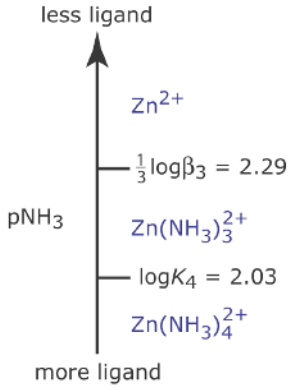


Figure 6.6.7 . Ladder diagram for Zn^{2+}–NH_3 metal–ligand complexation reactions showing both a step based on a cumulative formation constant and a step based on a stepwise formation constant.

LADDER DIAGRAMS FOR OXIDATION/REDUCTION EQUILIBRIA

We also can construct ladder diagrams to help us evaluate redox equilibria. Figure 6.6.8 shows a typical ladder diagram for two half-reactions in which the scale is the potential, *E*.

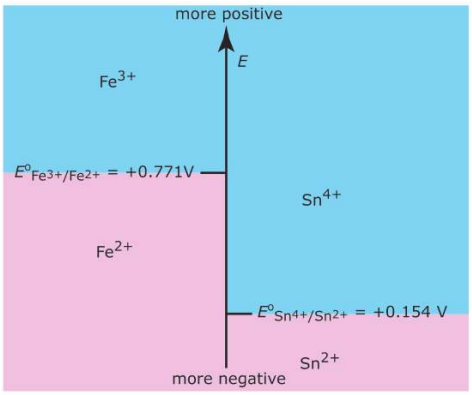


Figure 6.6.8 . Redox ladder diagram for Fe^{3+}/Fe^{2+} and for Sn^{4+}/Sn^{2+}. The areas shaded in blue show the potential range where the oxidized forms are the predominate species; the reduced forms are the predominate species in the areas shaded in pink. Note that a more positive potential favors the oxidized form.

The Nernst equation defines the areas of predominance. Using the Fe^{3+}/Fe^{2+} half-reaction as an example, we write

$$E = E^\circ - \frac{RT}{nF}\ln\frac{\left[\mathrm{Fe^{2+}}\right]}{\left[\mathrm{Fe^{3+}}\right]} = 0.771 - 0.05916\log\frac{\left[\mathrm{Fe^{2+}}\right]}{\left[\mathrm{Fe^{3+}}\right]}$$

At a potential more positive than the standard state potential, the predominate species is Fe^{3+}, whereas Fe^{2+} predominates at potentials more negative than E^o. When coupled with the step for the Sn^{4+}/Sn^{2+} half-reaction we see that Sn^{2+} is a useful reducing agent for Fe^{3+}. If Sn^{2+} is in excess, the potential of the resulting solution is near +0.154 V.

Because the steps on a redox ladder diagram are standard state potentials, a complication arises if solutes other than the oxidizing agent and reducing agent are present at non-standard state concentrations. For example, the potential for the half-reaction

$$\mathrm{UO_2^{2+}}(aq) + 4\mathrm{H_3O^+}(aq) + 2e^- \rightleftharpoons \mathrm{U^{4+}}(aq) + 6\mathrm{H_2O}(l)$$

depends on the solution's pH. To define areas of predominance in this case we begin with the Nernst equation

$$E = +0.327 - \frac{0.05916}{2}\log\frac{\left[\mathrm{U^{4+}}\right]}{\left[\mathrm{UO_2^{2+}}\right]\left[\mathrm{H_3O^+}\right]^4}$$

and factor out the concentration of H_3O^+.

$$E = +0.327 + \frac{0.05916}{2}\log\left[\mathrm{H_3O^+}\right]^4 - \frac{0.05916}{2}\log\frac{\left[\mathrm{U^{4+}}\right]}{\left[\mathrm{UO_2^{2+}}\right]}$$

From this equation we see that the area of predominance for UO_2^{2+} and U^{4+} is defined by a step at a potential where $[U^{4+}] = [UO_2^{2+}]$.

$$E = +0.327 + \frac{0.05916}{2}\log\left[\mathrm{H_3O^+}\right]^4 = +0.327 - 0.1183\mathrm{pH}$$

Figure 6.6.9 shows how pH affects the step for the UO_2^{2+} /U^{4+} half-reaction.

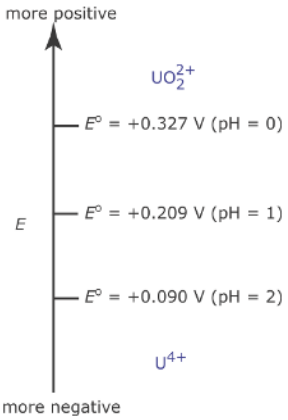


Figure 6.6.9 . Redox ladder diagram for the UO_2^{2+}/U^{4+} half-reaction showing the effect of pH on the step defined by the standard state's potential.

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8.7: SOLVING EQUILIBRIUM PROBLEMS

Ladder diagrams are a useful tool for evaluating chemical reactivity and for providing a reasonable estimate of a chemical system's composition at equilibrium. If we need a more exact quantitative description of the equilibrium condition, then a ladder diagram is insufficient; instead, we need to find an algebraic solution. In this section we will learn how to set-up and solve equilibrium problems. We will start with a simple problem and work toward more complex problems.

A SIMPLE PROBLEM: THE SOLUBILITY OF $PB(IO_3)_2$

If we place an insoluble compound such as $Pb(IO_3)_2$ in deionized water, the solid dissolves until the concentrations of Pb^{2+} and IO_3^- satisfy the solubility product for $Pb(IO_3)_2$. At equilibrium the solution is saturated with $Pb(IO_3)_2$, which means simply that no more solid can dissolve. How do we determine the equilibrium concentrations of Pb^{2+} and IO_3^-, and what is the molar solubility of $Pb(IO_3)_2$ in this saturated solution?

> When we first add solid $Pb(IO_3)_2$ to water, the concentrations of Pb^{2+} and IO_3^- are zero and the reaction quotient, Q_r, is
>
> $$Q_r = \left[Pb^{2+}\right]\left[IO_3^-\right]^2 = 0$$
>
> As the solid dissolves, the concentrations of these ions increase, but Q_r remains smaller than K_{sp}. We reach equilibrium and "satisfy the solubility product" when $Q_r = K_{sp}$.

We begin by writing the equilibrium reaction and the solubility product expression for $Pb(IO_3)_2$.

$$Pb(IO_3)_2(s) \rightleftharpoons Pb^{2+}(aq) + 2IO_3^-(aq)$$

e

$$K_{sp} = \left[Pb^{2+}\right]\left[IO_3^-\right]^2 = 2.5 \times 10^{-13} \tag{8.7.1}$$

As $Pb(IO_3)_2$ dissolves, two IO_3^- ions form for each ion of Pb^{2+}. If we assume that the change in the molar concentration of Pb^{2+} at equilibrium is x, then the change in the molar concentration of IO_3^- is $2x$. The following table helps us keep track of the initial concentrations, the change in con- centrations, and the equilibrium concentrations of Pb2+ and IO_3^-.

concentrations	$Pb(IO_3)_2$ (s)	⇌	Pb^{2+} (aq)	+	$2IO_3^-$ (aq)
initial	solid		0		0
change	solid		+x		+ 2x
equilibrium	solid		x		2x

> Because a solid, such as $Pb(IO_3)_2$, does not appear in the solubility product expression, we do not need to keep track of its concentration. Remember, however, that the K_{sp} value applies only if there is some solid $Pb(IO_3)_2$ present at equilibrium.

Substituting the equilibrium concentrations into Equation 8.7.1 and solving gives

$$(x)(2x)^2 = 4x^3 = 2.5 \times 10^{-13}$$

$$x = 3.97 \times 10^{-5}$$

Substituting this value of x back into the equilibrium concentration expressions for Pb^{2+} and IO_3^- gives their concentrations as

$$\left[Pb^{2+}\right] = x = 4.0 \times 10^{-5}\text{M and } \left[IO_3^-\right] = 2x = 7.9 \times 10^{-5}$$

Because one mole of $Pb(IO_3)_2$ contains one mole of Pb^{2+}, the molar solubility of $Pb(IO_3)_2$ is equal to the concentration of Pb^{2+}, or 4.0×10^{-5} M.

> We can express a compound's solubility in two ways: as its molar solubility (mol/L) or as its mass solubility (g/L). Be sure to express your answer clearly.

? EXERCISE 6.7.1

Calculate the molar solubility and the mass solubility for Hg_2Cl_2, given the following solubility reaction and K_{sp} value.

$$Hg_2Cl_2(s) \rightleftharpoons Hg_2^{2+}(aq) + 2Cl^-(aq) \quad K_{sp} = 1.2 \times 10^{-8}$$

Answer

When Hg_2Cl_2 dissolves, two Cl^- are produced for each ion of Hg_2^{2+}. If we assume x is the change in the molar concentration of Hg_2^{2+}, then the change in the molar concentration of Cl^- is $2x$. The following table helps us keep track of our solution to this problem.

concentration	Hg_2Cl_2 (s)	$\rightleftharpoons$	Hg_2^{2+} (aq)	+	Cl^- (aq)
initial	solid		0		0
change	solid		$+x$		$+2x$
equilibrium	solid		x		$2x$

Substituting the equilibrium concentrations into the K_{sp} expression forHg_2Cl_2 gives

$$K_{sp} = \left[Hg_2^{2+}\right]\left[Cl^-\right]^2 = (x)(2x)^2 = 4x^3 = 1.2 \times 10^{-18}$$

$$x = 6.69 \times 10^{-7}$$

Substituting x back into the equilibrium expressions for Hg_2^{2+} and Cl^- gives their concentrations as

$$\left[Hg_2^{2+}\right] = x = 6.7 \times 10^{-7}\ M \quad \left[Cl^-\right] = 2x = 1.3 \times 10^{-6}\ M$$

The molar solubility is equal to $[Hg_2^{2+}]$, or 6.7×10^{-7} mol/L.

A MORE COMPLEX PROBLEM: THE COMMON ION EFFECT

Calculating the solubility of $Pb(IO_3)_2$ in deionized water is a straightforward problem because the solid's dissolution is the only source of Pb^{2+} and IO_3^-. But what if we add $Pb(IO_3)_2$ to a solution of 0.10 M $Pb(NO_3)_2$? Before we set-up and solve this problem algebraically, think about the system's chemistry and decide whether the solubility of $Pb(IO_3)_2$ will increase, decrease, or remain the same. Beginning a problem by thinking about the likely answer is a good habit to develop. Knowing what answers are reasonable will help you spot errors in your calculations and give you more confidence that your solution to a problem is correct. Because the solution already contains a source of Pb^{2+}, we can use Le Châtelier's principle to predict that the solubility of $Pb(IO_3)_2$ is smaller than that in our previous problem.

We begin by setting up a table to help us keep track of the concentrations of Pb^{2+} and IO_3^- as this system moves toward and reaches equilibrium.

concentrations	$Pb(IO_3)_2$ (s)	$\rightleftharpoons$	Pb^{2+} (aq)	+	$2IO_3^-$ (aq)
initial	solid		0.10		0
change	solid		$+x$		$+ 2x$
equilibrium	solid		$0.10 + x$		$2x$

Substituting the equilibrium concentrations into Equation 8.7.1

$$(0.10 + x)(2x)^2 = 2.5 \times 10^{-13}$$

and multiplying out the terms on the equation's left side leaves us with

$$4x^3 + 0.40x^2 = 2.5 \times 10^{-13} \tag{8.7.2}$$

This is a more difficult equation to solve than that for the solubility of $Pb(IO_3)_2$ in deionized water, and its solution is not immediately obvious. We can find a rigorous solution to Equation 8.7.2 using computational software packages and spreadsheets, some of which are described in Chapter 6.10.

> There are several approaches to solving cubic equations, but none are computationally easy using just paper and pencil.

How might we solve Equation 8.7.2 if we do not have access to a computer? One approach is to use our understanding of chemistry to simplify the problem. From Le Châtelier's principle we know that a large initial concentration of Pb^{2+} will decrease significantly the solubility of $Pb(IO_3)_2$. One reasonable assumption is that the initial concentration of Pb^{2+} is very close to its equilibrium concentration. If this assumption is correct, then the following approximation is reasonable

$$\left[Pb^{2+}\right] = 0.10 + x \approx 0.10$$

Substituting this approximation into Equation 8.7.1 and solving for x gives

$$(0.10)(2x)^2 = 0.4x^2 = 2.5 \times 10^{-13}$$

$$x = 7.91 \times 10^{-7}$$

Before we accept this answer, we must verify that our approximation is reasonable. The difference between the actual concentration of Pb^{2+}, which is 0.10 + *x* M, and our assumption that the concentration of Pb^{2+} is 0.10 M is 7.9×10^{-7}, or 7.9×10^{-4} % of the assumed concentration. This is a negligible error. If we accept the result of our calculation, we find that the equilibrium concentrations of Pb^{2+} and IO_3^- are

$$\left[Pb^{2+}\right] = 0.10 + x \approx 0.10 \text{ M and } \left[IO_3^-\right] = 2x = 1.6 \times 10^{-6} \text{ M}$$

$$\begin{aligned} \%\text{ error } &= \frac{\text{actual } - \text{ assumed}}{\text{assumed}} \times 100 \\ &= \frac{(0.10 + x) - 0.10}{0.10} \times 100 \\ &= \frac{7.91 \times 10^{-7}}{0.10} \times 100 \\ &= 7.91 \times 10^{-4}\% \end{aligned}$$

The molar solubility of $Pb(IO_3)_2$ is equal to the additional concentration of Pb^{2+} in solution, or 7.9×10^{-4} mol/L. As expected, we find that $Pb(IO_3)_2$ is less soluble in the presence of a solution that already contains one of its ions. This is known as the ***common ion effect***.

As outlined in the following example, if an approximation leads to an error that is unacceptably large, then we can extend the process of making and evaluating approximations.

One "rule of thumb" when making an approximation is that it should not introduce an error of more than ±5%. Although this is not an unreasonable choice, what matters is that the error makes sense within the context of the problem you are solving.

EXAMPLE 6.7.1

Calculate the solubility of $Pb(IO_3)_2$ in 1.0×10^{-4} M $Pb(NO_3)_2$.

Solution

If we let *x* equal the change in the concentration of Pb^{2+}, then the equilibrium concentrations of Pb^{2+} and IO_3^- are

$$\left[Pb^{2+}\right] = 1.0 \times 10^{-4} + x \text{ and } \left[IO_3^-\right] = 2x$$

Substituting these concentrations into Equation 8.7.1 leaves us with

$$\left(1.0 \times 10^{-4} + x\right)(2x)^2 = 2.5 \times 10^{-13}$$

To solve this equation for *x*, let's make the following assumption

$$\left[Pb^{2+}\right] = 1.0 \times 10^{-4} + x \approx 1.0 \times 10^{-4} \text{ M}$$

Solving for *x* gives its value as 2.50×10^{-5}; however, when we substitute this value for *x* back, we find that the calculated concentration of Pb^{2+} at equilibrium

$$\left[Pb^{2+}\right] = 1.0 \times 10^{-4} + x = 1.0 \times 10^{-4} + 2.50 \times 10^{-5} = 1.25 \times 10^{-4} \text{ M}$$

is 25% greater than our assumption of 1.0×10^{-4} M. This error is unreasonably large.

Rather than shouting in frustration, let's make a new assumption. Our first assumption—that the concentration of Pb^{2+} is 1.0×10^{-4} M—was too small. The calculated concentration of 1.25×10^{-4} M, therefore, probably is a too large, but closer to the correct concentration than was our first assumption. For our second approximation, let's assume that

$$\left[Pb^{2+}\right] = 1.0 \times 10^{-4} + x = 1.25 \times 10^{-4}\text{M}$$

Substituting into Equation 8.7.1 and solving for *x* gives its value as 2.24×10^{-5}. The resulting concentration of Pb^{2+} is

$$\left[Pb^{2+}\right] = 1.0 \times 10^{-4} + 2.24 \times 10^{-5} = 1.22 \times 10^{-4} \text{ M}$$

which differs from our assumption of 1.25×10^{-4} M by 2.4%. Because the original concentration of Pb^{2+} is given to two significant figure, this is a more reasonable error. Our final solution, to two significant figures, is

$$\left[Pb^{2+}\right] = 1.2 \times 10^{-4}\ M \text{ and } \left[IO_3\right] = 4.5 \times 10^{-5}\ M$$

and the molar solubility of $Pb(IO_3)_2$ is 2.2×10^{-5} mol/L. This iterative approach to solving the problems is known as the ***method of successive approximations***.

EXERCISE 6.7.2

Calculate the molar solubility for Hg_2Cl_2 in 0.10 M NaCl and compare your answer to its molar solubility in deionized water (see Exercise 6.7.1).

Answer

We begin by setting up a table to help us keep track of the concentrations Hg_2^{2+} and Cl^- as this system moves toward and reaches equilibrium.

concentration	Hg_2Cl_2 (*s*)	⇌	Hg_2^{2+} (*aq*)	+	Cl^- (*aq*)
initial	solid		0		0.10
change	solid		+*x*		+2*x*
equilibrium	solid		*x*		0.1 + 2*x*

Substituting the equilibrium concentrations into the K_{sp} expression for Hg_2Cl_2 leaves us with a difficult to solve cubic equation.

$$K_{sp} = \left[Hg_2^{2+}\right]\left[Cl^-\right]^2 = (x)(0.10+2x)^2 = 4x^3 + 0.40x^2 + 0.010x$$

Let's make an assumption to simplify this problem. Because we expect the value of *x* to be small, let's assume that

$$\left[Cl^-\right] = 0.10 + 2x \approx 0.10$$

This simplifies our problem to

$$K_{sp} = \left[Hg_2^{2+}\right]\left[Cl^-\right]^2 = (x)(0.10)^2 = 0.010x = 1.2 \times 10^{-18}$$

which gives the value of *x* as 1.2×10^{-16} M. The difference between the actual concentration of Cl^-, which is (0.10 + 2*x*) M, and our assumption that it is 0.10 M introduces an error of 2.4×10^{-13} %. This is a negligible error. The molar solubility of Hg_2Cl_2 is the same as the concentration of Hg_2^{2+}, or 1.2×10^{-16} M. As expected, the molar solubility in 0.10 M NaCl is less than 6.7×10^{-7} mol/L, which is its solubility in water (see solution to Exercise 6.7.1).

A SYSTEMATIC APPROACH TO SOLVING EQUILIBRIUM PROBLEMS

Calculating the solubility of $Pb(IO_3)_2$ in a solution of $Pb(NO_3)_2$ is more complicated than calculating its solubility in deionized water. The calculation, however, is still relatively easy to organize and the simplifying assumptions are fairly obvious. This problem is reasonably straightforward because it involves only one equilibrium reaction and one equilibrium constant.

Determining the equilibrium composition of a system with multiple equilibrium reactions is more complicated. In this section we introduce a systematic approach to setting-up and solving equilibrium problems. As shown in Table 6.7.1 , this approach involves four steps.

Table 6.7.1 . Systematic Approach to Solving Equilibrium Problems

Step 1 Write all relevant equilibrium reactions and equilibrium constant expressions.
Step 2 Count the unique species that appear in the equilibrium constant expressions; these are your unknowns. You have enough information to solve the problem if the number of unknowns equals the number of equilibrium constant expressions. If not, add a mass balance equation and/or a charge balance equation. Continue adding equations until the number of equations equals the number of unknowns.
Step 3 Combine your equations and solve for one unknown. Whenever possible, simplify the algebra by making appropriate assumptions. If you make an assumption, set a limit for its error. This decision influences your evaluation of the assumption.
Step 4 Check your assumptions. If any assumption proves invalid, return to the previous step and continue solving. The problem is complete when you have an answer that does not violate any of your assumptions.

In addition to equilibrium constant expressions, two other equations are important to this systematic approach to solving an equilibrium problem. The first of these equations is a ***mass balance equation***, which simply is a statement that matter is conserved during a chemical reaction. In a solution of acetic acid, for example, the combined concentrations of the conjugate weak acid, CH_3COOH, and the conjugate weak base, CH_3COO^-, must equal acetic acid's initial concentration, C_{CH_3COOH}.

$$C_{\text{CH}_3\text{COOH}} = [\text{CH}_3\text{COOH}] + [\text{CH}_3\text{COO}^-]$$

> You may recall from Chapter 2 that this is the difference between a formal concentration and a molar concentration. The variable C represents a formal concentration.

The second equation is a ***charge balance equation***, which requires that the total positive charge from the cations equal the total negative charge from the anions. Mathematically, the charge balance equation is

$$\sum_{i=1}^{n} (z^+)_i [C^{z+}]_i = -\sum_{j=1}^{m} (z^-)_j [A^{z-}]_j$$

where $[C^{z+}]_i$ and $[A^{z-}]_j$ are, respectively, the concentrations of the ith cation and the jth anion, and $(z^+)_i$ and $(z^-)_j$ are the charges for the ith cation and the jth anion. Every ion in solution, even if it does not appear in an equilibrium reaction, must appear in the charge balance equation. For example, the charge balance equation for an aqueous solution of $Ca(NO_3)_2$ is

$$2 \times [\text{Ca}^{2+}] + [\text{H}_3\text{O}^+] = [\text{OH}^+] + [\text{NO}_3^-]$$

Note that we multiply the concentration of Ca^{2+} by two and that we include the concentrations of H_3O^+ and OH^-.

> A charge balance is a conservation of a charge. The minus sign in front of the summation term on the right side of the charge balance equation ensures that both summations are positive. There are situations where it is impossible to write a charge balance equation because we do not have enough information about the solution's composition. For example, suppose we fix a solution's pH using a buffer. If the buffer's composition is not specified, then we cannot write a charge balance equation.

✔ EXAMPLE 6.7.2

Write mass balance equations and a charge balance equation for a 0.10 M solution of $NaHCO_3$.

Solution

It is easier to keep track of the species in solution if we write down the reactions that define the solution's composition. These reactions are the dissolution of a soluble salt

$$\text{NaHCO}_3(s) \rightarrow \text{Na}^+(aq) + \text{HCO}_3^-(aq)$$

and the acid–base dissociation reactions of HCO_3^- and H_2O

$$\text{HCO}_3^-(aq) + \text{H}_2\text{O}(l) \rightleftharpoons \text{H}_3\text{O}^+(aq) + \text{CO}_3^{2-}(aq)$$

$$\text{HCO}_3^-(aq) + \text{H}_2\text{O}(l) \rightleftharpoons \text{OH}^-(aq) + \text{H}_2\text{CO}_3(aq)$$

$$2\text{H}_2\text{O}(l) \rightleftharpoons \text{H}_3\text{O}^+(aq) + \text{OH}^-(aq)$$

The mass balance equations are

$$0.10\text{M} = [\text{H}_2\text{CO}_3] + [\text{HCO}_3^-] + [\text{CO}_3^{2-}]$$

$$0.10\ \text{M} = [\text{Na}^+]$$

and the charge balance equation is

$$[\text{Na}^+] + [\text{H}_3\text{O}^+] = [\text{OH}^-] + [\text{HCO}_3^-] + 2 \times [\text{CO}_3^{2-}]$$

? EXERCISE 6.7.3

Write appropriate mass balance and charge balance equations for a solution containing 0.10 M KH_2PO_4 and 0.050 M Na_2HPO_4.

Answer

To help us determine what ions are in solution, let's write down all the reaction needed to prepare the solutions and the equilibrium reactions that take place within these solutions. These reactions are the dissolution of two soluble salts

$$\text{KH}_2\text{PO}_4(s) \longrightarrow \text{K}^+(aq) + \text{H}_2\text{PO}_4^-(aq)$$

$$\text{NaHPO}_4(s) \longrightarrow \text{Na}^+(aq) + \text{HPO}_4^{2-}(aq)$$

and the acid–base dissociation reactions for $H_2PO_4^-$, HPO_4^{2-}. and H_2O.

$$H_2PO_4^-(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + HPO_4^{2-}(aq)$$

$$H_2PO_4^-(aq) + H_2O(l) \rightleftharpoons OH^-(aq) + H_3PO_4(aq)$$

$$HPO_4^{2-}(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + PO_4^{3-}(aq)$$

$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq)$$

Note that we did not include the base dissociation reaction for HPO_4^{2-} because we already accounted for its product, $H_2PO_4^-$, in another reaction. The mass balance equations for K^+ and Na^+ are straightforward

$$\left[K^+\right] = 0.10\ \text{M and } \left[Na^+\right] = 0.10\ \text{M}$$

but the mass balance equation for phosphate takes a bit more thought. Both $H_2PO_4^-$ and HPO_4^{2-} produce the same ions in solution. We can, therefore, imagine that the solution initially contains 0.15 M KH_2PO_4, which gives the following mass balance equation.

$$[H_3PO_4] + \left[H_2PO_4^-\right] + \left[HPO_4^{2-}\right] + \left[PO_4^{3-}\right] = 0.15\ \text{M}$$

The charge balance equation is

$$\left[H_3O^+\right] + \left[K^+\right] + \left[Na^+\right] = \left[H_2PO_4^-\right] + 2 \times \left[HPO_4^{2-}\right] + 3 \times \left[PO_4^{3-}\right] + \left[OH^-\right]$$

PH OF A MONOPROTIC WEAK ACID

To illustrate the systematic approach to solving equilibrium problems, let's calculate the pH of 1.0 M HF. Two equilibrium reactions affect the pH. The first, and most obvious, is the acid dissociation reaction for HF

$$HF(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + F^-(aq)$$

for which the equilibrium constant expression is

$$K_a = \frac{\left[H_3O^+\right]\left[F^-\right]}{[HF]} = 6.8 \times 10^{-4} \tag{8.7.3}$$

The second equilibrium reaction is the dissociation of water, which is an obvious yet easily neglected reaction

$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq)$$

$$K_w = \left[H_3O^+\right]\left[OH^-\right] = 1.00 \times 10^{-14} \tag{8.7.4}$$

Counting unknowns, we find four: [HF], [F^-], [H_3O^+], and [OH^-]. To solve this problem we need two additional equations. These equations are a mass balance equation on hydrofluoric acid

$$C_{HF} = [HF] + \left[F^-\right] = 1.0\text{M} \tag{8.7.5}$$

and a charge balance equation

$$\left[H_3O^+\right] = \left[OH^-\right] + \left[F^-\right] \tag{8.7.6}$$

With four equations and four unknowns, we are ready to solve the problem. Before doing so, let's simplify the algebra by making two assumptions.

Assumption One. Because HF is a weak acid, we know that the solution is acidic. For an acidic solution it is reasonable to assume that

$$\left[H_3O^+\right] >> \left[OH^-\right]$$

which simplifies the charge balance equation to

$$\left[H_3O^+\right] = \left[F^-\right] \tag{8.7.7}$$

Assumption Two. Because HF is a weak acid, very little of it dissociates to form F^-. Most of the HF remains in its conjugate weak acid form and it is reasonable to assume that

$$[HF] >> \left[F^-\right]$$

which simplifies the mass balance equation to

$$C_{HF} = [HF] = 1.0\ M \tag{8.7.8}$$

For this exercise let's accept an assumption if it introduces an error of less than ±5%.

Substituting Equation 8.7.7 and Equation 8.7.8 into Equation 8.7.3, and solving for the concentration of H_3O^+ gives us

$$K_a = \frac{[H_3O^+][F^-]}{[HF]} = \frac{[H_3O^+][H_3O^+]}{C_{HF}} = \frac{[H_3O^+]^2}{C_{HF}} = 6.8 \times 10^{-4}$$

$$[H_3O^+] = \sqrt{K_a C_{HF}} = \sqrt{(6.8 \times 10^{-4})(1.0)} = 2.6 \times 10^{-2}$$

Before accepting this answer, we must verify our assumptions. The first assumption is that $[OH^-]$ is significantly smaller than $[H_3O^+]$. Using Equation 8.7.4, we find that

$$[OH^-] = \frac{K_w}{[H_3O^+]} = \frac{1.00 \times 10^{-14}}{2.6 \times 10^{-2}} = 3.8 \times 10^{-13}$$

Clearly this assumption is acceptable. The second assumption is that $[F^-]$ is significantly smaller than [HF]. From Equation 8.7.7 we have

$$[F^-] = 2.6 \times 10^{-2}\ M$$

Because $[F^-]$ is 2.60% of C_{HF}, this assumption also is acceptable. Given that $[H_3O^+]$ is 2.6×10^{-2} M, the pH of 1.0 M HF is 1.59.

How does the calculation change if we require that the error introduced in our assumptions be less than ±1%? In this case we no longer can assume that [HF] >> $[F^-]$ and we cannot simplify the mass balance equation. Solving the mass balance equation for [HF]

$$[HF] = C_{HF} - [F^-] = C_{HF} - [H_3O^+]$$

and substituting into the K_a expression along with Equation 8.7.7 gives

$$K_a = \frac{[H_3O^+]^2}{C_{HF} - [H_3O^+]}$$

Rearranging this equation leaves us with a quadratic equation

$$[H_3O^+]^2 + K_a[H_3O^+] - K_a C_{HF} = 0$$

which we solve using the quadratic formula

$$x = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$$

where *a*, *b*, and *c* are the coefficients in the quadratic equation

$$ax^2 + bx + c = 0$$

Solving a quadratic equation gives two roots, only one of which has chemical significance. For our problem, the equation's roots are

$$x = \frac{-6.8 \times 10^{-4} \pm \sqrt{(6.8 \times 10^{-4})^2 - (4)(1)(-6.8 \times 10^{-4})}}{(2)(1)}$$

$$x = \frac{-6.8 \times 10^{-4} \pm 5.22 \times 10^{-2}}{2}$$

$$x = 2.57 \times 10^{-2} \text{ or } -2.64 \times 10^{-2}$$

Only the positive root is chemically significant because the negative root gives a negative concentration for H_3O^+. Thus, $[H_3O^+]$ is 2.57×10^{-2} M and the pH is 1.59.

You can extend this approach to calculating the pH of a monoprotic weak base by replacing K_a with K_b, replacing C_{HF} with the weak base's concentration, and solving for $[OH^-]$ in place of $[H_3O^+]$.

? EXERCISE 6.7.4

Calculate the pH of 0.050 M NH_3. State any assumptions you make in solving the problem, limiting the error for any assumption to ±5%. The K_b value for NH_3 is 1.75×10^{-5}.

Answer

To determine the pH of 0.050 M NH_3, we need to consider two equilibrium reactions: the base dissociation reaction for NH_3

$$NH_3(aq) + H_2O(l) \rightleftharpoons OH^-(aq) + NH_4^+(aq)$$

and water's dissociation reaction.

$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq)$$

These two reactions contain four species whose concentrations we need to consider: NH_3, NH_4^+, H_3O^+, and OH^-. We need four equations to solve the problem—these equations are the K_b equation for NH_3

$$K_b = \frac{\left[NH_4^+\right]\left[OH^-\right]}{\left[NH_3\right]} = 1.75 \times 10^{-5}$$

the K_w equation for H_2O

$$K_w = \left[H_3O^+\right]\left[OH^-\right]$$

a mass balance equation on ammonia

$$C_{NH_3} = 0.050\ \text{M} = \left[NH_3\right] + \left[NH_4^+\right]$$

and a charge balance equation

$$\left[H_3O^+\right] + \left[NH_4^+\right] = \left[OH^-\right]$$

To solve this problem, we will make two assumptions. Because NH_3 is a base, our first assumption is

$$\left[OH^-\right] >> \left[H_3O^+\right]$$

which simplifies the charge balance equation to

$$\left[NH_4^+\right] = \left[OH^-\right]$$

Because NH_3 is a weak base, our second assumption is

$$\left[NH_3\right] >> \left[NH_4^+\right]$$

which simplifies the mass balance equation to

$$C_{NH_3} = 0.050\ \text{M} = \left[NH_3\right]$$

Substituting the simplified charge balance equation and mass balance equation into the K_b equation leave us with

$$K_b = \frac{\left[NH_4^+\right]\left[OH^-\right]}{\left[NH_3\right]} = \frac{\left[OH^-\right]\left[OH^-\right]}{C_{NH_3}} = \frac{\left[OH^-\right]^2}{C_{NH_3}} = 1.75 \times 10^{-5}$$

$$\left[OH^-\right] = \sqrt{K_b C_{NH_3}} = \sqrt{\left(1.75 \times 10^{-5}\right)(0.050)} = 9.35 \times 10^{-4}$$

Before we accept this answer, we must verify our two assumptions. The first assumption is that the concentration of OH^- is significantly greater than the concentration of H_3O^+. Using K_w, we find that

$$\left[H_3O^+\right] = \frac{K_w}{\left[OH^-\right]} = \frac{1.00 \times 10^{-14}}{9.35 \times 10^{-4}} = 1.07 \times 10^{-11}$$

Clearly this assumption is acceptable. Our second assumption is that the concentration of NH_3 is significantly greater than the concentration of NH_4^+. Using our simplified charge balance equation, we find that

$$\left[NH_4^+\right] = \left[OH^-\right] = 9.35 \times 10^{-4}$$

Because the concentration of NH_4^+ is 1.9% of C_{NH_3}, our second assumption also is reasonable. Given that $[H_3O^+]$ is 1.07×10^{-11}, the pH is 10.97.

PH OF A POLYPROTIC ACID OR BASE

A more challenging problem is to find the pH of a solution that contains a polyprotic weak acid or one of its conjugate species. As an example, consider the amino acid alanine, whose structure is shown in Figure 6.7.1 . The ladder diagram in Figure 6.7.2 shows alanine's three acid–base forms and their respective areas of predominance. For simplicity, we identify these species as H_2L^+, HL, and L^-.

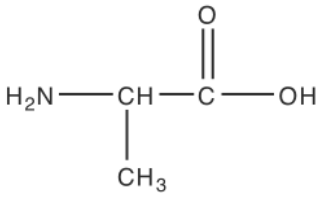


Figure 6.7.1 . Structure of the amino acid alanine, which has pK_a values of 2.348 (–COOH) and 9.867 ($–NH_2$).

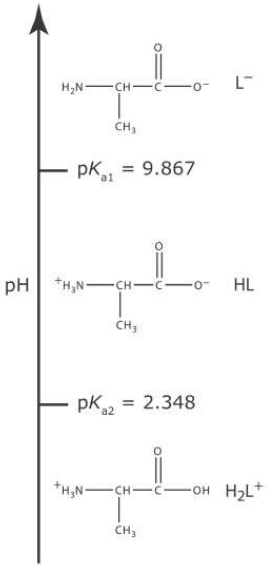


Figure 6.7.2 . Ladder diagram for alanine.

PH OF 0.10 M ALANINE HYDROCHLORIDE (H_2L^+)

Alanine hydrochloride is the salt of the diprotic weak acid H_2L^+ and Cl^-. Because H_2L^+ has two acid dissociation reactions, a complete systematic solution to this problem is more complicated than that for a monoprotic weak acid. The ladder diagram in Figure 6.7.2 helps us simplify the problem. Because the areas of predominance for H_2L^+ and L^- are so far apart, we can assume that a solution of H_2L^+ will not contain a significant amount of L^-. As a result, we can treat H_2L^+ as though it is a monoprotic weak acid. Calculating the pH of 0.10 M alanine hydrochloride, which is 1.72, is left to the reader as an exercise.

PH OF 0.10 M SODIUM ALANINATE (L^-)

The alaninate ion is a diprotic weak base. Because L^- has two base dissociation reactions, a complete systematic solution to this problem is more complicated than that for a monoprotic weak base. Once again, the ladder diagram in Figure 6.7.2 helps us simplify the problem. Because the areas of predominance for H_2L^+ and L^- are so far apart, we can assume that a solution of L^- will not contain a significant amount of H_2L^+. As a result, we can treat L^- as though it is a monoprotic weak base. Calculating the pH of 0.10 M sodium alaninate, which is 11.42, is left to the reader as an exercise.

PH OF 0.10 M ALANINE (HL)

Finding the pH of a solution of alanine is more complicated than our previous two examples because we cannot ignore the presence of either H_2L^+ or L^-. To calculate the solution's pH we must consider alanine's acid dissociation reaction

$$\mathrm{HL}(aq) + \mathrm{H_2O}(l) \rightleftharpoons \mathrm{H_3O^+}(aq) + \mathrm{L^-}(aq)$$

and its base dissociation reaction

$$\mathrm{HL}(aq) + \mathrm{H_2O}(l) \rightleftharpoons \mathrm{OH^-}(aq) + \mathrm{H_2L^+}(aq)$$

and, as always, we must also consider the dissociation of water

$$2\mathrm{H_2O}(l) \rightleftharpoons \mathrm{H_3O^+}(aq) + \mathrm{OH^-}(aq)$$

This leaves us with five unknowns—$[H_2L^+]$, [HL], $[L^-]$, $[H_3O^+]$, and $[OH^-]$—for which we need five equations. These equations are K_{a2} and K_{b2} for alanine

$$K_{a2} = \frac{[\mathrm{H_3O^+}]\,[\mathrm{L^-}]}{[\mathrm{HL}]}$$

$$K_{b2} = \frac{K_w}{K_{a1}} = \frac{\left[OH^-\right]\left[H_2L^+\right]}{[HL]}$$

the K_w equation

$$K_w = \left[H_3O^+\right]\left[OH^-\right]$$

a mass balance equation for alanine

$$C_{HL} = \left[H_2L^+\right] + [HL] + [L^-]$$

and a charge balance equation

$$\left[H_2L^+\right] + \left[H_3O^+\right] = [OH^-] + [L^-]$$

Because HL is a weak acid and a weak base, it seems reasonable to assume that little of it will dissociate and that

$$[HL] >> \left[H_2L^+\right] + [L^-]$$

which allows us to simplify the mass balance equation to

$$C_{HL} = [HL]$$

Next we solve K_{b2} for $[H_2L^+]$

$$\left[H_2L^+\right] = \frac{K_w[HL]}{K_{a1}\left[OH^-\right]} = \frac{\left[H_3O^+\right][HL]}{K_{a1}} = \frac{C_{HL}\left[H_3O^+\right]}{K_{a1}}$$

and solve K_{a2} for $[L^-]$

$$[L^-] = \frac{K_{a2}[HL]}{\left[H_3O^+\right]} = \frac{K_{a2}C_{HL}}{\left[H_3O^+\right]}$$

Substituting these equations for $[H_2L^+]$ and $[L^-]$, and the equation for K_w, into the charge balance equation give us

$$\frac{C_{HL}\left[H_3O^+\right]}{K_{a1}} + \left[H_3O^+\right] = \frac{K_w}{\left[H_3O^+\right]} + \frac{K_{a2}C_{HL}}{\left[H_3O^+\right]}$$

which we simplify to

$$\left[H_3O^+\right]\left(\frac{C_{HL}}{K_{a1}} + 1\right) = \frac{1}{\left[H_3O^+\right]}(K_w + K_{a2}C_{HL})$$

$$\left[H_3O^+\right]^2 = \frac{(K_{a2}C_{HL} + K_w)}{\frac{C_{HL}}{K_{a1}} + 1} = \frac{K_{a1}\left(K_{a2}C_{HL} + K_w\right)}{C_{HL} + K_{a1}}$$

$$\left[H_3O^+\right] = \sqrt{\frac{(K_{a1}K_{a2}C_{HL} + K_{a1}K_w)}{C_{HL} + K_{a1}}}$$

We can further simplify this equation if $K_{a1}K_w << K_{a1}K_{a2}C_{HL}$, and if $K_{a1} << C_{HL}$, leaving us with

$$\left[H_3O^+\right] = \sqrt{K_{a1}K_{a2}}$$

For a solution of 0.10 M alanine the $[H_3O^+]$ is

$$\left[H_3O^+\right] = \sqrt{\left(4.487 \times 10^{-3}\right)\left(1.358 \times 10^{-10}\right)} = 7.806 \times 10^{-7}\ \text{M}$$

or a pH of 6.11.

? EXERCISE 6.7.5

Verify that each assumption in our solution for the pH of 0.10 M alanine is reasonable, using ±5% as the limit for the acceptable error.

Answer

In solving for the pH of 0.10 M alanine, we made the following three assumptions: (a) [HL] >> [H_2L^+] + [L^-]; (b) $K_{a1}K_w$ << $K_{a1}K_{a2}C_{HL}$; and (c) K_{a1} << C_{HL}. Assumptions (b) and (c) are easy to check. The value of K_{a1} (4.487×10^{-3}) is 4.5% of C_{HL} (0.10), and K_{a1}Kw (4.487×10^{-17}) is 0.074% of $K_{a1}K_{a2}C_{HL}$ (6.093×10^{-14}). Each of these assumptions introduces an error of less than ±5%.

To test assumption (a) we need to calculate the concentrations of H_2L^+ and L^-, which we accomplish using the equations for K_{a1} and K_{a2}.

$$\left[H_2L^+\right] = \frac{\left[H_3O^+\right][HL]}{K_{a1}} = \frac{\left(7.807 \times 10^{-7}\right)(0.10)}{4.487 \times 10^{-3}} = 1.74 \times 10^{-5}$$

$$\left[L^-\right] = \frac{K_{a2}[HL]}{\left[H_3O^+\right]} = \frac{\left(1.358 \times 10^{-10}\right)(0.10)}{7.807 \times 10^{-7}} = 1.74 \times 10^{-5}$$

Because these concentrations are less than ±5% of *C*HL, the first assumption also is acceptable.

EFFECT OF COMPLEXATION ON SOLUBILITY

One method for increasing a precipitate's solubility is to add a ligand that forms soluble complexes with one of the precipitate's ions. For example, the solubility of AgI increases in the presence of NH_3 due to the formation of the soluble $Ag(NH_3)_2^+$ complex. As a final illustration of the systematic approach to solving equilibrium problems, let's calculate the molar solubility of AgI in 0.10 M NH_3.

We begin by writing the relevant equilibrium reactions, which includes the solubility of AgI, the acid–base chemistry of NH_3 and H_2O, and the metal-ligand complexation chemistry between Ag^+ and NH_3.

$$AgI(s) \rightleftharpoons Ag^+(aq) + I^-(aq)$$
$$NH_3(aq) + H_2O(l) \rightleftharpoons OH^-(aq) + NH_4^+(aq)$$
$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq)$$
$$Ag^+(aq) + 2NH_3(aq) \rightleftharpoons Ag(NH_3)_2^+(aq)$$

This leaves us with seven unknowns—[Ag^+], [I^-], [NH_3], [NH_4^+], [OH^-], [H_3O^+], and [$Ag(NH_3)_2^+$]—and a need for seven equations. Four of the equations we need to solve this problem are the equilibrium constant expressions

$$K_{sp} = \left[Ag^+\right]\left[I^-\right] = 8.3 \times 10^{-17} \tag{8.7.9}$$

$$K_b = \frac{\left[NH_4^+\right]\left[OH^-\right]}{\left[NH_3\right]} = 1.75 \times 10^{-5} \tag{8.7.10}$$

$$K_w = \left[H_3O^+\right]\left[OH^-\right] = 1.00 \times 10^{-14} \tag{8.7.11}$$

$$\beta_2 = \frac{\left[Ag(NH_3)_2^+\right]}{\left[Ag^+\right]\left[NH_3\right]^2} = 1.7 \times 10^7 \tag{8.7.12}$$

We still need three additional equations. The first of these equations is a mass balance for NH_3.

$$C_{NH_3} = \left[NH_3\right] + \left[NH_4^+\right] + 2 \times \left[Ag(NH_3)_2^+\right] \tag{8.7.13}$$

In writing this mass balance equation we multiply the concentration of $Ag(NH_3)_2^+$ by two since there are two moles of NH_3 per mole of $Ag(NH_3)_2^+$. The second additional equation is a mass balance between iodide and silver. Because AgI is the only source of I^- and Ag^+, each iodide in solution must have an associated silver ion, which may be Ag^+ or $Ag(NH_3)_2^+$; thus

$$\left[I^-\right] = \left[Ag^+\right] + \left[Ag(NH_3)_2^+\right] \tag{8.7.14}$$

Finally, we include a charge balance equation.

$$\left[Ag^+\right] + \left[Ag(NH_3)_2^+\right] + \left[NH_4^+\right] + \left[H_3O^+\right] = \left[OH^-\right] + \left[I^-\right] \tag{8.7.15}$$

Although the problem looks challenging, three assumptions greatly simplify the algebra.

Assumption One. Because the formation of the $Ag(NH_3)_2^+$ complex is so favorable (β_2 is 1.7×10^7), there is very little free Ag^+ in solution and it is reasonable to assume that

$$\left[Ag^+\right] << \left[Ag(NH_3)_2^+\right]$$

Assumption Two. Because NH_3 is a weak base we may reasonably assume that most uncomplexed ammonia remains as NH_3; thus

$$\left[\mathrm{NH_4^+}\right] << \left[\mathrm{NH_3}\right]$$

Assumption Three. Because K_{sp} for AgI is significantly smaller than β_2 for $\mathrm{Ag(NH_3)_2^+}$, the solubility of AgI probably is small enough that very little ammonia is needed to form the metal–ligand complex; thus

$$\left[\mathrm{Ag(NH_3)_2^+}\right] << \left[\mathrm{NH_3}\right]$$

As we use these assumptions to simplify the algebra, let's set ±5% as the limit for error.

Assumption two and assumption three suggest that the concentration of NH_3 is much larger than the concentrations of either $\mathrm{NH_4^+}$ or $\mathrm{Ag(NH_3)_2^+}$, which allows us to simplify the mass balance equation for NH_3 to

$$C_{\mathrm{NH_3}} = \left[\mathrm{NH_3}\right] \tag{8.7.16}$$

Finally, using assumption one, which suggests that the concentration of $\mathrm{Ag(NH_3)_2^+}$ is much larger than the concentration of Ag^+, we simplify the mass balance equation for I^- to

$$\left[\mathrm{I^-}\right] = \left[\mathrm{Ag(NH_3)_2^+}\right] \tag{8.7.17}$$

Now we are ready to combine equations and to solve the problem. We begin by solving Equation 8.7.9 for [Ag^+] and substitute it into β_2 (Equation 8.7.12), which leaves us with

$$\beta_2 = \frac{\left[\mathrm{Ag(NH_3)_2^+}\right]\left[\mathrm{I^-}\right]}{K_{sp}\left[\mathrm{NH_3}\right]^2} \tag{8.7.18}$$

Next we substitute Equation 8.7.16 and Equation 8.7.17 into Equation 8.7.18, obtaining

$$\beta_2 = \frac{\left[\mathrm{I^-}\right]^2}{K_{sp}\left(C_{\mathrm{NH_3}}\right)^2} \tag{8.7.19}$$

Solving Equation 8.7.19 for [I^-] gives

$$\left[\mathrm{I^-}\right] = C_{\mathrm{NH_3}}\sqrt{\beta_2 K_{sp}} =$$

$$(0.10)\sqrt{\left(1.7\times10^{7}\right)\left(8.3\times10^{-17}\right)} = 3.76\times10^{-6}\ \mathrm{M}$$

Because one mole of AgI produces one mole of I^-, the molar solubility of AgI is the same as the [I^-], or 3.8×10^{-6} mol/L.

Before we accept this answer we need to check our assumptions. Substituting [I^-] into Equation 8.7.9, we find that the concentration of Ag^+ is

$$\left[\mathrm{Ag^+}\right] = \frac{K_{\mathrm{p}}}{\left[\mathrm{I^-}\right]} = \frac{8.3\times10^{-17}}{3.76\times10^{-6}} = 2.2\times10^{-11}\ \mathrm{M}$$

Substituting the concentrations of I^- and Ag+ into the mass balance equation for iodide (Equation 8.7.14), gives the concentration of $\mathrm{Ag(NH_3)_2^+}$ as

$$\left[\mathrm{Ag\,(NH_3)_2^+}\right] = \left[\mathrm{I^-}\right] - \left[\mathrm{Ag^+}\right] = 3.76\times10^{-6} - 2.2\times10^{-11} = 3.76\times10^{-6}\ \mathrm{M}$$

Our first assumption that [Ag^+] is significantly smaller than the [$\mathrm{Ag(NH_3)_2^+}$] is reasonable.

Substituting the concentrations of Ag^+ and $\mathrm{Ag(NH_3)_2^+}$ into Equation 8.7.12 and solving for [NH_3], gives

$$\left[\mathrm{NH_3}\right] = \sqrt{\frac{\left[\mathrm{Ag(NH_3)_2^+}\right]}{\left[\mathrm{Ag^+}\right]\beta_2}} = \sqrt{\frac{3.76\times10^{-6}}{\left(2.2\times10^{-11}\right)\left(1.7\times10^{7}\right)}} = 0.10\ \mathrm{M}$$

From the mass balance equation for NH3 (Equation 8.7.12) we see that [$\mathrm{NH_4^+}$] is negligible, verifying our second assumption that [$\mathrm{NH_4^+}$] is significantly smaller than [NH_3]. Our third assumption that [$\mathrm{Ag(NH_3)_2^+}$] is significantly smaller than [NH_3] also is reasonable.

> Did you notice that our solution to this problem did not make use of Equation 8.7.15, the charge balance equation? The reason for this is that we did not try to solve for the concentration of all seven species. If we need to know the reaction mixture's complete composition at equilibrium, then we will need to incorporate the charge balance equation into our solution.

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8.8: ACTIVITY EFFECTS

Careful measurements on the metal–ligand complex $Fe(SCN)^{2+}$ suggest its stability decreases in the presence of inert ions [Lister, M. W.; Rivington, D. E. *Can. J. Chem.* **1995**, *33*, 1572–1590]. We can demonstrate this by adding an inert salt to an equilibrium mixture of Fe^{3+} and SCN^-. Figure 6.9.1 a shows the result of mixing together equal volumes of 1.0 mM $FeCl_3$ and 1.5 mM KSCN, both of which are colorless. The solution's reddish–orange color is due to the formation of $Fe(SCN)^{2+}$.

$$Fe^{3+}(aq) + SCN^-(aq) \rightleftharpoons Fe(SCN)^{2+}(aq) \tag{8.8.1}$$

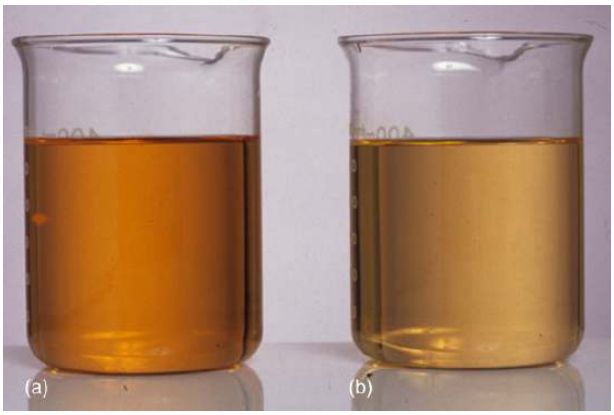


Figure 6.9.1 . The effect of a inert salt on a reaction's equilibrium position is shown by the solutions in these two beakers. The beaker on the left contains equal volumes of 1.0 mM $FeCl_3$ and 1.5 mM KSCN. The solution's color is due to the formation of the metal–ligand complex $Fe(SCN)^{2+}$. Adding 10 g of KNO_3 to the beaker on the left produces the result shown on the right. The lighter color suggests that there is less $Fe(SCN)^{2+}$ as a result of the equilibrium in reaction 8.8.1 shifting to the left.

Adding 10 g of KNO_3 to the solution and stirring to dissolve the solid, produces the result shown in Figure 6.9.1 b. The solution's lighter color suggests that adding KNO_3 shifts reaction 8.8.1 to the left, decreasing the concentration of $Fe(SCN)^{2+}$ and increasing the concentrations of Fe^{3+} and SCN^-. The result is a decrease in the complex's formation constant, K_1.

$$K_1 = \frac{[Fe(SCN)^{2+}]}{[Fe^{3+}]\,[SCN^-]} \tag{8.8.2}$$

Why should adding an inert electrolyte affect a reaction's equilibrium position? We can explain the effect of KNO_3 on the formation of $Fe(SCN)^{2+}$ if we consider the reaction on a microscopic scale. The solution in Figure 6.9.1 b contains a variety of cations and anions: Fe^{3+}, SCN^-, K^+, NO_3^-, H_3O^+, and OH^-. Although the solution is homogeneous, on average, there are slightly more anions in regions near the Fe^{3+} ions, and slightly more cations in regions near the SCN^- ions. As shown in Figure 6.9.2 , each Fe^{3+} ion and each SCN^- ion is surrounded by an ionic atmosphere of opposite charge (δ^- and δ^+) that partially screen the ions from each other. Because each ion's apparent charge at the edge of its ionic atmosphere is less than its actual charge, the force of attraction between the two ions is smaller. As a result, the formation of $Fe(SCN)^{2+}$ is slightly less favorable and the formation constant in Equation 8.8.2 is slightly smaller. Higher concentrations of KNO_3 increase δ^- and δ^+, resulting in even smaller values for the formation constant.

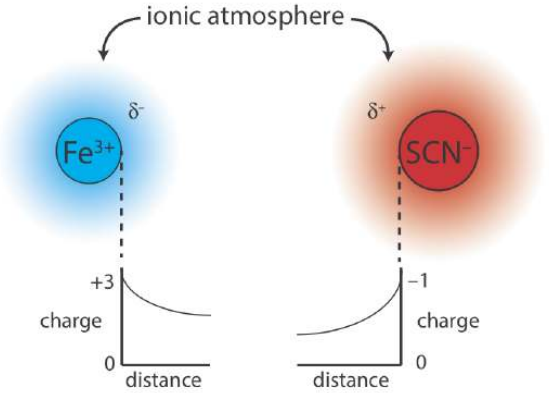


Figure 6.9.2 . Ions of Fe^{3+} and SCN^- are surrounded by ionic atmospheres with net charges of δ^- and δ^+. Because of these ionic atmospheres, each ion's apparent charge at the edge of its ionic atmosphere is less than the ion's actual charge.

IONIC STRENGTH

To factor the concentration of ions into the formation constant for $Fe(SCN)^{2+}$, we need a way to express that concentration in a meaningful way. Because both an ion's concentration and its charge are important, we define the solution's ***ionic strength***, μ as

$$\mu = \frac{1}{2}\sum_{i=1}^{n} c_i z_i^2$$

where c_i and z_i are the concentration and charge of the ith ion.

EXAMPLE 6.9.1

Calculate the ionic strength of a solution of 0.10 M NaCl. Repeat the calculation for a solution of 0.10 M Na_2SO_4.

Solution

The ionic strength for 0.10 M NaCl is

$$\mu = \tfrac{1}{2}\left\{\left[Na^+\right] \times (+1)^2 + \left[Cl^-\right] \times (-1)^2\right\}$$
$$\mu = \tfrac{1}{2}\left\{(0.10) \times (+1)^2 + (0.10) \times (-1)^2\right\} = 0.10\ M$$

For 0.10 M Na_2SO_4 the ionic strength is

$$\mu = \tfrac{1}{2}\left\{\left[Na^+\right] \times (+1)^2 + \left[SO_4^{2-}\right] \times (-2)^2\right\}$$
$$\mu = \tfrac{1}{2}\left\{(0.20) \times (+1)^2 + (0.10) \times (-2)^2\right\} = 0.30\ M$$

In calculating the ionic strengths of these solutions we are ignoring the presence of H_3O^+ and OH^-, and, in the case of Na_2SO_4, the presence of HSO_4^- from the base dissociation reaction of SO_4^{2-}. In the case of 0.10 M NaCl, the concentrations of H_3O^+ and OH^- are 1.0×10^{-7}, which is significantly smaller than the concentrations of Na^+ and Cl^-. Because SO_4^{2-} is a very weak base (K_b = 1.0×10^{-12}), the solution is only slightly basic (pH = 7.5), and the concentrations of H_3O^+, OH^-, and HSO_4^- are negligible. Although we can ignore the presence of H_3O^+, OH^-, and HSO_4^- when we calculate the ionic strength of these two solutions, be aware that an equilibrium reaction can generate ions that might affect the solution's ionic strength.

Note that the unit for ionic strength is molarity, but that a salt's ionic strength need not match its molar concentration. For a 1:1 salt, such as NaCl, ionic strength and molar concentration are identical. The ionic strength of a 2:1 electrolyte, such as Na_2SO_4, is three times larger than the electrolyte's molar concentration.

ACTIVITY AND ACTIVITY COEFFICIENTS

Figure 6.9.1 shows that adding KNO_3 to a mixture of Fe^{3+} and SCN^- decreases the formation constant for $Fe(SCN)^{2+}$. This creates a contradiction. Earlier in this chapter we showed that there is a relationship between a reaction's standard-state free energy, ΔG^o, and its equilibrium constant, K.

$$\triangle G^\circ = -RT \ln K$$

Because a reaction has only one standard-state, its equilibrium constant must be independent of solution conditions. Although ionic strength affects the *apparent* formation constant for $Fe(SCN)^{2+}$, reaction 8.8.1 must have an underlying *thermodynamic* formation constant that is independent of ionic strength.

The apparent formation constant for $Fe(SCN)^{2+}$, as shown in Equation 8.8.2, is a function of concentrations. In place of concentrations, we define the true thermodynamic equilibrium constant using activities. The activity of species A, a_A, is the product of its concentration, $[A]$, and a solution-dependent activity coefficient, γ_A

$$a_A = [A]\gamma_A$$

The true thermodynamic formation constant for $Fe(SCN)^{2+}$, therefore, is

$$K_1 = \frac{a_{Fe(SCN)^{2+}}}{a_{Fe^{3+}} \times a_{SCN^-}} = \frac{\left[Fe(SCN)^{2+}\right]\gamma_{Fe(SCN)^{2+}}}{\left[Fe^{3+}\right]\gamma_{Fe^{3+}}\left[SCN^-\right]\gamma_{SCN^-}}$$

> Unless otherwise specified, the equilibrium constants in the appendices are thermodynamic equilibrium constants.

A species' ***activity coefficient*** corrects for any deviation between its physical concentration and its ideal value. For a gas, a pure solid, a pure liquid, or a non-ionic solute, the activity coefficient is approximately one under most reasonable experimental conditions.

For a gas the proper terms are fugacity and fugacity coefficient, instead of activity and activity coefficient.

For a reaction that involves only these species, the difference between activity and concentration is negligible. The activity coefficient for an ion, however, depends on the solution's ionic strength, the ion's charge, and the ion's size. It is possible to estimate activity coefficients using the extended ***Debye-Hückel equation***

$$\log \gamma_A = \frac{-0.51 \times z_A^2 \times \sqrt{\mu}}{1 + 3.3 \times \alpha_A \times \sqrt{\mu}} \tag{8.8.3}$$

where z_A is the ion's charge, α_A is the hydrated ion's effective diameter in nanometers (Table 6.2), μ is the solution's ionic strength, and 0.51 and 3.3 are constants appropriate for an aqueous solution at 25°C. A hydrated ion's effective radius is the radius of the ion plus those water molecules closely bound to the ion. The effective radius is greater for smaller, more highly charged ions than it is for larger, less highly charged ions.

Table 6.9.1 . Effective Diameters (α) for Selected Ions

ion	effective diameter (nm)
H_3O^+	0.9
Li^+	0.6
Na^+, IO_3^-, HSO_3^-, HCO_3^-, $H_2PO_4^-$	0.45
OH^-, F^-, SCN^-, HS^-, ClO_3^-, ClO_4^-, MnO_4^-	0.35
K^+, Cl^-, Br^-, I^-, CN^-, NO_2^-, NO_3^-	0.3
Cs^+, Tl^+, Ag^+, NH_4^+	0.25
Mg^{2+}, Be^{2+}	0.8
Ca^{2+}, Cu^{2+}, Zn^{2+}, Sn^{2+}, Mn^{2+}, Fe^{2+}, Ni^{2+}, Co^{2+}	0.6
Sr^{2+}, Ba^{2+}, Cd^{2+}, Hg^{2+}, S^{2-}	0.5
Pb^{2+}, SO_4^{2-}, SO_3^{2-}	0.45
Hg_2^{2+}, SO_4^{2-}, $S_2O_3^{2-}$, CrO_4^{2-}, HPO_4^{2-}	0.40
Al^{3+}, Fe^{3+}, Cr^{3+}	0.9
PO_4^{3-}, $Fe(CN)_6^{3-}$	0.4
Zr^{4+}, Ce^{4+}, Sn^{4+}	1.1
$Fe(CN)_6^{4-}$	0.5

Source: Kielland, J. *J. Am. Chem. Soc.* **1937**, *59*, 1675–1678.

Several features of Equation 8.8.3 deserve our attention. First, as the ionic strength approaches zero an ion's activity coefficient approaches a value of one. In a solution where $\mu = 0$, an ion's activity and its concentration are identical. We can take advantage of this fact to determine a reaction's thermodynamic equilibrium constant by measuring the apparent equilibrium constant for several increasingly smaller ionic strengths and extrapolating back to an ionic strength of zero. Second, an activity coefficient is smaller, and the effect of activity is more important, for an ion with a higher charge and a smaller effective radius. Finally, the extended Debye-Hückel equation provides a reasonable estimate of an ion's activity coefficient when the ionic strength is less than 0.1. Modifications to Equation 8.8.3 extend the calculation of activity coefficients to higher ionic strengths [Davies, C. W. *Ion Association*, Butterworth: London, 1962].

INCLUDING ACTIVITY COEFFICIENTS WHEN SOLVING EQUILIBRIUM PROBLEMS

Earlier in this chapter we calculated the solubility of $Pb(IO_3)_2$ in deionized water, obtaining a result of 4.0×10^{-5} mol/L. Because the only significant source of ions is from the solubility reaction, the ionic strength is very low and we can assume that $\gamma \approx 1$ for both Pb^{2+} and IO_3^-. In calculating the solubility of $Pb(IO_3)_2$ in deionized water, we do not need to account for ionic strength. But what if we need to know the solubility of $Pb(IO_3)_2$ in a solution that contains other, inert ions? In this case we need to include activity coefficients in our calculation.

✔ EXAMPLE 6.9.2

Calculate the solubility of $Pb(IO_3)_2$ in a matrix of 0.020 M $Mg(NO_3)_2$.

Solution

We begin by calculating the solution's ionic strength. Since $Pb(IO_3)_2$ is only sparingly soluble, we will assume we can ignore its contribution to the ionic strength; thus

$$\mu = \frac{1}{2}\{(0.020)(+2)^2 + (0.040)(-1)^2\} = 0.060 \text{ M}$$

Next, we use Equation 8.8.3 to calculate the activity coefficients for Pb^{2+} and IO_3^-.

$$\log \gamma_{Pb^{2+}} = \frac{-0.51 \times (+2)^2 \times \sqrt{0.060}}{1 + 3.3 \times 0.45 \times \sqrt{0.060}} = -0.366$$

$$\gamma_{Pb^{2+}} = 0.431$$

$$\log \gamma_{IO_3^-} = \frac{-0.51 \times (-1)^2 \times \sqrt{0.060}}{1 + 3.3 \times 0.45 \times \sqrt{0.060}} = -0.0916$$

$$\gamma_{IO_3^-} = 0.810$$

Defining the equilibrium concentrations of Pb^{2+} and IO_3^- in terms of the variable *x*

Concentrations	$Pb(IO_3)_2$ (*s*)	⇌	Pb^{2+} (*aq*)	+	$2IO_3^-$ (*aq*)
initial	solid		0		0
change	solid		+*x*		+2*x*
equilibrium	solid		*x*		2*x*

and substituting into the thermodynamic solubility product for $Pb(IO_3)_2$ leaves us with

$$K_{sp} = a_{Pb^{2+}} \times a_{IO_3^-}^2 = \gamma_{Pb^{2+}} \left[Pb^{2+}\right] \times \gamma_{IO_3^-}^2 \left[IO_3^-\right]^2 = 2.5 \times 10^{-13}$$

$$K_{sp} = (0.431)(x)(0.810)^2(2x)^2 = 2.5 \times 10^{-13}$$

$$K_{sp} = 1.131x^3 = 2.5 \times 10^{-13}$$

Solving for *x* gives 6.0×10^{-5} and a molar solubility of 6.0×10^{-5} mol/L for $Pb(IO_3)_2$. If we ignore activity, as we did in our earlier calculation, we report the molar solubility as 4.0×10^{-5} mol/L. Failing to account for activity in this case underestimates the molar solubility of $Pb(IO_3)_2$ by 33%.

The solution's equilibrium composition is

$$\left[Pb^{2+}\right] = 6.0 \times 10^{-5}\ M$$
$$\left[IO_3^-\right] = 1.2 \times 10^{-4}\ M$$
$$\left[Mg^{2+}\right] = 0.020\ M$$
$$\left[NO_3^-\right] = 0.040\ M$$

Because the concentrations of both Pb^{2+} and IO_3^- are much smaller than the concentrations of Mg^{2+} and NO_3^- our decision to ignore the contribution of Pb^{2+} and IO_3^- to the ionic strength is reasonable.

How do we handle the calculation if we can not ignore the concentrations of Pb^{2+} and IO_3^- when calculating the ionic strength. One approach is to use the method of successive approximations. First, we recalculate the ionic strength using the concentrations of all ions, including Pb^{2+} and IO_3^-. Next, we recalculate the activity coefficients for Pb^{2+} and IO_3^- using this new ionic strength and then recalculate the molar solubility. We continue this cycle until two successive calculations yield the same molar solubility within an acceptable margin of error.

? EXERCISE 6.9.1

Calculate the molar solubility of Hg_2Cl_2 in 0.10 M NaCl, taking into account the effect of ionic strength. Compare your answer to that from Exercise 6.7.2 in which you ignored the effect of ionic strength.

Answer

We begin by calculating the solution's ionic strength. Because NaCl is a 1:1 ionic salt, the ionic strength is the same as the concentration of NaCl; thus μ = 0.10 M. This assumes, of course, that we can ignore the contributions of Hg_2^{2+} and Cl^- from the solubility of Hg_2Cl_2.

Next we use Equation 8.8.3 to calculate the activity coefficients for Hg_2^{2+} and Cl^-.

$$\log \gamma_{Hg_2^{2+}} = \frac{-0.51 \times (+2)^2 \times \sqrt{0.10}}{1 + 3.3 \times 0.40 \times \sqrt{0.10}} = -0.455$$

$$\gamma_{Hg_2^{2+}} = 0.351$$

$$\log \gamma_{Cl^-} = \frac{-0.51 \times (-1)^2 \times \sqrt{0.10}}{1 + 3.3 \times 0.3 \times \sqrt{0.10}} = -0.12$$

$$\gamma_{Cl^-} = 0.75$$

Defining the equilibrium concentrations of Hg_2^{2+} and Cl^- in terms of the variable *x*

concentrations	Hg2Cl2 (*s*)	⇌	Hg_2^{2+} (*aq*)	+	$2Cl^-$ (*aq*)
initial	solid		0		0.10
change	solid		+*x*		+2*x*
equilibrium	solid		*x*		0.10 + 2*x*

and substituting into the thermodynamic solubility product for Hg_2Cl_2, leave us with

$$K_{sp} = a_{Hg_2^{2+}} (a_{Cl^-})^2 = \gamma_{Hg_2^{2+}} \left[Hg_2^{2+}\right] (\gamma_{Cl^-})^2 \left[Cl^-\right]^2 = 1.2 \times 10^{-18}$$

Because the value of *x* likely is small, let's simplify this equation to

$$(0.351)(x)(0.75)^2(0.1)^2 = 1.2 \times 10^{-18}$$

Solving for *x* gives its value as 6.1×10^{-16} . Because *x* is the concentration of Hg_2^{2+} and 2*x* is the concentration of Cl^-, our decision to ignore their contributions to the ionic strength is reasonable. The molar solubility of Hg_2Cl_2 in 0.10 M NaCl is 6.1×10^{-16} mol/L. In Exercise 6.7.2, where we ignored ionic strength, we determined that the molar solubility of Hg_2Cl_2 is 1.2×10^{-16} mol/L, a result that is $5\times$ smaller than the its actual value.

As Example 6.9.2 and Exercise 6.9.1 show, failing to correct for the effect of ionic strength can lead to a significant error in an equilibrium calculation. Nevertheless, it is not unusual to ignore activities and to assume that the equilibrium constant is expressed in terms of concentrations. There is a practical reason for this—in an analysis we rarely know the exact composition, much less the ionic strength of aqueous samples or of solid samples brought into solution. Equilibrium calculations are a useful guide when we develop an analytical method; however, it only is when we complete an analysis and evaluate the results that can we judge whether our theory matches reality. In the end, work in the laboratory is the most critical step in developing a reliable analytical method.

This is a good place to revisit the meaning of pH. In Chapter 2 we defined pH as

$$pH = -\log\left[H_3O^+\right]$$

Now we see that the correct definition is

$$pH = -\log a_{H_3O^+}$$
$$pH = -\log \gamma_{H_3O^+} \left[H_3O^+\right]$$

Failing to account for the effect of ionic strength can lead to a significant error in the reported concentration of H_3O^+. For example, if the pH of a solution is 7.00 and the activity coefficient for H_3O^+ is 0.90, then the concentration of H_3O^+ is 1.11×10^{-7} M, not 1.00×10^{-7} M, an error of +11%. Fortunately, when we develop and carry out an analytical method, we are more interested in controlling pH than in calculating $[H_3O^+]$. As a result, the difference between the two definitions of pH rarely is of significant concern.

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8.9: USING EXCEL AND R TO SOLVE EQUILIBRIUM PROBLEMS

In solving equilibrium problems we typically make one or more assumptions to simplify the algebra. These assumptions are important because they allow us to reduce the problem to an equation in *x* that we can solve by simply taking a square-root, a cube-root, or by using the quadratic equation. Without these assumptions, most equilibrium problems result in a cubic equation (or a higher-order equation) that is more challenging to solve. Both Excel and R are useful tools for solving such equations.

> Although we focus here on the use of Excel and R to solve equilibrium problems, you also can use WolframAlpha; for details, see Cleary, D. A. "Use of WolframAlpha in Equilibrium Calculations," *Chem. Educator*, **2014**, *19*, 182–186.

EXCEL

Excel offers a useful tool—the Solver function—for finding the chemically significant root of a polynomial equation. In addition, it is easy to solve a system of simultaneous equations by constructing a spreadsheet that allows you to test and evaluate multiple solutions. Let's work through two examples.

EXAMPLE 1: SOLUBILITY OF $PB(IO_3)_2$ IN 0.10 M $PB(NO_3)_2$

In our earlier treatment of this problem we arrived at the following cubic equation

$$4x^3 + 0.40x^2 = 2.5 \times 10^{-13}$$

where *x* is the equilibrium concentration of Pb^{2+}. Although there are several approaches for solving cubic equations with paper and pencil, none are computationally easy. One approach is to iterate in on the answer by finding two values of *x*, one that leads to a result larger than 2.5×10^{-13} and one that gives a result smaller than 2.5×10^{-13}. With boundaries established for the value of *x*, we shift the upper limit and the lower limit until the precision of our answer is satisfactory. Without going into details, this is how Excel's Solver function works.

To solve this problem, we first rewrite the cubic equation so that its right-side equals zero.

$$4x^3 + 0.40x^2 - 2.5 \times 10^{-13} = 0$$

Next, we set up the spreadsheet shown in Figure 6.10.1 a, placing the formula for the cubic equation in cell B2, and entering our initial guess for *x* in cell B1. Because $Pb(IO_3)_2$ is not very soluble, we expect that *x* is small and set our initial guess to 0. Finally, we access the Solver function by selecting **Solver...** from the **Tools** menu, which opens the *Solver Parameters* window.

(a)

	A	B
1	x =	0
2	function	=4*b1^3+0.4*b1^2–2.5e–13

(b)

	A	B
1	x =	7.90565E–07
2	function	–5.71156E–19

Figure 6.10.1 . Spreadsheet demonstrating the use of Excel's Solver function to find the root of a cubic equation. The spreadsheet in (a) shows the cubic equation in cell B2 and the initial guess for the value of *x* in cell B1; Excel replaces the formula with its equivalent value. The spreadsheet in (b) shows the results of running Excel's Solver function.

To define the problem, place the cursor in the box for *Set Target Cell* and then click on cell B2. Select the *Value of:* radio button and enter 0 in the box. Place the cursor in the box for *By Changing Cells:* and click on cell B1. Together, these actions instruct the Solver function to change the value of *x*, which is in cell B1, until the cubic equation in cell B2 equals zero. Before we actually solve the function, we need to consider whether there are any limitations for an acceptable result. For example, we know that *x* cannot be smaller than 0 because a negative concentration is not possible. We also want to ensure that the solution's precision is acceptable. Click on the button labeled **Options...** to open the *Solver Options* window. Checking the option for *Assume Non-Negative* forces the Solver to maintain a positive value for the contents of cell B1, meeting one of our criteria. Setting the precision requires a bit more thought. The Solver function uses the precision to decide when to stop its search, doing so when

$$|\text{expected value} - \text{calculated value}| \times 100 = \text{precision (\%)}$$

where *expected value* is the target cell's desired value (0 in this case), *calculated value* is the function's current value (cell B1 in this case), and *precision* is the value we enter in the box for *Precision*. Because our initial guess of *x* = 0 gives a calculated result of 2.5×10^{-13}, accepting the Solver's default precision of 1×10^{-6} will stop the search after one cycle. To be safe, let's set the precision to 1×10^{-18}. Click **OK** and then **Solve**. When the Solver function finds a solution, the results appear in your spreadsheet (see Figure 6.10.1 b). Click **OK**

to keep the result, or **Cancel** to return to the original values. Note that the answer here agrees with our earlier result of 7.91×10^{-7} M for the solubility of $Pb(IO_3)_2$.

> Be sure to evaluate the reasonableness of Solver's answer. If necessary, repeat the process using a smaller value for the precision.

EXAMPLE 2: PH OF 1.0 M HF

In developing our earlier solution to this problem we began by identifying four unknowns and writing out the following four equations.

$$K_a = \frac{\left[H_3O^+\right]\left[F^-\right]}{[HF]} = 6.8 \times 10^{-4}$$

$$K_w = \left[H_3O^+\right]\left[OH^-\right] = 1.00 \times 10^{-14}$$

$$C_{HF} = [HF] + \left[F^-\right]$$

$$\left[H_3O^+\right] = \left[OH^-\right] + \left[F^-\right]$$

Next, we made two assumptions that allowed us to simplify the problem to an equation that is easy to solve.

$$\left[H_3O^+\right] = \sqrt{K_a C_{HF}} = \sqrt{\left(6.8 \times 10^{-4}\right)(1.0)} = 2.6 \times 10^{-2}$$

Although we did not note this at the time, without making assumptions the solution to our problem is a cubic equation

$$\left[H_3O^+\right]^3 + K_a\left[H_3O^+\right]^2 - \left(K_a C_{HF} + K_w\right)\left[H_3O^+\right] - K_a K_w = 0 \tag{8.9.1}$$

that we can solve using Excel's Solver function. Of course, this assumes that we successfully complete the derivation!

Another option is to use Excel to solve the four equations simultaneously by iterating in on values for [HF], $[F^-]$, $[H_3O^+]$, and $[OH^-]$. Figure 6.10.2 a shows a spreadsheet for this purpose. The cells in the first row contain initial guesses for the equilibrium pH. Using the ladder diagram in Figure 6.8.1, pH values between 1 and 3 seems reasonable. You can add additional columns if you wish to include more pH values. The formulas in rows 2–5 use the definition of pH to calculate $[H_3O^+]$, K_w to calculate $[OH^-]$, the charge balance equation to calculate $[F^-]$, and K_a to calculate [HF]. To evaluate the initial guesses, we use the mass balance expression for HF, rewriting it as

$$[HF] + \left[F^-\right] - C_{HF} = [HF] + [F] - 1.0 = 0$$

and entering it in the last row; the values in these cells gives the calculation's error for each pH.

(a)

	A	B	C	D
1	pH =	3.00	2.00	1.00
2	[H3O+] =	= 10^–b1	= 10^–c1	= 10^–d1
3	[OH-] =	= 1e–14/b2	= 1e–14/c2	= 1e–14/d2
4	[F-] =	= b2 – b3	= c2 – c3	= d2 – d3
5	[HF] =	= (b2 * b4)/6.8e–4	= (c2 * c4)/6.8e–4	= (d2 * d4)/6.8e–4
6	error	= b5 + b4 – 1	= c5 + c4 – 1	= d5 + d4 – 1

(b)

	A	B	C	D
1	pH =	3.00	2.00	1.00
2	[H3O+] =	1.00E-03	1.00E-02	1.00E-1
3	[OH-] =	1.00E–11	1.00E–12	1.00E–13
4	[F-] =	1.00E–03	1.00E–02	1.00E–01
5	[HF] =	0.001470588	0.147058824	14.70588235
6	error	-9.98E-01	-8.43E-01	1.38E+01

(c)

	A	B	C	D
1	pH =	1.59	1.58	1.57
2	[H3O+] =	2.57E-02	2.63E-02	2.69E-02
3	[OH-] =	3.89E-13	3.80E-13	3.72E-13
4	[F-] =	2.57E-02	2.63E-02	2.69E-02
5	[HF] =	0.971608012	1.017398487	1.065347
6	error	-2.69E-03	4.37E-02	9.23E-02

Figure 6.10.2 . Spreadsheet demonstrating the use of Excel to solve a set of simultaneous equations. The spreadsheet in (a) shows the initial guess for $[H_3O^+]$ in the first row, and the formulas that we enter in rows 2–6. Enter the formulas in cells B2–B6 and then copy and paste them into the appropriate cells in the remaining columns. As shown in (b), Excel replaces the formulas with their equivalent values. The spreadsheet in (c) shows the results after our final iteration. See the text for further details.

Figure 6.10.2 b shows the actual values for the spreadsheet in Figure 6.10.2 a. The negative value in cells B6 and C6 means that the combined concentrations of HF and F^- are too small, and the positive value in cell D6 means that their combined concentrations are too large. The actual pH, therefore, is between 1.00 and 2.00. Using these pH values as new limits for the spreadsheet's first row, we continue to narrow the range for the actual pH. Figure 6.10.2 c shows a final set of guesses, with the actual pH falling between 1.59 and 1.58. Because the error for 1.59 is smaller than that for 1.58, we accept a pH of 1.59 as the answer. Note that this is an agreement with our earlier result.

You also can solve this set of simultaneous equations using Excel's Solver function. To do so, create the spreadsheet in Figure 6.10.2 a, but omit all columns other than A and B. Select **Solver...** from the **Tools** menu and define the problem by using B6 for *Set Target Cell*, setting its desired value to 0, and selecting B1 for *By Changing Cells:*. You may need to play with the Solver's options to find a suitable solution to the problem, and it is wise to try several different initial guesses. The Solver function works well for relatively simple problems, such as finding the pH of 1.0 M HF. As problems become more complex and include more unknowns, the Solver function becomes a less reliable tool for solving equilibrium problems.

? EXERCISE 6.10.1

Using Excel, calculate the solubility of AgI in 0.10 M NH_3 without making any assumptions. See our earlier treatment of this problem for the relevant equilibrium reactions and constants.

Answer

For a list of the relevant equilibrium reactions and equilibrium constants, see our earlier treatment of this problem. To solve this problem using Excel, let's set up the following spreadsheet

	A	B
1	pI =	3
2	[I-] =	= 10^–b1
3	[Ag+] =	= 8.3e–17/b2
4	[Ag(NH3)2+] =	= b2 – b3
5	[NH3] =	= (b4/(b3*1.7e7))^0.5
6	[NH4+] =	= 0.10 – b5-2*b4
7	[OH-] =	= 1.75e–5*b5/b6
8	[H3O+] =	= 1.00e–14/b7
9	error	= b3 + b4 + b6 + b8 – b2 – b7

copying the contents of cells B1-B9 into several additional columns. The initial guess for pI in cell B1 gives the concentration of I^- in cell B2. Cells B3–B8 calculate the remaining concentrations, using the K_{sp} to obtain $[Ag^+]$, using the mass balance on iodide and silver to obtain $[Ag(NH_3)_2^+]$, using b2 to calculate $[NH_3]$, using the mass balance on ammonia to find $[NH_4^+]$, using K_b to calculate $[OH^-]$, and using K_w to calculate $[H_3O^+]$. The system's charge balance equation provides a means for determining the calculation's error.

$$\left[Ag^+\right] + \left[Ag(NH_3)_2^+\right] + \left[NH_4^+\right] + \left[H_3O^+\right] - \left[I^-\right] + \left[OH^-\right] = 0$$

The largest possible value for pI, which corresponds to the smallest concentration of I^- and the lowest possible solubility, occurs for a simple, saturated solution of AgI. When $[Ag^+] = [I^-]$, the concentration of iodide is

$$\left[I^-\right] = \sqrt{K_{sp}} = \sqrt{8.3 \times 10^{-17}} = 9.1 \times 10^{-9}$$

which corresponds to a pI of 8.04. Entering initial guesses for pI of 4, 5, 6, 7, and 8 shows that the error changes sign between a pI of 5 and 6. Continuing in this way to narrow down the range for pI, we find that the error function is closest to zero at a pI of 5.42. The concentration of I^- at equilibrium, and the molar solubility of AgI, is 3.8×10^{-6} mol/L, which agrees with our earlier solution to this problem.

R

R has a simple command—**uniroot**—for finding the chemically significant root of a polynomial equation. In addition, it is easy to write a function to solve a set of simultaneous equations by iterating in on a solution. Let's work through two examples.

EXAMPLE 1: SOLUBILITY OF $PB(IO_3)_2$ IN 0.10 M $PB(NO_3)_2$

In our earlier treatment of this problem we arrived at the following cubic equation

$$4x^3 + 0.40x^2 = 2.5 \times 10^{-13}$$

where x is the equilibrium concentration of Pb^{2+}. Although there are several approaches for solving cubic equations with paper and pencil, none are computationally easy. One approach to solving the problem is to iterate in on the answer by finding two values of x, one that leads to a result larger than 2.5×10^{-13} and one that gives a result smaller than 2.5×10^{-13}. Having established boundaries for the value of x, we then shift the upper limit and the lower limit until the precision of our answer is satisfactory. Without going into details, this is how the **uniroot** command works.

The general form of the **uniroot** command is

uniroot(*function*, *lower*, *upper*, *tol*)

where *function* is an object that contains the equation whose root we seek, *lower* and *upper* are boundaries for the root, and *tol* is the desired precision for the root. To create an object that contains the equation, we rewrite it so that its right-side equals zero.

$$4x^3 + 0.40x^2 - 2.5 \times 10^{-13} = 0$$

Next, we enter the following code, which defines our cubic equation as a function with the name *eqn*.

```
> eqn = function(x) {4*x^3 + 0.4*x^2 – 2.5e–13}
```

Because our equation is a function, the **uniroot** command can send a value of x to *eqn* and receive back the equation's corresponding value.

For example, entering

```
> eqn(2)
```

passes the value x = 2 to the function and returns an answer of 33.6.

Finally, we use the **uniroot** command to find the root.

> **uniroot**(eqn, lower = 0, upper = 0.1, tol = 1e–18)

Because $Pb(IO_3)_2$ is not very soluble, we expect that *x* is small and set the lower limit to 0. The choice for the upper limit is less critical. To ensure that the solution has sufficient precision, we set the tolerance to a value that is smaller than the expected root. Figure 6.10.3 shows the resulting output. The value *$root* is the equation's root, which is in good agreement with our earlier result of 7.91×10^{-7} for the molar solubility of $Pb(IO_3)_2$. The other results are the equation's value for the root, the number of iterations needed to find the root, and the root's estimated precision.

```
$root
[1] 7.905663e-07

$f.root
[1] 0

$iter
[1] 46

$estim.prec
[1] 1.827271e-12
```

Figure 6.10.3 . The summary of R's output from the **uniroot** command. See the text for a discussion of how to interpret the results.

EXAMPLE 2: PH OF 1.0 M HF

In developing our earlier solution to this problem we began by identifying four unknowns and writing out the following four equations.

$$K_a = \frac{\left[H_3O^+\right]\left[F^-\right]}{[HF]} = 6.8 \times 10^{-4}$$

$$K_w = \left[H_3O^+\right]\left[OH^-\right] = 1.00 \times 10^{-14}$$

$$C_{HF} = [HF] + \left[F^-\right]$$

$$\left[H_3O^+\right] = \left[OH^-\right] + \left[F^-\right]$$

Next, we made two assumptions that allowed us to simplify the problem to an equation that is easy to solve.

$$\left[H_3O^+\right] = \sqrt{K_a C_{HF}} = \sqrt{\left(6.8 \times 10^{-4}\right)(1.0)} = 2.6 \times 10^{-2}$$

Although we did not note this at the time, without making assumptions the solution to our problem is a cubic equation

$$\left[H_3O^+\right]^3 + K_a\left[H_3O^+\right]^2 - \left(K_a C_{HF} + K_w\right)\left[H_3O^+\right] - K_a K_w = 0$$

that we can solve using the **uniroot** command. Of course, this assumes that we successfully complete the derivation!

Another option is to write a function to solve the four equations simultaneously. Here is the code for this function, which we will call *eval*.

```
> eval = function(pH){
+ h3o = 10^–pH
+ oh = 1e–14/h3o
+ hf = (h3o * f )/6.8e–4
+ error= hf + f – 1
+ output= data.frame(pH, error)
+ print(output)
+}
```

The open curly braces, {, tells R that we intend to enter our function over several lines. When we press enter at the end of a line, R changes its prompt from > to +, indicating that we are continuing to enter the same command. The closed curly brace, }, on the last line indicates that we have completed the function. The command data.frame combines two or more objects into a table, which we then

print out so that we can view the results of the calculations. You can adapt this function to other problems by changing the variable you pass to the function and the equations you include within the function.

Let's examine more closely how this function works. The function accepts a guess for the pH and uses the definition of pH to calculate [H_3O^+], K_w to calculate [OH^-], the charge balance equation to calculate [F^-], and K_a to calculate [HF]. The function then evaluates the solution using the mass balance expression for HF, rewriting it as

$$[\mathrm{HF}] + \left[\mathrm{F}^-\right] - C_{\mathrm{HF}} = [\mathrm{HF}] + \left[\mathrm{F}^-\right] - 1.0 = 0$$

The function then gathers together the initial guess for the pH and the error and prints them as a table.

The beauty of this function is that the object we pass to it, *pH*, can contain many values, which makes it easy to search for a solution. Because HF is an acid, we know that the solution is acidic. This sets an upper limit of 7 for the pH. We also know that the pH of 1.0 M HF is no smaller than 0 as this is the pH if HF was a strong acid. For our first pass, let's enter the following code

> pH= c(7, 6, 5, 4, 3, 2, 1)

> eval(pH)

which varies the pH within these limits. The result, which is shown in Figure 6.10.4 a, indicates that the pH is less than 2 and greater than 1 because it is in this interval that the error changes sign.

(a)

	pH	error
1	7	-1.0000000
2	6	-0.9999990
3	5	-0.9999899
4	4	-0.9998853
5	3	-0.9975294
6	2	-0.8429412
7	1	13.8058824
8	0	1470.5882353

(b)

	pH	error
1	2.0	-0.84294118
2	1.9	-0.75433822
3	1.8	-0.61475600
4	1.7	-0.39459566
5	1.6	-0.04700269
6	1.5	0.50221101
7	1.4	1.37053600
8	1.3	2.74406936
9	1.2	4.91761295
10	1.1	8.35821730
11	1.0	13.80588235

(c)

	pH	error
1	1.60	-0.047002688
2	1.59	-0.002688030
3	1.58	0.043701167
4	1.57	0.092262348
5	1.56	0.143097544
6	1.55	0.196313586
7	1.54	0.252022331
8	1.53	0.310340901
9	1.52	0.371391928
10	1.51	0.435303816
11	1.50	0.502211012

Figure 6.10.4 . The output of three iterations to find the pH for a solution of 1.0 M HF. The results are for pH values between (a) 7 and 0, (b) 2.0 and 1.0, and (c) 1.60 M and 1.50. The columns labeled "error" show an evaluation of the mass balance equation for HF, with positive values indicating that the pH is too low and negative values indicating that the pH is too high.

For our second pass, let's explore pH values between 2.0 and 1.0 to further narrow down the problem's solution.

> pH = c(2.0, 1.9, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, 1.2, 1.1, 1.0)

> eval(pH)

The result in Figure 6.10.4 b show that the pH must be less than 1.6 and greater than 1.5. A third pass between these limits gives the result shown in Figure 6.10.4 c, which is consistent with our earlier result of a pH 1.59.

? EXERCISE 6.10.2

Using R, calculate the solubility of AgI in 0.10 M NH_3 without making any assumptions. See our earlier treatment of this problem for the relevant equilibrium reactions and constants.

Answer

To solve this problem, let's use the following function

```
> eval = function(pI){
+ I = 10^–pI
+ Ag = 8.3e–17/I
+ AgNH3 = Ag – I
+ NH3 = (AgNH3/(1.7e7*Ag))^0.5
+ NH4 = 0.10-NH3 – 2 * AgNH3
```

+ OH = 1.75e–5 * NH3/NH4

+ H3O = 1e–14/OH

+ error = Ag + AgNH3 + NH4 + H3O – OH – I

+ output = data.frame(pI, error)

+ print(output)

+}

The function accepts an initial guess for pI and calculates the concentrations of each species in solution using the definition of pI to calculate $[I^-]$, using the K_{sp} to obtain $[Ag^+]$, using the mass balance on iodide and silver to obtain $[Ag(NH_3)_2^+]$, using β_2 to calculate $[NH_3]$, using the mass balance on ammonia to find $[NH_4^+]$, using K_b to calculate $[OH^-]$, and using K_w to calculate $[H_3O^+]$. The system's charge balance equation provides a means for determining the calculation's error.

$$\left[Ag^+\right] + \left[Ag(NH_3)_2^+\right] + \left[NH_4^+\right] + \left[H_3O^+\right] - \left[I^-\right] + \left[OH^-\right] = 0$$

The largest possible value for pI—corresponding to the smallest concentration of I^- and the lowest possible solubility—occurs for a simple, saturated solution of AgI. When $[Ag^+] = [I^-]$, the concentration of iodide is

$$\left[I^-\right] = \sqrt{K_{sp}} = \sqrt{8.3 \times 10^{-17}} = 9.1 \times 10^{-9}$$

corresponding to a pI of 8.04. The following session shows the function in action.

> pI=c(4, 5, 6, 7, 8)

> eval(pI)

pI error
1 4 -2.56235615
2 5 -0.16620930
3 6 0.07337101
4 7 0.09734824
5 8 0.09989073

> pI =c(5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0)

> eval(pI)

pI error
1 5.1 -0.11144658
2 5.2 -0.06794105
3 5.3 -0.03336475
4 5.4 -0.00568116
5 5.5 0.01571549
6 5.6 0.03308929
7 5.7 0.04685937
8 5.8 0.05779214
9 5.9 0.06647475
10 6.0 0.07337101

> pI =c(5.40, 5.41, 5.42, 5.43, 5.44, 5.45, 5.46, 5.47, 5.48, 5.49, 5.50)

> eval(pI)

pI error
1 5.40 -0.0056811605
2 5.41 -0.0030715484
3 5.42 0.0002310369
4 5.43 -0.0005134898
5 5.44 0.0028281878
6 5.45 0.0052370980
7 5.46 0.0074758181
8 5.47 0.0096260370

9 5.48 0.0117105498

10 5.49 0.0137387291

11 5.50 0.0157154889

The error function is closest to zero at a pI of 5.42. The concentration of I^- at equilibrium, and the molar solubility of AgI, is 3.8×10^{-6} mol/L, which agrees with our earlier solution to this problem.

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8.10: SOME FINAL THOUGHTS ON EQUILIBRIUM CALCULATIONS

In this chapter we developed several tools to evaluate the composition of a system at equilibrium. These tools differ in how precisely they allow us to answer questions involving equilibrium chemistry. They also differ in how easy they are to use. An important part of having several tools to choose from is knowing when to each is most useful. If you need to know whether a reaction if favorable or you need to estimate a solution's pH, then a ladder diagram usually will meet your needs. On the other hand, if you require a more accurate or more precise estimate of a compound's solubility, then a rigorous calculation that includes activity coefficients is necessary.

A critical part of solving an equilibrium problem is to know what equilibrium reactions to include. The need to include all relevant reactions is obvious, and at first glance this does not appear to be a significant problem—it is, however, a potential source of significant errors. The tables of equilibrium constants in this textbook, although extensive, are a small subset of all known equilibrium constants, which makes it easy to overlook an important equilibrium reaction. Commercial and freeware computational programs with extensive databases are available for equilibrium modeling, two examples of which are Visual Minteq (Windows only) and CurTiPot (for Excel); Visual Minteq can model acid–base, solubility, complexation, and redox equilibria; CurTiPot is limited to acid–base equilibria. Both programs account for the effect of activity. The R package CHNOSZ is used to model aqueous geochemistry systems and the properities of proteins.

An integrated set of tools for thermodynamic calculations in aqueous geochemistry and geobiochemistry. Functions are provided for writing balanced reactions to form species from user-selected basis species and for calculating the standard molal properties of species and reactions, including the standard Gibbs energy and equilibrium constant. Calculations of the non-equilibrium chemical affinity and equilibrium chemical activity of species can be portrayed on diagrams as a function of temperature, pressure, or activity of basis species; in two dimensions, this gives a maximum affinity or predominance diagram. The diagrams have formatted chemical formulas and axis labels, and water stability limits can be added to Eh-pH, oxygen fugacity- temperature, and other diagrams with a redox variable. The package has been developed to handle common calculations in aqueous geochemistry, such as solubility due to complexation of metal ions, mineral buffers of redox or pH, and changing the basis species across a diagram ("mosaic diagrams"). CHNOSZ also has unique capabilities for comparing the compositional and thermodynamic properties of different proteins.

Finally, a consideration of equilibrium chemistry can only help us decide if a reaction is favorable; however, it does not guarantee that the reaction occurs. How fast a reaction approaches its equilibrium position does not depend on the reaction's equilibrium constant because the rate of a chemical reaction is a kinetic, not a thermodynamic, phenomenon. We will consider kinetic effects and their application in analytical chemistry in Chapter 13.

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8.11: PROBLEMS

1. Write equilibrium constant expressions for the following reactions. What is the value for each reaction's equilibrium constant?

(a) $NH_3(aq) + H_3O^+(aq) \rightleftharpoons NH_4^+(aq)$

(b) $PbI_2(s) + S^{2-}(aq) \rightleftharpoons PbS(s) + 2I^-(aq)$

(c) $CdY^{2-}(aq) + 4CN^-(aq) \rightleftharpoons Cd(CN)_4^{2-}(aq) + Y^{4-}(aq)$; *note: Y is the shorthand symbol for EDTA*

(d) $AgCl(s) + 2NH_3(aq) \rightleftharpoons Ag(NH_3)_2^+(aq) + Cl^-(aq)$

(e) $BaCO_3(s) + 2H_3O^+(aq) \rightleftharpoons Ba^{2+}(aq) + H_2CO_3(aq) + 2H_2O(l)$

2. Use a ladder diagram to explain why the first reaction is favorable and why the second reaction is unfavorable.

$$H_3PO_4(aq) + F^-(aq) \rightleftharpoons HF(aq) + H_2PO_4^-(aq)$$

$$H_3PO_4(aq) + 2F^-(aq) \rightleftharpoons 2HF(aq) + HPO_4^{2-}(aq)$$

Determine the equilibrium constant for these reactions and verify that they are consistent with your ladder diagram.

3. Calculate the potential for the following redox reaction for a solution in which [Fe^{3+}] = 0.050 M, [Fe^{2+}] = 0.030 M, [Sn^{2+}] = 0.015 M and [Sn^{4+}] = 0.020 M.

$$2Fe^{3+}(aq) + Sn^{2+}(aq) \rightleftharpoons Sn^{4+}(aq) + 2Fe^{2+}(aq)$$

4. Calculate the standard state potential and the equilibrium constant for each of the following redox reactions. Assume that [H_3O^+] is 1.0 M for an acidic solution and that [OH^-] is 1.0 M for a basic solution. Note that these reactions are not balanced. Reactions (a) and (b) are in acidic solution; reaction (c) is in a basic solution.

(a) $MnO_4^-(aq) + H_2SO_3(aq) \rightleftharpoons Mn^{2+}(aq) + SO_4^{2-}(aq)$

(b) $IO_3^-(aq) + I^-(aq) \rightleftharpoons I_2(aq)$

(c) $ClO^-(aq) + I^-(aq) \rightleftharpoons IO_3^-(aq) + Cl^-(aq)$

5. One analytical method for determining the concentration of sulfur is to oxidize it to SO_4^{2-} and then precipitate it as $BaSO_4$ by adding $BaCl_2$. The mass of the resulting precipitate is proportional to the amount of sulfur in the original sample. The accuracy of this method depends on the solubility of $BaSO_4$, the reaction for which is shown here.

$$BaSO_4(s) \rightleftharpoons Ba^{2+}(aq) + SO_4^{2-}(aq)$$

For each of the following, predict the affect on the solubility of $BaSO_4$: (a) decreasing the solution's pH; (b) adding more $BaCl_2$; and (c) increasing the solution's volume by adding H_2O.

6. Write a charge balance equation and one or more mass balance equations for the following solutions.

(a) 0.10 M NaCl

(b) 0.10 M HCl

(c) 0.10 M HF

(d) 0.10 M NaH_2PO_4

(e) $MgCO_3$ (saturated solution)

(f) 0.10 M $Ag(CN)_2^-$ (prepared using $AgNO_3$ and KCN)

(g) 0.10 M HCl and 0.050 M $NaNO_2$

7. Use the systematic approach to equilibrium problems to calculate the pH of the following solutions. Be sure to state and justify any assumptions you make in solving the problems.

(a) 0.050 M $HClO_4$

(b) 1.00×10^{-7} M HCl

(c) 0.025 M HClO

(d) 0.010 M HCOOH

(e) 0.050 M $Ba(OH)_2$

(f) 0.010 M C_5H_5N

8. Construct ladder diagrams for the following diprotic weak acids (H_2A) and estimate the pH of 0.10 M solutions of H_2A, NaHA, and Na_2A.

(a) maleic acid

(b) malonic acid

(c) succinic acid

9. Use the systematic approach to solving equilibrium problems to calculate the pH of (a) malonic acid, H_2A; (b) sodium hydrogenmalonate, NaHA; and (c) sodium malonate, Na_2A. Be sure to state and justify any assumptions you make in solving the problems.

10. Ignoring activity effects, calculate the molar solubility of Hg_2Br_2 in the following solutions. Be sure to state and justify any assumption you make in solving the problems.

(a) a saturated solution of Hg_2Br_2

(b) 0.025 M $Hg_2(NO_3)_2$ saturated with Hg_2Br_2

(c) 0.050 M NaBr saturated with Hg_2Br_2

11. The solubility of CaF_2 is controlled by the following two reactions

$$\mathrm{CaF_2}(s) \rightleftharpoons \mathrm{Ca^{2+}}(aq) + 2\mathrm{F^-}(aq)$$

$$\mathrm{HF}(aq) + \mathrm{H_2O}(l) \rightleftharpoons \mathrm{H_3O^+}(aq) + \mathrm{F^-}(aq)$$

Calculate the molar solubility of CaF_2 in a solution that is buffered to a pH of 7.00. Use a ladder diagram to help simplify the calculations. How would your approach to this problem change if the pH is buffered to 2.00? What is the solubility of CaF_2 at this pH? Be sure to state and justify any assumptions you make in solving the problems.

12. Calculate the molar solubility of $Mg(OH)_2$ in a solution buffered to a pH of 7.00. How does this compare to its solubility in unbuffered deionized water with an initial pH of 7.00? Be sure to state and justify any assumptions you make in solving the problem.

13. Calculate the solubility of Ag_3PO_4 in a solution buffered to a pH of 9.00. Be sure to state and justify any assumptions you make in solving the problem.

14. Determine the equilibrium composition of saturated solution of AgCl. Assume that the solubility of AgCl is influenced by the following reactions

$$\mathrm{AgCl}(s) \rightleftharpoons \mathrm{Ag^+}(aq) + \mathrm{Cl^-}(aq)$$

$$\mathrm{Ag^+}(aq) + \mathrm{Cl^-}(aq) \rightleftharpoons \mathrm{AgCl}(aq)$$

$$\mathrm{AgCl}(aq) + \mathrm{Cl^-}(aq) \rightleftharpoons \mathrm{AgCl_2^-}(aq)$$

Be sure to state and justify any assumptions you make in solving the problem.

15. Calculate the ionic strength of the following solutions

(a) 0.050 M NaCl

(b) 0.025 M $CuCl_2$

(c) 0.10 M Na_2SO_4

16. Repeat the calculations in Problem 10, this time correcting for the effect of ionic strength. Be sure to state and justify any assumptions you make in solving the problems.

17. Over what pH range do you expect $Ca_3(PO_4)_2$ to have its minimum solubility?

18. Construct ladder diagrams for the following systems, each of which consists of two or three equilibrium reactions. Using your ladder diagrams, identify all reactions that are likely to occur in each system?

(a) HF and H_3PO_4

(b) $\mathrm{Ag(CN)_2^-}$, $\mathrm{Ni(CN)_4^{2-}}$, and $\mathrm{Fe(CN)_6^{3-}}$

(c) $\mathrm{Cr_2O_7^{2-}/Cr^{3+}}$ and $\mathrm{Fe^{3+}/Fe^{2+}}$

19. Calculate the pH of the following acid–base buffers. Be sure to state and justify any assumptions you make in solving the problems.

(a) 100.0 mL of 0.025 M formic acid and 0.015 M sodium formate

(b) 50.00 mL of 0.12 M NH_3 and 3.50 mL of 1.0 M HCl

(c) 5.00 g of Na_2CO_3 and 5.00 g of $NaHCO_3$ diluted to 0.100 L

20. Calculate the pH of the buffers in Problem 19 after adding 5.0 mL of 0.10 M HCl. Be sure to state and justify any assumptions you make in solving the problems.

21. Calculate the pH of the buffers in Problem 19 after adding 5.0 mL of 0.10 M NaOH. Be sure to state and justify any assumptions you make in solving the problems.

22. Consider the following hypothetical complexation reaction between a metal, M, and a ligand, L

$$\mathrm{M}(aq) + \mathrm{L}(aq) \rightleftharpoons \mathrm{ML}(aq)$$

for which the formation constant is 1.5×10^8 . (a) Derive an equation similar to the Henderson–Hasselbalch equation that relates pM to the concentrations of L and ML. (b) What is the pM for a solution that contains 0.010 mol of M and 0.020 mol of L? (c) What is pM if you add 0.002 mol of M to this solution? Be sure to state and justify any assumptions you make in solving the problem.

23. A redox buffer contains an oxidizing agent and its conjugate reducing agent. Calculate the potential of a solution that contains 0.010 mol of Fe^{3+} and 0.015 mol of Fe^{2+}. What is the potential if you add sufficient oxidizing agent to convert 0.002 mol of Fe^{2+} to Fe^{3+}? Be sure to state and justify any assumptions you make in solving the problem.

24. Use either Excel or R to solve the following problems. For these problems, make no simplifying assumptions.

(a) the solubility of CaF_2 in deionized water

(b) the solubility of AgCl in deionized water

(c) the pH of 0.10 M fumaric acid

25. Derive equation 6.10.1 for the rigorous solution to the pH of 0.1 M HF.

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8.12: ADDITIONAL RESOURCES

The following experiments involve the experimental determination of equilibrium constants, the characterization of buffers, and, in some cases, demonstrations of the importance of activity effects.

- "The Effect of Ionic Strength on an Equilibrium Constant (A Class Study)" in *Chemical Principles in Practice*, J. A. Bell, Ed., Addison-Wesley: Reading, MA, 1967.
- "Equilibrium Constants for Calcium Iodate Solubility and Iodic Acid Dissociation" in *Chemical Principles in Practice*, J. A. Bell, Ed., Addison-Wesley: Reading, MA, 1967.
- "The Solubility of Silver Acetate" in *Chemical Principles in Practice*, J. A. Bell, Ed., Addison-Wesley: Reading, MA, 1967.
- Cobb, C. L.; Love, G. A. "Iron(III) Thiocyanate Revisited: A Physical Chemistry Equilibrium Lab Incorporating Ionic Strength Effects," *J. Chem. Educ.* **1998**, *75*, 90–92.
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- Russo, S. O.; Hanania, I. H. "Buffer Capacity," *J. Chem. Educ.* **1987**, *64*, 817–819.
- Stolzberg, R. J. "Discovering a Change in Equilibrium Constant with Change in Ionic Strength," *J. Chem. Educ.* **1999**, *76*, 640–641.
- Wiley, J. D. "The Effect of Ionic Strength on the Solubility of an Electrolyte," *J. Chem. Educ.* **2004**, *81*, 1644–1646.

A nice discussion of Berthollet's discovery of the reversibility of reactions is found in

- Roots-Bernstein, R. S. *Discovering*, Harvard University Press: Cambridge, MA, 1989.

The following texts provide additional coverage of equilibrium chemistry.

- Butler, J. N. *Ionic Equilibria: A Mathematical Approach*; Addison-Wesley: Reading, MA, 1964.
- Butler, J. N. *Solubility and pH Calculations*; Addison-Wesley: Reading, MA, 1973.
- Fernando, Q.; Ryan, M. D. *Calculations in Analytical Chemistry*, Harcourt Brace Jovanovich: New York, 1982.
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- Freiser, H. *Concepts and Calculations in Analytical Chemistry*, CRC Press: Boca Raton, 1992.
- Gordus, A. A. *Schaum's Outline of Analytical Chemistry*; McGraw-Hill: New York, 1985.
- Ramette, R. W. *Chemical Equilibrium and Analysis*, Addison-Wesley: Reading, MA, 1981.

The following papers discuss a variety of general aspects of equilibrium chemistry.

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- Gordus, A. A. "Chemical Equilibrium I. The Thermodynamic Equilibrium Concept," *J. Chem. Educ.* **1991**, *68*, 138–140.
- Gordus, A. A. "Chemical Equilibrium II. Deriving an Exact Equilibrium Equation," *J. Chem. Educ.* **1991**, *68*, 215–217.
- Gordus, A. A. "Chemical Equilibrium III. A Few Math Tricks," *J. Chem. Educ.* **1991**, *68*, 291–293.
- Gordus, A. A. "Chemical Equilibrium IV. Weak Acids and Bases," *J. Chem. Educ.* **1991**, *68*, 397–399.
- Gordus, A. A. "Chemical Equilibrium VI. Buffer Solutions," *J. Chem. Educ.* **1991**, *68*, 656–658.
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- Reijenga, J.; Van Hoof, A.; van Loon, A.; Teunissen, B. "Development of Methods for the Determination of pK_a Values," *Analytical Chemistry Insights*, **2013**, *8*, 53–71.
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- Chaston, S. "Calculating Complex Equilibrium Concentrations by a Next Guess Factor Method," *J. Chem. Educ.* **1993**, *70*, 622–624.
- Donato, H. "Graphing Calculator Strategies for Solving Chemical Equilibrium Problems," J. Chem. Educ. 1999, 76, 632–634.
- Glaser, R. E. Delarosa, M. A.; Salau, A. O.; Chicone, C. "Dynamical Approach to Multiequilibria Problems for Mixtures of Acids and Their Conjugate Bases," *J. Chem. Educ.* **2014**, *91*, 1009–1016.
- Olivieri, A. C. "Solution of Acid-Base Equilibria by Successive Approximations," *J. Chem. Educ.* **1990**, *67*, 229–231.
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- Weltin, E. "Calculating Equilibrium Concentrations," *J. Chem. Educ.* **1992**, *69*, 393–396.

- Weltin, E. “Calculating Equilibrium Concentrations for Stepwise Binding of Ligands and Polyprotic Acid-Base Systems,” *J. Chem. Educ.* **1993**, *70*, 568–571.
- Weltin, E. “Equilibrium Calculations are Easier Than You Think - But You do Have to Think!” *J. Chem. Educ.* **1993**, *70*, 571–573.
- Weltin, E. “Calculating Equilibrium Concentrations by Iteration: Recycle Your Approximations,” J. Chem. Educ. 1995, 72, 36–38.

Additional historical background on the development of the Henderson-Hasselbalch equation is provided by the following papers.

- de Levie, R. “The Henderson Approximation and the Mass Action Law of Guldberg and Waage,” *Chem. Educator* **2002**, *7*, 132–135.
- de Levie, R. “The Henderson-Hasselbalch Equation: Its History and Limitations,” *J. Chem. Educ.* **2003**, *80*, 146.

A simulation is a useful tool for helping students gain an intuitive understanding of a topic. Gathered here are some simulations for teaching equilibrium chemistry.

- Edmonson, L. J.; Lewis, D. L. “Equilibrium Principles: A Game for Students,” *J. Chem. Educ.* **1999**, *76*, 502.
- Huddle, P. A.; White, M. W.; Rogers, F. “Simulations for Teaching Chemical Equilibrium,” *J. Chem. Educ.* **2000**, *77*, 920–926.

The following papers provide additional resources on ionic strength, activity, and the effect of ionic strength and activity on equilibrium reactions and pH.

- Clark, R. W.; Bonicamp, J. M. “The K_{sp}-Solubility Conundrum,” *J. Chem. Educ.* **1998**, *75*, 1182– 1185.
- de Levie, R. “On Teaching Ionic Activity Effects: What, When, and Where?” *J. Chem. Educ.* **2005**, *82*, 878–884.
- McCarty, C. G.; Vitz, E. “pH Paradoxes: Demonstrating That It Is Not True That pH = –log[H^+],”*J. Chem. Educ.* **2006**, *83*, 752–757.
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- Solomon, T. “The Definition and Unit of Ionic Strength,” *J. Chem. Educ.* **2001**, *78*, 1691–1692.

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- Hawkes, S. J. “What Should We Teach Beginners About Solubility and Solubility Products?” *J. Chem. Educ.* **1998**, *75*, 1179–1181.
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8.13: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

Analytical chemistry is more than a collection of techniques; it is the application of chemistry to the analysis of samples. As we will see in later chapters, almost all analytical methods use chemical reactivity to accomplish one or more of the following: dissolve a sample, separate analytes from interferents, transform an analyte into a more useful form, or provide a signal. Equilibrium chemistry and thermodynamics provide us with a means for predicting which reactions are likely to be favorable.

The most important types of reactions are precipitation reactions, acid–base reactions, metal-ligand complexation reactions, and oxidation–reduction reactions. In a precipitation reaction two or more soluble species combine to produce an insoluble precipitate, which we characterize using a solubility product.

An acid–base reaction occurs when an acid donates a proton to a base. The reaction's equilibrium position is described using either an acid dissociation constant, K_a, or a base dissociation constant, K_b. The product of K_a and K_b for an acid and its conjugate base is the dissociation constant for water, K_w.

When a ligand donates one or more pairs of electron to a metal ion, the result is a metal–ligand complex. Two types of equilibrium constants are used to describe metal–ligand complexation: stepwise formation constants and overall formation constants. There are two stepwise formation constants for the metal–ligand complex ML_2, each of which describes the addition of one ligand; thus, K_1 represents the addition of the first ligand to M, and K_2 represents the addition of the second ligand to ML. Alternatively, we can use a cumulative, or overall formation constant, β_2, for the metal–ligand complex ML_2, in which both ligands are added to M.

In an oxidation–reduction reaction, one of the reactants is oxidized and another reactant is reduced. Instead of using an equilibrium constants to characterize an oxidation–reduction reactions, we use the potential, positive values of which indicate a favorable reaction. The Nernst equation relates this potential to the concentrations of reactants and products.

Le Châtelier's principle provides a means for predicting how a system at equilibrium responds to a change in conditions. If we apply a stress to a system at equilibrium—by adding a reactant or product, by adding a reagent that reacts with a reactant or product, or by changing the volume—the system will respond by moving in the direction that relieves the stress.

You should be able to describe a system at equilibrium both qualitatively and quantitatively. You can develop a rigorous solution to an equilibrium problem by combining equilibrium constant expressions with appropriate mass balance and charge balance equations. Using this systematic approach, you can solve some quite complicated equilibrium problems. If a less rigorous answer is acceptable, then a ladder diagram may help you estimate the equilibrium system's composition.

Solutions that contain relatively similar amounts of a weak acid and its conjugate base experience only a small change in pH upon the addition of a small amount of strong acid or of strong base. We call these solutions buffers. A buffer can also be formed using a metal and its metal–ligand complex, or an oxidizing agent and its conjugate reducing agent. Both the systematic approach to solving equilibrium problems and ladder diagrams are useful tools for characterizing buffers.

A quantitative solution to an equilibrium problem may give an answer that does not agree with experimental results if we do not consider the effect of ionic strength. The true, thermodynamic equilibrium constant is a function of activities, a, not concentrations. A species' activity is related to its molar concentration by an activity coefficient, γ. Activity coefficients are estimated using the extended Debye-Hückel equation, making possible a more rigorous treatment of equilibria.

KEY TERMS

acid	acid dissociation constant	activity
activity coefficient	amphiprotic	base
base dissociation constant	buffer	buffer capacity
charge balance equation	common ion effect	cumulative formation constant
dissociation constant	enthalpy	entropy
equilibrium	equilibrium constant	extended Debye-Hückel equation
formation constant	Gibb's free energy	half-reaction
Henderson–Hasselbalch equation	ionic strength	ladder diagram
Le Châtelier's principle	ligand	mass balance equation
metal–ligand complex	method of successive approximations	monoprotic
Nernst equation	oxidation	oxidizing agent
pH scale	polyprotic	potential
precipitate	redox reaction	reducing agent
reduction	standard-state	standard potential
steady state	stepwise formation constant	solubility product

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CHAPTER OVERVIEW

9: TITRIMETRIC METHODS

Titrimetry, in which volume serves as the analytical signal, first appears as an analytical method in the early eighteenth century. Titrimetric methods were not well received by the analytical chemists of that era because they could not duplicate the accuracy and precision of a gravimetric analysis. Not surprisingly, few standard texts from that era include titrimetric methods of analysis.

Precipitation gravimetry first developed as an analytical method without a general theory of precipitation. An empirical relationship between a precipitate's mass and the mass of analyte in a sample—what analytical chemists call a gravimetric factor—was determined experimentally by taking a known mass of analyte through the procedure. Today, we recognize this as an early example of an external standardization. Gravimetric factors were not calculated using the stoichiometry of a precipitation reaction because chemical formulas and atomic weights were not yet available! Unlike gravimetry, the development and acceptance of titrimetry required a deeper understanding of stoichiometry, of thermodynamics, and of chemical equilibria. By the 1900s, the accuracy and precision of titrimetric methods were comparable to that of gravimetric methods, establishing titrimetry as an accepted analytical technique.

9.1: Buffer Solutions
9.2: Overview of Titrimetry
9.3: Acid–Base Titrations
9.4: Complexation Titrations
9.5: Problems
9.6: Additional Resources
9.7: Chapter Summary and Key Terms

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9.1: BUFFER SOLUTIONS

Adding as little as 0.1 mL of concentrated HCl to a liter of H_2O shifts the pH from 7.0 to 3.0. Adding the same amount of HCl to a liter of a solution that 0.1 M in acetic acid and 0.1 M in sodium acetate, however, results in a negligible change in pH. Why do these two solutions respond so differently to the addition of HCl?

A mixture of acetic acid and sodium acetate is one example of an acid–base ***buffer***. To understand how this buffer works to limit the change in pH, we need to consider its acid dissociation reaction

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq)$$

and its corresponding acid dissociation constant

$$K_a = \frac{\left[CH_3COO^-\right]\left[H_3O^+\right]}{\left[CH_3COOH\right]} = 1.75 \times 10^{-5} \tag{9.1.1}$$

Taking the negative log of the terms in Equation 9.1.1 and solving for pH leaves us with the result shown here.

$$\mathrm{pH} = \mathrm{p}K_\mathrm{a} + \log \frac{\left[CH_3COO^-\right]}{\left[CH_3COOH\right]}$$

$$\mathrm{pH} = 4.76 + \log \frac{\left[CH_3COO^-\right]}{\left[CH_3COOH\right]} \tag{9.1.2}$$

> You may recall that we developed these same equations in Chapter 6.6 when we introduced ladder diagrams.

Buffering occurs because of the logarithmic relationship between pH and the concentration ratio of acetate and acetic acid. Here is an example to illustrate this point. If the concentrations of acetic acid and acetate are equal, the buffer's pH is 4.76. If we convert 10% of the acetate to acetic acid, by adding a strong acid, the ratio $[CH_3COO^-]/[CH_3COOH]$ changes from 1.00 to 0.818, and the pH decreases from 4.76 to 4.67—a decrease of only 0.09 pH units.

> The ratio $[CH_3COO^-]/[CH_3COOH]$ becomes 0.9/1.1 = 0.818 and the pH becomes
>
> $$\mathrm{pH} = 4.76 + \log(0.818) = 4.67$$

SYSTEMATIC SOLUTION TO BUFFER PROBLEMS

Equation 9.1.2 is written in terms of the equilibrium concentrations of CH_3COOH and of CH_3COO^-. A more useful relationship relates a buffer's pH to the initial concentrations of the weak acid and the weak base. We can derive a general buffer equation by considering the following reactions for a weak acid, HA, and the soluble salt of its conjugate weak base, NaA.

$$NaA(s) \rightarrow Na^+(aq) + A^-(aq)$$
$$HA(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + A^-(aq)$$
$$2H_2O(l) \rightleftharpoons H_3O^+(aq) + OH^-(aq)$$

Because the concentrations of Na^+, A^-, HA, H_3O^+, and OH^- are unknown, we need five equations to define the solution's composition. Two of these equations are the equilibrium constant expressions for HA and H_2O.

$$K_a = \frac{\left[H_3O^+\right]\left[A^-\right]}{\left[HA\right]} \tag{9.1.3}$$

$$K_w = \left[H_3O^+\right]\left[OH^-\right]$$

The remaining three equations are mass balance equations for HA and Na^+

$$C_{HA} + C_{NaA} = \left[HA\right] + \left[A^-\right] \tag{9.1.4}$$

$$C_{NaA} = \left[Na^+\right] \tag{9.1.5}$$

and a charge balance equation

$$\left[H_3O^+\right] + \left[Na^+\right] = \left[OH^-\right] + \left[A^-\right] \tag{9.1.6}$$

Substituting Equation 9.1.5 into Equation 9.1.6 and solving for [A⁻] gives

$$\left[\mathrm{A}^-\right] = C_{\mathrm{NaA}} - \left[\mathrm{OH}^-\right] + \left[\mathrm{H_3O}^+\right] \tag{9.1.7}$$

Next, we substitute Equation 9.1.7 into Equation 9.1.4, which gives the concentration of HA as

$$[\mathrm{HA}] = C_{\mathrm{HA}} + \left[\mathrm{OH}^-\right] - \left[\mathrm{H_3O}^+\right] \tag{9.1.8}$$

Finally, we substitute Equation 9.1.7 and Equation 9.1.8 into Equation 9.1.3 and solve for pH to arrive at a general equation for a buffer's pH.

$$\mathrm{pH} = \mathrm{p}K_\mathrm{a} + \log \frac{C_{\mathrm{NaA}} - \left[\mathrm{OH}^-\right] + \left[\mathrm{H_3O}^+\right]}{C_{\mathrm{HA}} + \left[\mathrm{OH}^-\right] - \left[\mathrm{H_3O}^+\right]}$$

If the initial concentrations of the weak acid, C_{HA}, and the weak base, C_{NaA}. are significantly greater than $[\mathrm{H_3O}^+]$ and $[\mathrm{OH}^-]$, then we can simplify the general equation to the ***Henderson–Hasselbalch equation***.

$$\mathrm{pH} = \mathrm{p}K_\mathrm{a} + \log \frac{C_{\mathrm{NaA}}}{C_{\mathrm{HA}}} \tag{9.1.9}$$

As outlined below, the Henderson–Hasselbalch equation provides a simple way to calculate the pH of a buffer, and to determine the change in pH upon adding a strong acid or strong base.

Lawrence Henderson (1878-1942) first developed a relationship between $[\mathrm{H_3O}^+]$, [HA], and $[\mathrm{A}^-]$ while studying the buffering of blood. Kurt Hasselbalch (1874-1962) modified Henderson's equation by transforming it to the logarithmic form shown in Equation 9.1.9. The assumptions that lead to Equation 9.1.9 result in a minimal error in pH (<±5%) for larger concentrations of HA and A^-, for concentrations of HA and A^- that are similar in magnitude, and for weak acid's with pK_a values closer to 7. For most problems in this textbook, Equation 9.1.9 provides acceptable results. Be sure, however, to test your assumptions. For a discussion of the Henderson–Hasselbalch equation, including the error inherent in Equation 9.1.9, see Po, H. N.; Senozan, N. M. "The Henderson–Hasselbalch Equation: Its History and Limitations," *J. Chem. Educ.* **2001**, *78*, 1499–1503.

EXAMPLE 6.8.1

Calculate the pH of a buffer that is 0.020 M in $\mathrm{NH_3}$ and 0.030 M in $\mathrm{NH_4Cl}$. What is the pH after we add 1.0 mL of 0.10 M NaOH to 0.10 L of this buffer?

Solution

The acid dissociation constant for $\mathrm{NH_4^+}$ is 5.70×10^{-10}, which is a pK_a of 9.24. Substituting the initial concentrations of $\mathrm{NH_3}$ and $\mathrm{NH_4Cl}$ into Equation 9.1.9 and solving, we find that the buffer's pH is

$$\mathrm{pH} = 9.24 + \log \frac{0.020}{0.030} = 9.06$$

With a pH of 9.06, the concentration of $\mathrm{H_3O}^+$ is 8.71×10^{-10} and the concentration of OH^- is 1.15×10^{-5}. Because both of these concentrations are much smaller than either $C_{\mathrm{NH_3}}$ or $C_{\mathrm{NH_4Cl}}$, the approximations used to derive Equation 9.1.9 are reasonable.

Adding NaOH converts a portion of the $\mathrm{NH_4^+}$ to $\mathrm{NH_3}$ following reaction

$$\mathrm{NH_4^+}(aq) + \mathrm{OH}^-(aq) \rightleftharpoons \mathrm{H_2O}(l) + \mathrm{NH_3}(aq)$$

Because this reaction's equilibrium constant is so large (it is equal to $(K_\mathrm{b})^{-1}$ or 5.7×10^4), we may treat the reaction as if it goes to completion. The new concentrations of $\mathrm{NH_4^+}$ and $\mathrm{NH_3}$ are

$$C_{\mathrm{NH_4^+}} = \frac{\text{mol } \mathrm{NH_4^+} - \text{ mol}\mathrm{OH}^-}{V_{\text{total}}}$$

$$C_{\mathrm{NH_4^+}} = \frac{(0.030\ \mathrm{M})(0.10\ \mathrm{L}) - (0.10\ \mathrm{M})\left(1.0 \times 10^{-3}\ \mathrm{L}\right)}{0.10\ \mathrm{L} + 1.0 \times 10^{-3}\ \mathrm{L}} = 0.029\ \mathrm{M}$$

$$C_{\mathrm{NH_3}} = \frac{\text{mol } \mathrm{NH_3} + \text{mol } \mathrm{OH}^-}{V_{\text{total}}}$$

$$C_{\mathrm{NH_3}} = \frac{(0.020\ \mathrm{M})(0.10\ \mathrm{L}) + (0.10\ \mathrm{M})\left(1.0 \times 10^{-3}\ \mathrm{L}\right)}{0.10\ \mathrm{L} + 1.0 \times 10^{-3}\ \mathrm{L}} = 0.021\ \mathrm{M}$$

Substituting these concentrations into the equation 6.60 gives a pH of

$$\text{pH} = 9.24 + \log \frac{0.021}{0.029} = 9.10$$

Note that adding NaOH increases the pH from 9.06 to 9.10. As we expect, adding a base makes the pH more basic. Checking to see that the pH changes in the right direction is one way to catch a calculation error.

? EXERCISE 6.8.1

Calculate the pH of a buffer that is 0.10 M in KH_2PO_4 and 0.050 M in Na_2HPO_4. What is the pH after we add 5.0 mL of 0.20 M HCl to 0.10 L of this buffer. Use Appendix 11 to find the appropriate K_a value.

Answer

The acid dissociation constant for $H_2PO_4^-$ is 6.32×10^{-8}, or a pK_a of 7.199. Substituting the initial concentrations of $H_2PO_4^-$ and HPO_4^{2-} into Equation 9.1.9 and solving gives the buffer's pH as

$$\text{pH} = 7.199 + \log \frac{\left[HPO_4^{2-}\right]}{\left[H_2PO_4^-\right]} = 7.199 + \log \frac{0.050}{0.10} = 6.898 \approx 6.90$$

Adding HCl converts a portion of HPO_4^{2-} to $H_2PO_4^-$ as a result of the following reaction

$$HPO_4^{2-}(aq) + H_3O^+(aq) \rightleftharpoons H_2O(l) + H_2PO_4^-(aq)$$

Because this reaction's equilibrium constant is so large (it is 1.59×10^7), we may treat the reaction as if it goes to completion. The new concentrations of $H_2PO_4^-$ and HPO_4^{2-} are

$$C_{H_2PO_4^{4-}} = \frac{\text{mol } H_2PO_4^- + \text{mol HCl}}{V_{\text{total}}}$$

$$C_{H_2PO_4^{4-}} = \frac{(0.10\text{ M})(0.10\text{ L}) + (0.20\text{ M})\left(5.0 \times 10^{-3}\text{ L}\right)}{0.10\text{ L} + 5.0 \times 10^{-3}\text{ L}} = 0.105\text{ M}$$

$$C_{HPO_4^{2-}} = \frac{\text{mol } HPO_4^{2-} - \text{mol HCl}}{V_{\text{total}}}$$

$$C_{HPO_4^{2-}} = \frac{(0.05\text{ M})(0.10\text{ L}) - (0.20\text{ M})\left(5.0 \times 10^{-3}\text{ L}\right)}{0.10\text{ L} + 5.0 \times 10^{-3}\text{ L}} = 0.0381\text{ M}$$

Substituting these concentrations into Equation 9.1.9 gives a pH of

$$\text{pH} = 7.199 + \log \frac{\left[HPO_4^{2-}\right]}{\left[H_2PO_4^-\right]} = 7.199 + \log \frac{0.0381}{0.105} = 6.759 \approx 6.76$$

As we expect, adding HCl decreases the buffer's pH by a small amount, dropping from 6.90 to 6.76.

We can use a multiprotic weak acid to prepare buffers at as many different pH's as there are acidic protons, with the Henderson–Hasselbalch equation applying in each case. For example, for malonic acid (pK_{a1} = 2.85 and pK_{a2} = 5.70) we can prepare buffers with pH values of

$$\text{pH} = 2.85 + \log \frac{C_{HM^-}}{C_{H_2M}}$$

$$\text{pH} = 5.70 + \log \frac{C_{M^{2-}}}{C_{HM^-}}$$

where H_2M, HM^- and M^{2-} are malonic acid's different acid–base forms.

Although our treatment of buffers is based on acid–base chemistry, we can extend buffers to equilibria that involve complexation or redox reactions. For example, the Nernst equation for a solution that contains Fe^{2+} and Fe^{3+} is similar in form to the Henderson-Hasselbalch equation.

$$E = E^\circ_{Fe^{3+}/Fe^{2+}} - 0.05916 \log \frac{\left[Fe^{2+}\right]}{\left[Fe^{3+}\right]}$$

A solution that contains similar concentrations of Fe^{2+} and Fe^{3+} is buffered to a potential near the standard state reduction potential for Fe^{3+}. We call such solutions redox buffers. Adding a strong oxidizing agent or a strong reducing agent to a redox buffer results in a small change in potential.

REPRESENTING BUFFER SOLUTIONS WITH LADDER DIAGRAMS

A ladder diagram provides a simple way to visualize a solution's predominate species as a function of solution conditions. It also provides a convenient way to show the range of solution conditions over which a buffer is effective. For example, an acid–base buffer exists when the concentrations of the weak acid and its conjugate weak base are similar. For convenience, let's assume that an acid–base buffer exists when

$$\frac{1}{10} \leq \frac{[CH_3COO^-]}{[CH_3COOH]} \leq \frac{10}{1}$$

Substituting these ratios into the Henderson–Hasselbalch equation

$$\mathrm{pH} = \mathrm{p}K_\mathrm{a} + \log\frac{1}{10} = \mathrm{p}K_\mathrm{a} - 1$$
$$\mathrm{pH} = \mathrm{p}K_\mathrm{a} + \log\frac{10}{1} = \mathrm{p}K_\mathrm{a} + 1$$

shows that an acid–base buffer works over a pH range of $pK_a \pm 1$.

Using the same approach, it is easy to show that a metal-ligand complexation buffer for ML_n exists when

$$\mathrm{pL} = \log K_n \pm 1 \text{ or } \mathrm{pL} = \log \beta_n \pm \frac{1}{n}$$

where K_n or β_n is the relevant stepwise or overall formation constant. For an oxidizing agent and its conjugate reducing agent, a redox buffer exists when

$$E = E^\circ \pm \frac{1}{n} \times \frac{RT}{F} = E^\circ \pm \frac{0.05916}{n} (\text{ at } 25^\circ\mathrm{C})$$

Figure 6.8.1 shows ladder diagrams with buffer regions for several equilibrium systems.

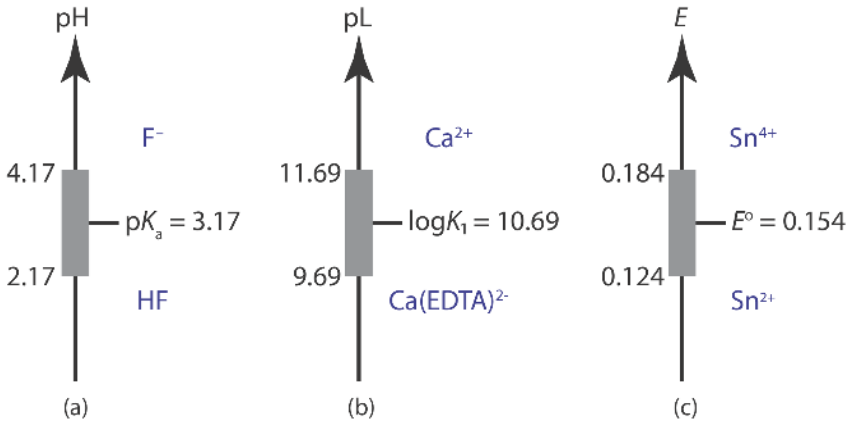


Figure 6.8.1 . Ladder diagrams showing buffer regions shaded in grey for (a) an acid–base buffer of HF and F^-; (b) a metal–ligand complexation buffer of Ca^{2+} and $Ca(EDTA)^{2-}$; and (c) an oxidation–reduction (redox) buffer of Sn^{4+} and Sn^{2+}.

PREPARING A BUFFER

Buffer capacity is the ability of a buffer to resist a change in pH when we add to it a strong acid or a strong base. A buffer's capacity to resist a change in pH is a function of the concentrations of the weak acid and the weak base, as well as their relative proportions. The importance of the weak acid's concentration and the weak base's concentration is obvious. The more moles of weak acid and weak base a buffer has, the more strong base or strong acid it can neutralize without a significant change in its pH.

> Although a higher concentration of buffering agents provides greater buffer capacity, there are reasons for using smaller concentrations, including the formation of unwanted precipitates and the tolerance of biological systems for high concentrations of dissolved salts.

The relative proportions of a weak acid and a weak base also affects how much the pH changes when we add a strong acid or a strong base. A buffer that is equimolar in weak acid and weak base requires a greater amount of strong acid or strong base to bring about a one unit change in pH. Consequently, a buffer is most effective against the addition of strong acids or strong bases when its pH is near the weak acid's pK_a value.

Buffer solutions are often prepared using standard "recipes" found in the chemical literature [see, for example, (a) Bower, V. E.; Bates, R. G. *J. Res. Natl. Bur. Stand. (U. S.)* **1955**, *55*, 197– 200; (b) Bates, R. G. *Ann. N. Y. Acad. Sci.* **1961**, *92*, 341–356; (c) Bates, R. G. *Determination of pH*, 2nd ed.; Wiley-Interscience: New York, 1973]. In addition, there are computer programs and on-line calculators to aid in preparing buffers [(a) Lambert, W. J. J. Chem. Educ. 1990, 67, 150–153; (b) http://www.bioinformatics.org/JaMBW/5/4/index.html.]. Perhaps the simplest way to make a buffer, however, is to prepare a solution that contains an appropriate conjugate weak acid and weak base, measure its pH, and then adjust the pH to the desired value by adding small portions of either a strong acid or a strong base.

> A good "rule of thumb" when choosing a buffer is to select one whose reagents have a pK_a value close to your desired pH.

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9.2: OVERVIEW OF TITRIMETRY

In ***titrimetry*** we add a reagent, called the ***titrant***, to a solution that contains another reagent, called the ***titrand***, and allow them to react. The type of reaction provides us with a simple way to divide titrimetry into four categories: acid–base titrations, in which an acidic or basic titrant reacts with a titrand that is a base or an acid; complexometric titrations , which are based on metal–ligand complexation; redox titrations, in which the titrant is an oxidizing or reducing agent; and precipitation titrations, in which the titrand and titrant form a precipitate.

> We will deliberately avoid the term analyte at this point in our introduction to titrimetry. Although in most titrations the analyte is the titrand, there are circumstances where the analyte is the titrant. Later, when we discuss specific titrimetric methods, we will use the term analyte where appropriate.

Despite their difference in chemistry, all titrations share several common features. Before we consider individual titrimetric methods in greater detail, let's take a moment to consider some of these similarities. As you work through this chapter, this overview will help you focus on the similarities between different titrimetric methods. You will find it easier to understand a new analytical method when you can see its relationship to other similar methods.

EQUIVALENCE POINTS AND END POINTS

If a titration is to give an accurate result we must combine the titrand and the titrant in stoichiometrically equivalent amounts. We call this stoichiometric mixture the ***equivalence point***. Unlike precipitation gravimetry, where we add the precipitant in excess, an accurate titration requires that we know the exact volume of titrant at the equivalence point, V_{eq}. The product of the titrant's equivalence point volume and its molarity, M_T, is equal to the moles of titrant that react with the titrand.

$$\text{moles titrant } = M_T \times V_{eq}$$

If we know the stoichiometry of the titration reaction, then we can calculate the moles of titrand.

Unfortunately, for most titration reactions there is no obvious sign when we reach the equivalence point. Instead, we stop adding the titrant at an ***end point*** of our choosing. Often this end point is a change in the color of a substance, called an ***indicator***, that we add to the titrand's solution. The difference between the end point's volume and the equivalence point's volume is a determinate ***titration error***. If the end point and the equivalence point volumes coincide closely, then this error is insignificant and is safely ignored. Clearly, selecting an appropriate end point is of critical importance.

VOLUME AS A SIGNAL

> Instead of measuring the titrant's volume, we may choose to measure its mass. Although generally we can measure mass more precisely than we can measure volume, the simplicity of a volumetric titration makes it the more popular choice.

Almost any chemical reaction can serve as a titrimetric method provided that it meets the following four conditions. The first condition is that we must know the stoichiometry between the titrant and the titrand. If this is not the case, then we cannot convert the moles of titrant used to reach the end point to the moles of titrand in our sample. Second, the titration reaction effectively must proceed to completion; that is, the stoichiometric mixing of the titrant and the titrand must result in their complete reaction. Third, the titration reaction must occur rapidly. If we add the titrant faster than it can react with the titrand, then the end point and the equivalence point will differ significantly. Finally, we must have a suitable method for accurately determining the end point. These are significant limitations and, for this reason, there are several common titration strategies.

> Depending on how we are detecting the endpoint, we may stop the titration too early or too late. If the end point is a function of the titrant's concentration, then adding the titrant too quickly leads to an early end point. On the other hand, if the end point is a function of the titrand's concentration, then the end point exceeds the equivalence point.

A simple example of a titration is an analysis for Ag^+ using thiocyanate, SCN^-, as a titrant.

$$Ag^+(aq) + SCN^-(aq) \rightleftharpoons Ag(SCN)(s)$$

This reaction occurs quickly and with a known stoichiometry, which satisfies two of our requirements. To indicate the titration's end point, we add a small amount of Fe^{3+} to the analyte's solution before we begin the titration. When the reaction between Ag^+ and SCN^- is

complete, formation of the red-colored $Fe(SCN)^{2+}$ complex signals the end point. This is an example of a ***direct titration*** since the titrant reacts directly with the analyte.

> This is an example of a precipitation titration. You will find more information about precipitation titrations later in this chapter.

If the titration's reaction is too slow, if a suitable indicator is not available, or if there is no useful direct titration reaction, then an indirect analysis may be possible. Suppose you wish to determine the concentration of formaldehyde, H_2CO, in an aqueous solution. The oxidation of H_2CO by I_3^-

$$H_2CO(aq) + I_3^-(aq) + 3OH^-(aq) \rightleftharpoons HCO_2^-(aq) + 3I^-(aq) + 2H_2O(1)$$

is a useful reaction, but it is too slow for a titration. If we add a known excess of I_3^- and allow its reaction with H_2CO to go to completion, we can titrate the unreacted I_3^- with thiosulfate, $S_2O_3^{2-}$.

$$I_3^-(aq) + 2S_2O_3^{2-}(aq) \rightleftharpoons S_4O_6^{2-}(aq) + 3I^-(aq)$$

The difference between the initial amount of I_3^- and the amount in excess gives us the amount of I_3^- that reacts with the formaldehyde. This is an example of a ***back titration***.

> This is an example of a redox titration. You will find more information about redox titrations later in this chapter.

Calcium ions play an important role in many environmental systems. A direct analysis for Ca^{2+} might take advantage of its reaction with the ligand ethylenediaminetetraacetic acid (EDTA), which we represent here as Y^{4-}.

$$Ca^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons CaY^{2-}(aq)$$

Unfortunately, for most samples this titration does not have a useful indicator. Instead, we react the Ca^{2+} with an excess of MgY^{2-}

$$Ca^{2+}(aq) + MgY^{2-}(aq) \rightleftharpoons CaY^{2-}(aq) + Mg^{2+}(aq)$$

releasing an amount of Mg^{2+} equivalent to the amount of Ca^{2+} in the sample. Because the titration of Mg^{2+} with EDTA

$$Mg^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons MgY^{2-}(aq)$$

has a suitable end point, we can complete the analysis. The amount of EDTA used in the titration provides an indirect measure of the amount of Ca^{2+} in the original sample. Because the species we are titrating was displaced by the analyte, we call this a ***displacement titration***.

> MgY^{2-} is the Mg^{2+}–EDTA metal–ligand complex. You can prepare a solution of MgY^{2-} by combining equimolar solutions of Mg^{2+} and EDTA. This is an example of a complexation titration. You will find more information about complexation titrations later in this chapter.

If a suitable reaction with the analyte does not exist it may be possible to generate a species that we can titrate. For example, we can determine the sulfur content of coal by using a combustion reaction to convert sulfur to sulfur dioxide

$$S(s) + O_2(g) \rightarrow SO_2(g)$$

and then convert the SO_2 to sulfuric acid, H_2SO_4, by bubbling it through an aqueous solution of hydrogen peroxide, H_2O_2.

$$SO_2(g) + H_2O_2(aq) \longrightarrow H_2SO_4(aq)$$

Titrating H_2SO_4 with NaOH

$$H_2SO_4(aq) + 2NaOH(aq) \rightleftharpoons 2H_2O(l) + Na_2SO_4(aq)$$

provides an indirect determination of sulfur.

> This is an example of an acid–base titration. You will find more information about acid–base titrations later in this chapter.

TITRATION CURVES

To find a titration's end point, we need to monitor some property of the reaction that has a well-defined value at the equivalence point. For example, the equivalence point for a titration of HCl with NaOH occurs at a pH of 7.0. A simple method for finding the equivalence point is to monitor the titration mixture's pH using a pH electrode, stopping the titration when we reach a pH of 7.0. Alternatively, we can add an indicator to the titrand's solution that changes color at a pH of 7.0.

> Why a pH of 7.0 is the equivalence point for this titration is a topic we will cover later in the section on acid–base titrations.

Suppose the only available indicator changes color at a pH of 6.8. Is the difference between this end point and the equivalence point small enough that we safely can ignore the titration error? To answer this question we need to know how the pH changes during the titration.

A ***titration curve*** provides a visual picture of how a property of the titration reaction changes as we add the titrant to the titrand. The titration curve in Figure 9.1.1 , for example, was obtained by suspending a pH electrode in a solution of 0.100 M HCl (the titrand) and monitoring the pH while adding 0.100 M NaOH (the titrant). A close examination of this titration curve should convince you that an end point pH of 6.8 produces a negligible titration error. Selecting a pH of 11.6 as the end point, however, produces an unacceptably large titration error.

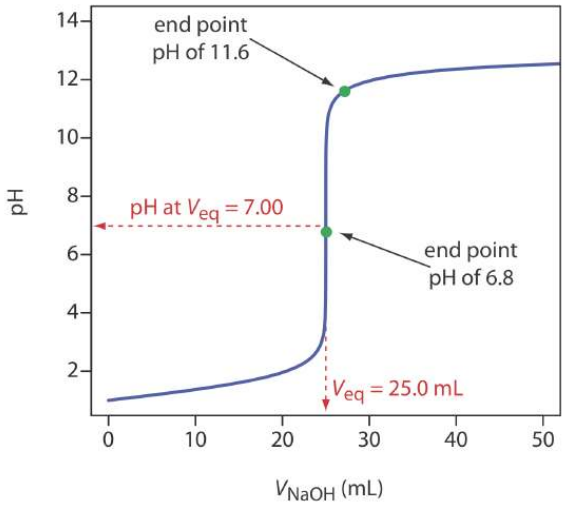


Figure 9.1.1 . Typical acid–base titration curve showing how the titrand's pH changes with the addition of titrant. The titrand is a 25.0 mL solution of 0.100 M HCl and the titrant is 0.100 M NaOH. The titration curve is the solid blue line, and the equivalence point volume (25.0 mL) and pH (7.00) are shown by the dashed red lines. The green dots show two end points. The end point at a pH of 6.8 has a small titration error, and the end point at a pH of 11.6 has a larger titration error.

> For the titration curve in Figure 9.1.1 , the volume of titrant to reach a pH of 6.8 is 24.99995 mL, a titration error of -2.00×10^{-4}% relative to the equivalence point of 25.00 mL. Typically, we can read the volume only to the nearest ±0.01 mL, which means this uncertainty is too small to affect our results. The volume of titrant to reach a pH of 11.6 is 27.07 mL, or a titration error of +8.28%. This is a significant error.

The shape of the titration curve in Figure 9.1.1 is not unique to an acid–base titration. Any titration curve that follows the change in concentration of a species in the titration reaction (plotted logarithmically) as a function of the titrant's volume has the same general sigmoidal shape. Several additional examples are shown in Figure 9.1.2 .

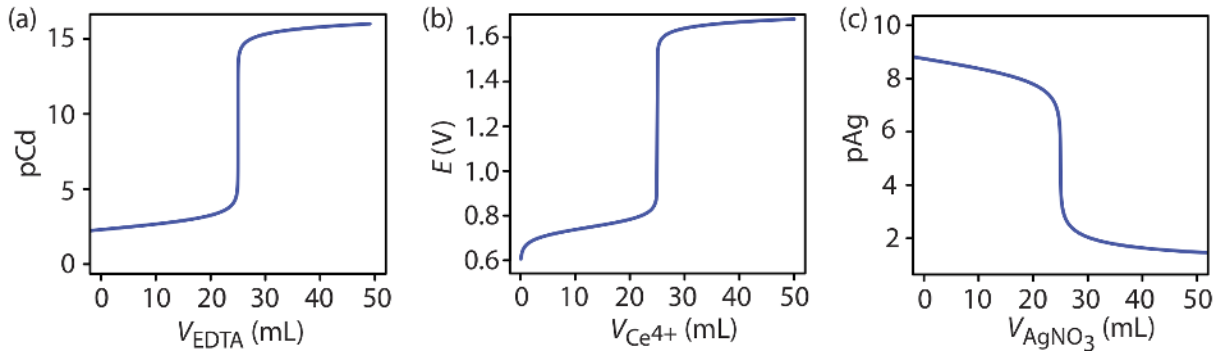


Figure 9.1.2 . Additional examples of titration curves. (a) Complexation titration of 25.0 mL of 1.0 mM Cd^{2+} with 1.0 mM EDTA at a pH of 10. The *y*-axis displays the titrand's equilibrium concentration as pCd. (b) Redox titration of 25.0 mL of 0.050 M Fe^{2+} with 0.050 M Ce^{4+} in 1 M $HClO_4$. The *y*-axis displays the titration mixture's electrochemical potential, *E*, which, through the Nernst equation is a logarithmic function of concentrations. (c) Precipitation titration of 25.0 mL of 0.10 M NaCl with 0.10 M $AgNO_3$. The *y*-axis displays the titrant's equilibrium concentration as pAg.

The titrand's or the titrant's concentration is not the only property we can use to record a titration curve. Other parameters, such as the temperature or absorbance of the titrand's solution, may provide a useful end point signal. Many acid–base titration reactions, for example, are exothermic. As the titrant and the titrand react, the temperature of the titrand's solution increases. Once we reach the equivalence point, further additions of titrant do not produce as exothermic a response. Figure 9.1.3 shows a typical ***thermometric titration curve*** where the intersection of the two linear segments indicates the equivalence point.

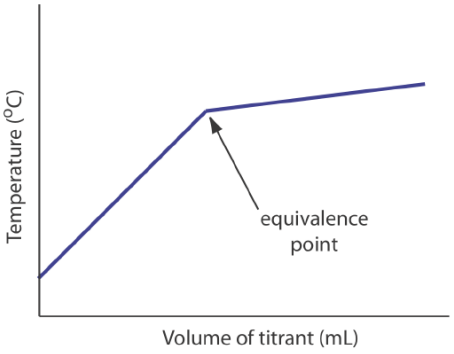


Figure 9.1.3 . Example of a thermometric titration curve showing the location of the equivalence point.

THE BURET

The only essential equipment for an acid–base titration is a means for delivering the titrant to the titrand's solution. The most common method for delivering titrant is a ***buret*** (Figure 9.1.4), which is a long, narrow tube with graduated markings and equipped with a stopcock for dispensing the titrant. The buret's small internal diameter provides a better defined meniscus, making it easier to read precisely the titrant's volume. Burets are available in a variety of sizes and tolerances (Table 9.1.1), with the choice of buret determined by the needs of the analysis. You can improve a buret's accuracy by calibrating it over several intermediate ranges of volumes using the method described in Chapter 5 for calibrating pipets. Calibrating a buret corrects for variations in the buret's internal diameter.

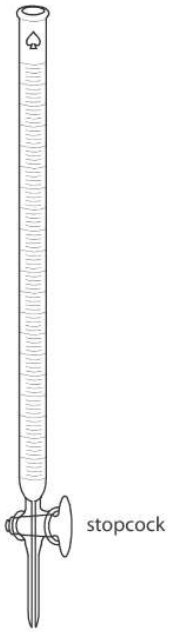


Figure 9.1.4 . A typical volumetric buret. The stopcock is shown here in the open position, which allows the titrant to flow into the titrand's solution. Rotating the stopcock controls the titrant's flow rate.

Table 9.1.1 . Specifications for Volumetric Burets

volume (mL)	class	subdivision (mL)	tolerance (±)
5	A	0.01	±0.01
	B	0.01	±0.01
10	A	0.02	±0.02
	B	0.02	±0.04
25	A	0.1	±0.03
	B	0.1	±0.06
50	A	0.1	±0.05
	B	0.1	±0.10
100	A	0.2	±0.10
	B	0.2	±0.20

An automated titration uses a pump to deliver the titrant at a constant flow rate (Figure 9.1.5). Automated titrations offer the additional advantage of using a microcomputer for data storage and analysis.



Figure 9.1.5 . Typical instrumentation for an automated acid–base titration showing the titrant, the pump, and the titrand. The pH electrode in the titrand's solution is used to monitor the titration's progress. You can see the titration curve in the lower-left quadrant of the computer's display. Modified from: Datamax (commons. Wikipedia.org).

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9.3: ACID–BASE TITRATIONS

Before 1800, most ***acid–base titrations*** used H_2SO_4, HCl, or HNO_3 as acidic titrants, and K_2CO_3 or Na_2CO_3 as basic titrants. A titration's end point was determined using litmus as an indicator, which is red in acidic solutions and blue in basic solutions, or by the cessation of CO_2 effervescence when neutralizing CO_3^{2-}. Early examples of acid–base titrimetry include determining the acidity or alkalinity of solutions, and determining the purity of carbonates and alkaline earth oxides.

> The determination of acidity and alkalinity continue to be important applications of acid–base titrimetry. We will take a closer look at these applications later in this section.

Three limitations slowed the development of acid–base titrimetry: the lack of a strong base titrant for the analysis of weak acids, the lack of suitable indicators, and the absence of a theory of acid–base reactivity. The introduction, in 1846, of NaOH as a strong base titrant extended acid–base titrimetry to the determination of weak acids. The synthesis of organic dyes provided many new indicators. Phenolphthalein, for example, was first synthesized by Bayer in 1871 and used as an indicator for acid–base titrations in 1877.

Despite the increased availability of indicators, the absence of a theory of acid–base reactivity made it difficult to select an indicator. The development of equilibrium theory in the late 19th century led to significant improvements in the theoretical understanding of acid–base chemistry, and, in turn, of acid–base titrimetry. Sørenson's establishment of the pH scale in 1909 provided a rigorous means to compare indicators. The determination of acid–base dissociation constants made it possible to calculate a theoretical titration curve, as outlined by Bjerrum in 1914. For the first time analytical chemists had a rational method for selecting an indicator, making acid–base titrimetry a useful alternative to gravimetry.

ACID–BASE TITRATION CURVES

In the overview to this chapter we noted that a titration's end point should coincide with its equivalence point. To understand the relationship between an acid–base titration's end point and its equivalence point we must know how the titrand's pH changes during a titration. In this section we will learn how to calculate a titration curve using the equilibrium calculations from Chapter 6. We also will learn how to sketch a good approximation of any acid–base titration curve using a limited number of simple calculations.

TITRATING STRONG ACIDS AND STRONG BASES

For our first titration curve, let's consider the titration of 50.0 mL of 0.100 M HCl using a titrant of 0.200 M NaOH. When a strong base and a strong acid react the only reaction of importance is

$$H_3O^+(aq) + OH^-(aq) \rightarrow 2H_2O(l) \tag{9.3.1}$$

> Although we have not written reaction 9.3.1 as an equilibrium reaction, it is at equilibrium; however, because its equilibrium constant is large—it is $(K_w)^{-1}$ or 1.00×10^{14} —we can treat reaction 9.3.1 as though it goes to completion.

The first task is to calculate the volume of NaOH needed to reach the equivalence point, V_{eq}. At the equivalence point we know from reaction 9.3.1 that

$$\begin{aligned} \text{moles HCl} &= \text{moles NaOH} \\ M_a \times V_a &= M_b \times V_b \end{aligned}$$

where the subscript 'a' indicates the acid, HCl, and the subscript 'b' indicates the base, NaOH. The volume of NaOH needed to reach the equivalence point is

$$V_{eq} = V_b = \frac{M_a V_a}{M_b} = \frac{(0.100\ \text{M})(50.0\ \text{mL})}{(0.200\ \text{M})} = 25.0\ \text{mL}$$

Before the equivalence point, HCl is present in excess and the pH is determined by the concentration of unreacted HCl. At the start of the titration the solution is 0.100 M in HCl, which, because HCl is a strong acid, means the pH is

$$\text{pH} = -\log\left[H_3O^+\right] = -\log[\text{HCl}] = -\log(0.100) = 1.00$$

After adding 10.0 mL of NaOH the concentration of excess HCl is

$$[\text{HCl}] = \frac{(\text{mol HCl})_{\text{initial}} - (\text{mol NaOH})_{\text{added}}}{\text{total volume}} = \frac{M_a V_a - M_b V_b}{V_a + V_b}$$

$$[\text{HCl}] = \frac{(0.100\ \text{M})(50.0\ \text{mL}) - (0.200\ \text{M})(10.0\ \text{mL})}{50.0\ \text{mL} + 10.0\ \text{mL}} = 0.0500\ \text{M}$$

and the pH increases to 1.30.

At the equivalence point the moles of HCl and the moles of NaOH are equal. Since neither the acid nor the base is in excess, the pH is determined by the dissociation of water.

$$K_w = 1.00 \times 10^{-14} = \left[H_3O^+\right]\left[OH^-\right] = \left[H_3O^+\right]^2$$
$$\left[H_3O^+\right] = 1.00 \times 10^{-7}$$

Thus, the pH at the equivalence point is 7.00.

For volumes of NaOH greater than the equivalence point, the pH is determined by the concentration of excess OH^-. For example, after adding 30.0 mL of titrant the concentration of OH^- is

$$\left[OH^-\right] = \frac{(\text{mol NaOH})_{\text{added}} - (\text{mol HCl})_{\text{initial}}}{\text{total volume}} = \frac{M_bV_b - M_aV_a}{V_a + V_b}$$
$$\left[OH^-\right] = \frac{(0.200\ \text{M})(30.0\ \text{mL}) - (0.100\ \text{M})(50.0\ \text{mL})}{30.0\ \text{mL} + 50.0\ \text{mL}} = 0.0125\ \text{M}$$

To find the concentration of H_3O^+ we use the K_w expression

$$\left[H_3O^+\right] = \frac{K_w}{\left[OH^-\right]} = \frac{1.00 \times 10^{-14}}{0.0125} = 8.00 \times 10^{-13}\ \text{M}$$

to find that the pH is 12.10. Table 9.2.1 and Figure 9.2.1 show additional results for this titration curve. You can use this same approach to calculate the titration curve for the titration of a strong base with a strong acid, except the strong base is in excess before the equivalence point and the strong acid is in excess after the equivalence point.

Table 9.2.1 . Titration of 50.0 mL of 0.100 M HCl with 0.200 M NaOH

volume of NaOH (mL)	pH	volume of NaOH (mL)	pH
0.00	1.00	26.0	11.42
5.00	1.14	28.0	11.89
10.0	1.30	30.0	12.10
15.0	1.51	35.0	12.37
20.0	1.85	40.0	12.52
22.0	2.08	45.0	12.63
24.0	2.57	50.0	12.70
25.0	7.00		

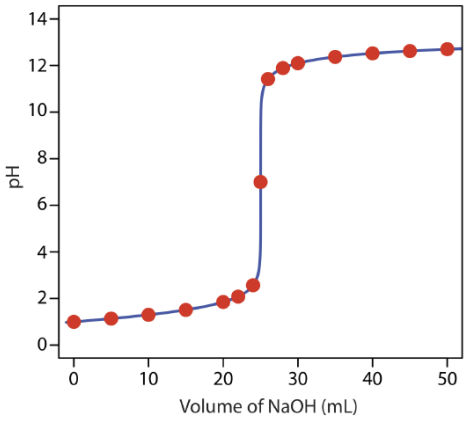


Figure 9.2.1 . Titration curve for the titration of 50.0 mL of 0.100 M HCl with 0.200 M NaOH. The red points correspond to the data in Table 9.2.1 . The blue line shows the complete titration curve.

? EXERCISE 9.2.1

Construct a titration curve for the titration of 25.0 mL of 0.125 M NaOH with 0.0625 M HCl.

Answer

The volume of HCl needed to reach the equivalence point is

$$V_{eq} = V_a = \frac{M_b V_b}{M_a} = \frac{(0.125\ \text{M})(25.0\ \text{mL})}{(0.0625\ \text{M})} = 50.0\ \text{mL}$$

Before the equivalence point, NaOH is present in excess and the pH is determined by the concentration of unreacted OH^-. For example, after adding 10.0 mL of HCl

$$\left[OH^-\right] = \frac{(0.125\ \text{M})(25.0\ \text{mL}) - (0.0625\text{M})(10.0\ \text{mL})}{25.0\ \text{mL} + 10.0\ \text{mL}} = 0.0714\ \text{M}$$

$$\left[H_3O^+\right] = \frac{K_w}{\left[OH^-\right]} = \frac{1.00 \times 10^{-14}}{0.0714\ \text{M}} = 1.40 \times 10^{-13}\ \text{M}$$

the pH is 12.85.

For the titration of a strong base with a strong acid the pH at the equivalence point is 7.00.

For volumes of HCl greater than the equivalence point, the pH is determined by the concentration of excess HCl. For example, after adding 70.0 mL of titrant the concentration of HCl is

$$[HCl] = \frac{(0.0625\ \text{M})(70.0\ \text{mL}) - (0.125\ \text{M})(25.0\ \text{mL})}{70.0\ \text{mL} + 25.0\ \text{mL}} = 0.0132\ \text{M}$$

giving a pH of 1.88. Some additional results are shown here.

volume of HCl (mL)	pH	volume of HCl (mL)	pH
0	13.10	60	2.13
10	12.85	70	1.88
20	12.62	80	1.75
30	12.36	90	1.66
40	11.98	100	1.60
50	7.00		

TITRATING A WEAK ACID WITH A STRONG BASE

For this example, let's consider the titration of 50.0 mL of 0.100 M acetic acid, CH_3COOH, with 0.200 M NaOH. Again, we start by calculating the volume of NaOH needed to reach the equivalence point; thus

$$\text{mol } CH_3COOH = \text{mol NaOH}$$

$$M_a \times V_a = M_b \times V_b$$

$$V_{eq} = V_b = \frac{M_a V_a}{M_b} = \frac{(0.100\ \text{M})(50.0\ \text{mL})}{(0.200\ \text{M})} = 25.0\ \text{mL}$$

Before we begin the titration the pH is that for a solution of 0.100 M acetic acid. Because acetic acid is a weak acid, we calculate the pH using the method outlined in Chapter 6

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq)$$

$$K_a = \frac{\left[H_3O^+\right]\left[CH_3COO^-\right]}{[CH_3COOH]} = \frac{(x)(x)}{0.100 - x} = 1.75 \times 10^{-5}$$

finding that the pH is 2.88.

Adding NaOH converts a portion of the acetic acid to its conjugate base, CH_3COO^-.

$$CH_3COOH(aq) + OH^-(aq) \longrightarrow H_2O(l) + CH_3COO^-(aq) \tag{9.3.2}$$

Because the equilibrium constant for reaction 9.3.2 is quite large

$$K = K_a / K_w = 1.75 \times 10^9$$

we can treat the reaction as if it goes to completion.

Any solution that contains comparable amounts of a weak acid, HA, and its conjugate weak base, A^-, is a buffer. As we learned in Chapter 6, we can calculate the pH of a buffer using the Henderson–Hasselbalch equation.

$$\text{pH} = \text{p}K_\text{a} + \log \frac{[\text{A}^-]}{[\text{HA}]}$$

Before the equivalence point the concentration of unreacted acetic acid is

$$[\text{CH}_3\text{COOH}] = \frac{(\text{mol CH}_3\text{COOH})_\text{initial} - (\text{mol NaOH})_\text{added}}{\text{total volume}} = \frac{M_a V_a - M_b V_b}{V_a + V_b}$$

and the concentration of acetate is

$$[\text{CH}_3\text{COO}^-] = \frac{(\text{mol NaOH})_\text{added}}{\text{total volume}} = \frac{M_b V_b}{V_a + V_b}$$

For example, after adding 10.0 mL of NaOH the concentrations of CH_3COOH and CH_3COO^- are

$$[\text{CH}_3\text{COOH}] = \frac{(0.100\text{ M})(50.0\text{ mL}) - (0.200\text{ M})(10.0\text{ mL})}{50.0\text{ mL} + 10.0\text{ mL}} = 0.0500\text{ M}$$

$$[\text{CH}_3\text{COO}^-] = \frac{(0.200\text{ M})(10.0\text{ mL})}{50.0\text{ mL} + 10.0\text{ mL}} = 0.0333\text{ M}$$

which gives us a pH of

$$\text{pH} = 4.76 + \log \frac{0.0333\text{ M}}{0.0500\text{ M}} = 4.58$$

At the equivalence point the moles of acetic acid initially present and the moles of NaOH added are identical. Because their reaction effectively proceeds to completion, the predominate ion in solution is CH_3COO^-, which is a weak base. To calculate the pH we first determine the concentration of CH_3COO^-

$$[\text{CH}_3\text{COO}^-] = \frac{(\text{mol NaOH})_\text{added}}{\text{total volume}} = \frac{(0.200\text{ M})(25.0\text{ mL})}{50.0\text{ mL} + 25.0\text{ mL}} = 0.0667\text{ M}$$

> Alternatively, we can calculate acetate's concentration using the initial moles of acetic acid; thus
>
> $$[\text{CH}_3\text{COO}^-] = \frac{(\text{mol CH}_3\text{COOH})_\text{initial}}{\text{total volume}} = \frac{(0.100\text{ M})(50.0\text{ mL})}{50.0\text{ mL} + 25.0\text{ mL}} = 0.0667\text{ M}$$

Next, we calculate the pH of the weak base as shown earlier in Chapter 6

$$\text{CH}_3\text{COO}^-(aq) + \text{H}_2\text{O}(l) \rightleftharpoons \text{OH}^-(aq) + \text{CH}_3\text{COOH}(aq)$$

$$K_\text{b} = \frac{[\text{OH}^-]\,[\text{CH}_3\text{COOH}]}{[\text{CH}_3\text{COO}^-]} = \frac{(x)(x)}{0.0667 - x} = 5.71 \times 10^{-10}$$

$$x = [\text{OH}^-] = 6.17 \times 10^{-6}\text{ M}$$

$$[\text{H}_3\text{O}^+] = \frac{K_\text{w}}{[\text{OH}^-]} = \frac{1.00 \times 10^{-14}}{6.17 \times 10^{-6}} = 1.62 \times 10^{-9}\text{ M}$$

finding that the pH at the equivalence point is 8.79.

After the equivalence point, the titrant is in excess and the titration mixture is a dilute solution of NaOH. We can calculate the pH using the same strategy as in the titration of a strong acid with a strong base. For example, after adding 30.0 mL of NaOH the concentration of OH^- is

$$[\text{OH}^-] = \frac{(0.200\text{ M})(30.0\text{ mL}) - (0.100\text{ M})(50.0\text{ mL})}{30.0\text{ mL} + 50.0\text{ mL}} = 0.0125\text{ M}$$

$$[\text{H}_3\text{O}^+] = \frac{K_\text{w}}{[\text{OH}^-]} = \frac{1.00 \times 10^{-14}}{0.0125} = 8.00 \times 10^{-13}\text{ M}$$

giving a pH of 12.10. Table 9.2.2 and Figure 9.2.2 show additional results for this titration. You can use this same approach to calculate the titration curve for the titration of a weak base with a strong acid, except the initial pH is determined by the weak base, the pH at the equivalence point by its conjugate weak acid, and the pH after the equivalence point by excess strong acid.

Table 9.2.2 . Titration of 50.0 mL of 0.100 M Acetic Acid with 0.200 M NaOH

volume of HCl (mL)	pH	volume of HCl (mL)	pH
0.00	2.88	26.0	11.43
5.00	4.16	28.0	11.89
10.0	4.58	30.0	12.10
15.0	4.94	35.0	12.37
20.0	5.36	40.0	12.52
22.0	5.63	45.0	12.63
24.0	6.14	50.0	12.70
25.0	8.79		

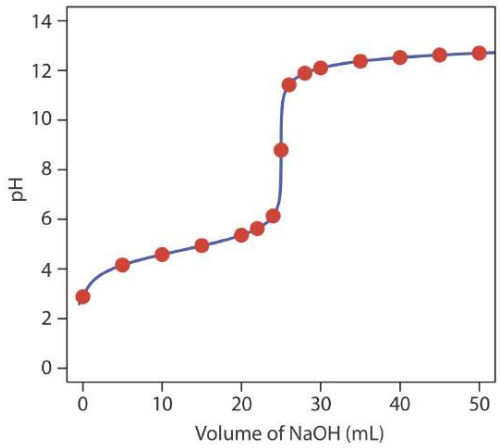


Figure 9.2.2 . Titration curve for the titration of 50.0 mL of 0.100 M CH_3COOH with 0.200 M NaOH. The red points correspond to the data in Table 9.2.2 . The blue line shows the complete titration curve.

EXERCISE 9.2.2

Construct a titration curve for the titration of 25.0 mL of 0.125 M NH_3 with 0.0625 M HCl.

Answer

The volume of HCl needed to reach the equivalence point is

$$V_{aq} = V_a = \frac{M_b V_b}{M_a} = \frac{(0.125\ \text{M})(25.0\ \text{mL})}{(0.0625\ \text{M})} = 50.0\ \text{mL}$$

Before adding HCl the pH is that for a solution of 0.100 M NH_3.

$$K_\text{b} = \frac{[\text{OH}^-]\,[\text{NH}_4^+]}{[\text{NH}_3]} = \frac{(x)(x)}{0.125 - x} = 1.75 \times 10^{-5}$$

$$x = [\text{OH}^-] = 1.48 \times 10^{-3}\ \text{M}$$

$$[\text{H}_3\text{O}^+] = \frac{K_\text{w}}{[\text{OH}^-]} = \frac{1.00 \times 10^{-14}}{1.48 \times 10^{-3}\ \text{M}} = 6.76 \times 10^{-12}\ \text{M}$$

The pH at the beginning of the titration, therefore, is 11.17.

Before the equivalence point the pH is determined by an NH_3/NH_4^+ buffer. For example, after adding 10.0 mL of HCl

$$[\text{NH}_3] = \frac{(0.125\ \text{M})(25.0\ \text{mL}) - (0.0625\ \text{M})(10.0\ \text{mL})}{25.0\ \text{mL} + 10.0\ \text{mL}} = 0.0714\ \text{M}$$

$$[\text{NH}_4^+] = \frac{(0.0625\ \text{M})(10.0\ \text{mL})}{25.0\ \text{mL} + 10.0\ \text{mL}} = 0.0179\ \text{M}$$

$$\text{pH} = 9.244 + \log\frac{0.0714\ \text{M}}{0.0179\ \text{M}} = 9.84$$

At the equivalence point the predominate ion in solution is NH_4^+. To calculate the pH we first determine the concentration of NH_4^+

$$\left[\mathrm{NH_4^+}\right] = \frac{(0.125\ \mathrm{M})(25.0\ \mathrm{mL})}{25.0\ \mathrm{mL} + 50.0\ \mathrm{mL}} = 0.0417\ \mathrm{M}$$

and then calculate the pH

$$K_\mathrm{a} = \frac{\left[\mathrm{H_3O^+}\right]\left[\mathrm{NH_3}\right]}{\left[\mathrm{NH_4^+}\right]} = \frac{(x)(x)}{0.0417 - x} = 5.70 \times 10^{-10}$$

obtaining a value of 5.31.

After the equivalence point, the pH is determined by the excess HCl. For example, after adding 70.0 mL of HCl

$$[\mathrm{HCl}] = \frac{(0.0625\ \mathrm{M})(70.0\ \mathrm{mL}) - (0.125\ \mathrm{M})(25.0\ \mathrm{mL})}{70.0\ \mathrm{mL} + 25.0\ \mathrm{mL}} = 0.0132\ \mathrm{M}$$

and the pH is 1.88. Some additional results are shown here.

volume of HCl (mL)	pH	volume of HCl (mL)	pH
0	11.17	60	2.13
10	9.84	70	1.88
20	9.42	80	1.75
30	9.07	90	1.66
40	8.64	100	1.60
50	5.31		

We can extend this approach for calculating a weak acid–strong base titration curve to reactions that involve multiprotic acids or bases, and mixtures of acids or bases. As the complexity of the titration increases, however, the necessary calculations become more time consuming. Not surprisingly, a variety of algebraic and spreadsheet approaches are available to aid in constructing titration curves.

The following papers provide information on algebraic approaches to calculating titration curves: (a) Willis, C. J. *J. Chem. Educ.* **1981**, *58*, 659–663; (b) Nakagawa, K. *J. Chem. Educ.* **1990**, *67*, 673–676; (c) Gordus, A. A. *J. Chem. Educ.* **1991**, *68*, 759–761; (d) de Levie, R. *J. Chem. Educ.* **1993**, *70*, 209–217; (e) Chaston, S. *J. Chem. Educ.* **1993**, *70*, 878–880; (f) de Levie, R. *Anal. Chem.* **1996**, *68*, 585–590.

The following papers provide information on the use of spreadsheets to generate titration curves: (a) Currie, J. O.; Whiteley, R. V. *J. Chem. Educ.* **1991**, *68*, 923–926; (b) Breneman, G. L.; Parker, O. J. *J. Chem. Educ.* **1992**, *69*, 46–47; (c) Carter, D. R.; Frye, M. S.; Mattson, W. A. *J. Chem. Educ.* **1993**, *70*, 67–71; (d) Freiser, H. *Concepts and Calculations in Analytical Chemistry*, CRC Press: Boca Raton, 1992.

SKETCHING AN ACID–BASE TITRATION CURVE

To evaluate the relationship between a titration's equivalence point and its end point we need to construct only a reasonable approximation of the exact titration curve. In this section we demonstrate a simple method for sketching an acid–base titration curve. Our goal is to sketch the titration curve quickly, using as few calculations as possible. Let's use the titration of 50.0 mL of 0.100 M CH_3COOH with 0.200 M NaOH to illustrate our approach. This is the same example that we used to develop the calculations for a weak acid–strong base titration curve. You can review the results of that calculation in Table 9.2.2 and in Figure 9.2.2 .

We begin by calculating the titration's equivalence point volume, which, as we determined earlier, is 25.0 mL. Next we draw our axes, placing pH on the *y*-axis and the titrant's volume on the *x*-axis. To indicate the equivalence point volume, we draw a vertical line that intersects the *x*-axis at 25.0 mL of NaOH. Figure 9.2.3 a shows the first step in our sketch.

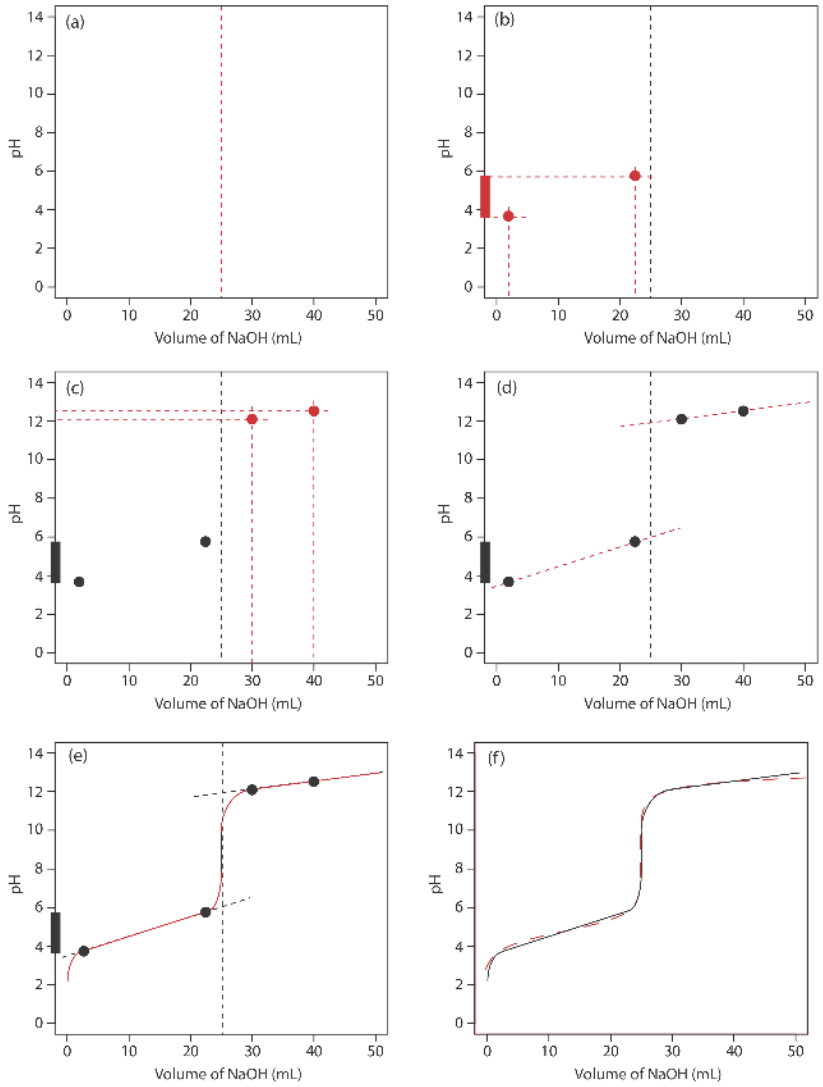


Figure 9.2.3 . Illustrations showing the steps used to sketch an approximate titration curve for the titration of 50.0 mL of 0.100 M CH_3COOH with 0.200 M NaOH: (a) locating the equivalence point volume; (b) plotting two points before the equivalence point; (c) plotting two points after the equivalence point; (d) preliminary approximation of titration curve using straight-lines; (e) final approximation of titration curve using a smooth curve; (f) comparison of approximate titration curve (solid black line) and exact titration curve (dashed red line). See the text for additional details.

Before the equivalence point the titrand's pH is determined by a buffer of acetic acid, CH_3COOH, and acetate, CH_3COO^-. Although we can calculate a buffer's pH using the Henderson–Hasselbalch equation, we can avoid this calculation by making a simple assumption. You may recall from Chapter 6 that a buffer operates over a pH range that extends approximately ±1 pH unit on either side of the weak acid's pK_a value. The pH is at the lower end of this range, pH = pK_a – 1, when the weak acid's concentration is 10× greater than that of its conjugate weak base. The buffer reaches its upper pH limit, pH = pK_a + 1, when the weak acid's concentration is 10× smaller than that of its conjugate weak base. When we titrate a weak acid or a weak base, the buffer spans a range of volumes from approximately 10% of the equivalence point volume to approximately 90% of the equivalence point volume.

> The actual values are 9.09% and 90.9%, but for our purpose, using 10% and 90% is more convenient; that is, after all, one advantage of an approximation!

Figure 9.2.3 b shows the second step in our sketch. First, we superimpose acetic acid's ladder diagram on the *y*-axis, including its buffer range, using its pK_a value of 4.76. Next, we add two points, one for the pH at 10% of the equivalence point volume (a pH of 3.76 at 2.5 mL) and one for the pH at 90% of the equivalence point volume (a pH of 5.76 at 22.5 mL).

The third step is to add two points after the equivalence point. The pH after the equivalence point is fixed by the concentration of excess titrant, NaOH. Calculating the pH of a strong base is straightforward, as we saw earlier. Figure 9.2.3 c includes points (see Table 9.2.2) for the pH after adding 30.0 mL and after adding 40.0 mL of NaOH.

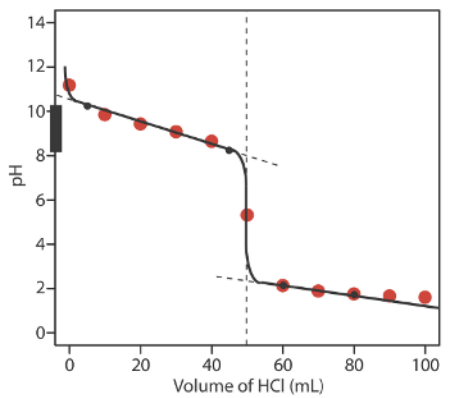
Next, we draw a straight line through each pair of points, extending each line through the vertical line that represents the equivalence point's volume (Figure 9.2.3 d). Finally, we complete our sketch by drawing a smooth curve that connects the three straight-line segments (Figure 9.2.3 e). A comparison of our sketch to the exact titration curve (Figure 9.2.3 f) shows that they are in close agreement.

? EXERCISE 9.2.3

Sketch a titration curve for the titration of 25.0 mL of 0.125 M NH_3 with 0.0625 M HCl and compare to the result from Exercise 9.2.2 .

Answer

The figure below shows a sketch of the titration curve. The black dots and curve are the approximate sketch of the titration curve. The points in red are the calculations from Exercise 9.2.2 . The two black points before the equivalence point (V_{HCl} = 5 mL, pH = 10.24 and V_{HCl} = 45 mL, pH= 8.24) are plotted using the pK_a of 9.244 for NH_4^+. The two black points after the equivalence point (V_{HCl} = 60 mL, pH = 2.13 and V_{HCl} = 80 mL, pH= 1.75) are from the answer to Exercise 9.2.2 .



As shown in the following example, we can adapt this approach to any acid–base titration, including those where exact calculations are more challenging, including the titration of polyprotic weak acids and bases, and the titration of mixtures of weak acids or weak bases.

✓ EXAMPLE 9.2.1

Sketch titration curves for the following two systems: (a) the titration of 50.0 mL of 0.050 M H_2A, a diprotic weak acid with a pK_{a1} of 3 and a pK_{a2} of 7; and (b) the titration of a 50.0 mL mixture that contains 0.075 M HA, a weak acid with a pK_a of 3, and 0.025 M HB, a weak acid with a pK_a of 7. For both titrations, assume that the titrant is 0.10 M NaOH.

Solution

Figure 9.2.4 a shows the titration curve for H_2A, including the ladder diagram for H_2A on the *y*-axis, the two equivalence points at 25.0 mL and at 50.0 mL, two points before each equivalence point, two points after the last equivalence point, and the straight-lines used to sketch the final titration curve. Before the first equivalence point the pH is controlled by a buffer of H_2A and HA^-. An HA^-/A^{2-} buffer controls the pH between the two equivalence points. After the second equivalence point the pH reflects the concentration of excess NaOH.

Figure 9.2.4 b shows the titration curve for the mixture of HA and HB. Again, there are two equivalence points; however, in this case the equivalence points are not equally spaced because the concentration of HA is greater than that for HB. Because HA is the stronger of the two weak acids it reacts first; thus, the pH before the first equivalence point is controlled by a buffer of HA and A^-. Between the two equivalence points the pH reflects the titration of HB and is determined by a buffer of HB and B^-. After the second equivalence point excess NaOH determines the pH.

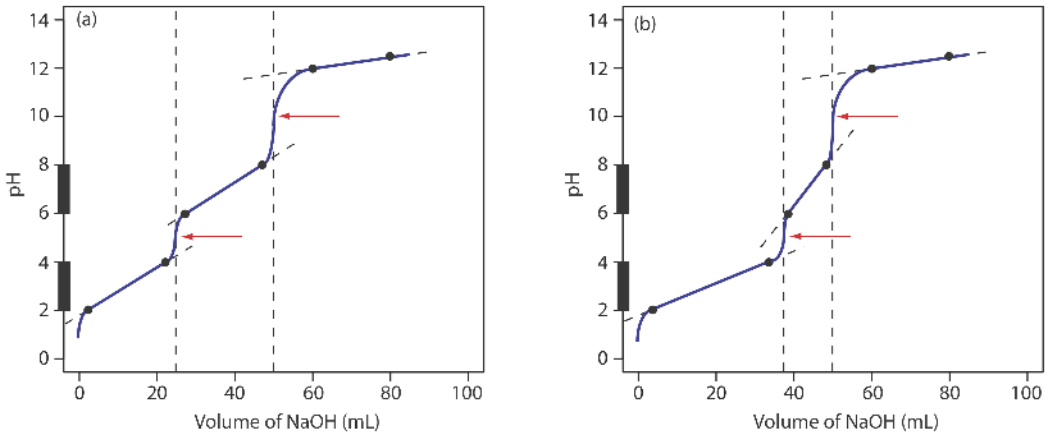


Figure 9.2.4 . Titration curves for Example 9.2.1 . The solid black dots show the points used to sketch the titration curves (shown in blue) and the red arrows show the locations of the equivalence points.

EXERCISE 9.2.4

Sketch the titration curve for 50.0 mL of 0.050 M H_2A, a diprotic weak acid with a pK_{a1} of 3 and a pK_{a2} of 4, using 0.100 M NaOH as the titrant. The fact that pK_{a2} falls within the buffer range of pK_{a1} presents a challenge that you will need to consider.

Answer

The figure below shows a sketch of the titration curve. The titration curve has two equivalence points, one at 25.0 mL $(H_2A \rightarrow HA^-)$ and one at 50.0 mL $(HA^- \rightarrow A^{2-})$. In sketching the curve, we plot two points before the first equivalence point using the pK_{a1} of 3 for H_2A

$$V_{HCl} = 2.5 \text{ mL}, \text{pH} = 2 \text{ and } V_{HCl} = 22.5 \text{ mL}, \text{pH} = 4$$

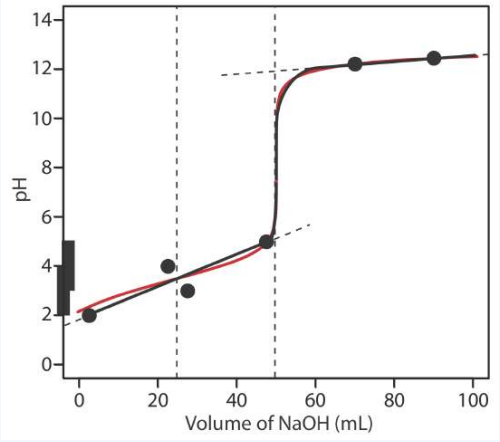
two points between the equivalence points using the pK_{a2} of 5 for HA^-

$$V_{HCl} = 27.5 \text{ mL}, \text{pH} = 3, \text{ and } V_{HCl} = 47.5 \text{ mL}, \text{pH} = 5$$

and two points after the second equivalence point

$$V_{HCl} = 70 \text{ mL}, \text{pH} = 12.22 \text{ and } V_{HCl} = 90 \text{ mL}, \text{pH} = 12.46$$

Drawing a smooth curve through these points presents us with the following dilemma—the pH appears to increase as the titrant's volume approaches the first equivalence point and then appears to decrease as it passes through the first equivalence point. This is, of course, absurd; as we add NaOH the pH cannot decrease. Instead, we model the titration curve before the second equivalence point by drawing a straight line from the first point (V_{HCl} = 2.5 mL, pH = 2) to the fourth point (V_{HCl} = 47.5 mL, pH= 5), ignoring the second and third points. The results is a reasonable approximation of the exact titration curve.



SELECTING AND EVALUATING THE END POINT

Earlier we made an important distinction between a titration's end point and its equivalence point. The difference between these two terms is important and deserves repeating. An equivalence point, which occurs when we react stoichiometrically equal amounts of the analyte and the titrant, is a theoretical not an experimental value. A titration's end point is an experimental result that represents our best estimate of the equivalence point. Any difference between a titration's equivalence point and its corresponding end point is a source of determinate error.

WHERE IS THE EQUIVALENCE POINT?

Earlier we learned how to calculate the pH at the equivalence point for the titration of a strong acid with a strong base, and for the titration of a weak acid with a strong base. We also learned how to sketch a titration curve with only a minimum of calculations. Can we also locate the equivalence point without performing any calculations. The answer, as you might guess, often is yes!

For most acid–base titrations the inflection point—the point on a titration curve that has the greatest slope—very nearly coincides with the titration's equivalence point. The red arrows in Figure 9.2.4 , for example, identify the equivalence points for the titration curves in Example 9.2.1 . An inflection point actually precedes its corresponding equivalence point by a small amount, with the error approaching 0.1% for weak acids and weak bases with dissociation constants smaller than 10^{-9}, or for very dilute solutions [Meites, L.; Goldman, J. A. *Anal. Chim. Acta* **1963**, *29*, 472–479].

The principal limitation of an inflection point is that it must be present and easy to identify. For some titrations the inflection point is missing or difficult to find. Figure 9.2.5 , for example, demonstrates the affect of a weak acid's dissociation constant, K_a, on the shape of its titration curve. An inflection point is visible, even if barely so, for acid dissociation constants larger than 10^{-9}, but is missing when K_a is 10^{-11}.

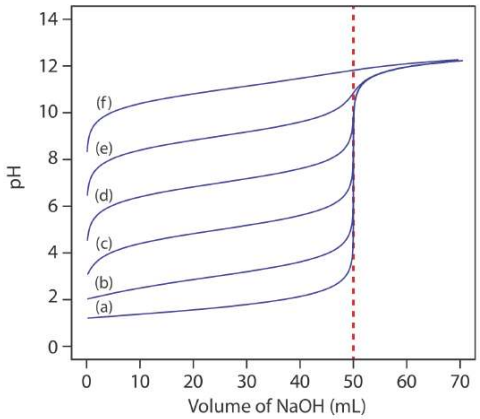


Figure 9.2.5 . Weak acid–strong base titration curves for the titration of 50.0 mL of 0.100 M HA with 0.100 M NaOH. The pK_a values for HA are (a) 1, (b) 3, (c) 5, (d) 7, (e) 9, and (f) 11. The dashed red line shows the equivalence point, which is 50.0 mL for all six analytes.

An inflection point also may be missing or difficult to see if the analyte is a multiprotic weak acid or weak base with successive dissociation constants that are similar in magnitude. To appreciate why this is true let's consider the titration of a diprotic weak acid, H_2A, with NaOH. During the titration the following two reactions occur.

$$H_2A(aq) + OH^-(aq) \longrightarrow H_2O(l) + HA^-(aq) \tag{9.3.3}$$

$$HA^-(aq) + OH^-(aq) \rightarrow H_2O(l) + A^{2-}(aq) \tag{9.3.4}$$

To see two distinct inflection points, reaction 9.3.3 must essentially be complete before reaction 9.3.4 begins.

Figure 9.2.6 shows titration curves for three diprotic weak acids. The titration curve for maleic acid, for which K_{a1} is approximately $20000\times$ larger than K_{a2}, has two distinct inflection points. Malonic acid, on the other hand, has acid dissociation constants that differ by a factor of approximately 690. Although malonic acid's titration curve shows two inflection points, the first is not as distinct as the second. Finally, the titration curve for succinic acid, for which the two K_a values differ by a factor of only $27\times$, has only a single inflection point that corresponds to the neutralization of $HC_2H_4O_4^-$ to $C_2H_4O_4^{2-}$. In general, we can detect separate inflection points when successive acid dissociation constants differ by a factor of at least 500 (a ΔK_a of at least 2.7).

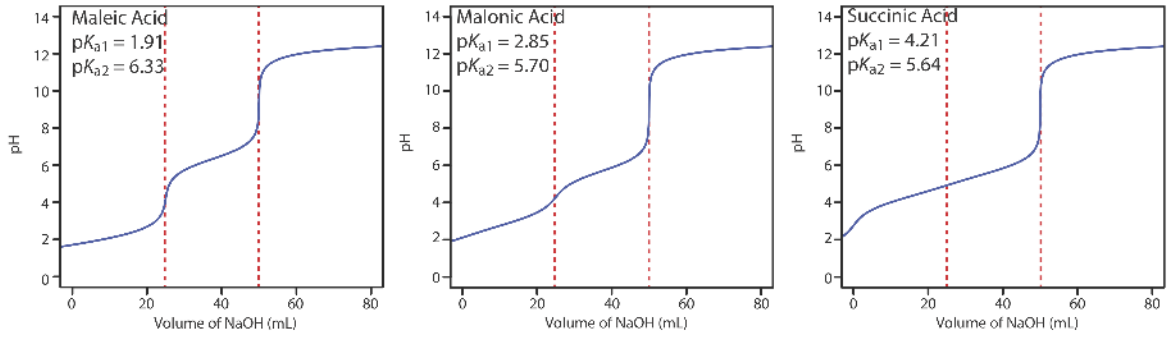


Figure 9.2.6 . Titration curves for the diprotic weak acids maleic acid, malonic acid, and succinic acid. Each titration curve is for 50.0 mL of 0.0500 M weak acid using 0.100 M NaOH as the titrant. Although each titration curve has equivalence points at 25.0 mL and 50.0 mL of NaOH (shown by the dashed red lines), the titration curve for succinic acid shows only one inflection point.

The same holds true for mixtures of weak acids or mixtures of weak bases. To detect separate inflection points when titrating a mixture of weak acids, their pK_a values must differ by at least a factor of 500.

FINDING THE END POINT WITH AN INDICATOR

One interesting group of weak acids and weak bases are organic dyes. Because an organic dye has at least one highly colored conjugate acid–base species, its titration results in a change in both its pH and its color. We can use this change in color to indicate the end point of a titration provided that it occurs at or near the titration's equivalence point.

As an example, let's consider an indicator for which the acid form, HIn, is yellow and the base form, In^-, is red. The color of the indicator's solution depends on the relative concentrations of HIn and In^-. To understand the relationship between pH and color we use the indicator's acid dissociation reaction

$$HIn(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + In^-(aq)$$

and its equilibrium constant expression.

$$K_a = \frac{[H_3O^+]\,[In^-]}{[HIn]} \tag{9.3.5}$$

Taking the negative log of each side of Equation 9.3.5, and rearranging to solve for pH leaves us with a equation that relates the solution's pH to the relative concentrations of HIn and In^-.

$$pH = pK_a + \log\frac{[In^-]}{[HIn]} \tag{9.3.6}$$

If we can detect HIn and In^- with equal ease, then the transition from yellow-to-red (or from red-to-yellow) reaches its midpoint, which is orange, when the concentrations of HIn and In^- are equal, or when the pH is equal to the indicator's pK_a. If the indicator's pK_a and the pH at the equivalence point are identical, then titrating until the indicator turns orange is a suitable end point. Unfortunately, we rarely know the exact pH at the equivalence point. In addition, determining when the concentrations of HIn and In^- are equal is difficult if the indicator's change in color is subtle.

We can establish the range of pHs over which the average analyst observes a change in the indicator's color by making two assumptions: that the indicator's color is yellow if the concentration of HIn is 10× greater than that of In^- and that its color is red if the concentration of HIn is 10× smaller than that of In^-. Substituting these inequalities into Equation 9.3.6

$$pH = pK_a + \log\tfrac{1}{10} = pK_a - 1$$
$$pH = pK_a + \log\tfrac{10}{1} = pK_a + 1$$

shows that the indicator changes color over a pH range that extends ±1 unit on either side of its pK_a. As shown in Figure 9.2.7 , the indicator is yel-ow when the pH is less than pK_a – 1 and it is red when the pH is greater than pK_a + 1. For pH values between pK_a – 1 and pK_a + 1 the indicator's color passes through various shades of orange. The properties of several common acid–base indicators are listed in Table 9.2.3 .

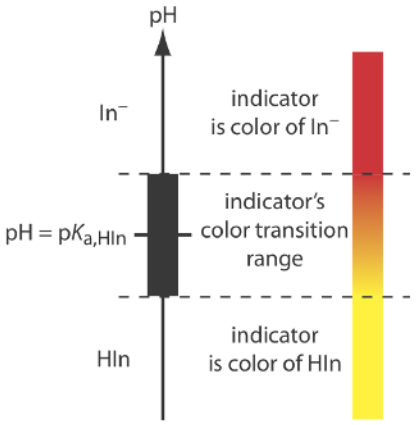


Figure 9.2.7 . Diagram showing the relationship between pH and an indicator's color. The ladder diagram defines pH values where HIn and In^- are the predominate species. The indicator changes color when the pH is between $pK_a - 1$ and $pK_a + 1$.

Table 9.2.3 . Properties of Selected Acid–Base Indicators

indicator	acid color	base color	pH range	pK_a
cresol red	red	yellow	0.2–1.8	—
thymol blue	red	yellow	1.2–2.8	1.7
bromothymol blue	yellow	blue	3.0–4.6	4.1
methyl orange	red	yellow	3.4–4.4	3.7
Congo red	blue	red	3.0–5.0	—
bromocresol green	yellow	blue	3.8–5.4	4.7
methyl red	red	yellow	4.2–6.3	5.0
bromocresol purple	yellow	purple	5.2–6.8	6.1
litmus	red	blue	5.0–8.0	—
bromothymol blue	yellow	blue	6.0–7.6	7.1
phenol red	yellow	blue	6.8–8.4	7.8
cresol red	yellow	red	7.2–8.8	8.2
thymol blue	yellow	red	8.0–9.6	8.9
phenolphthalein	colorless	red	8.3–10.0	9.6
alizarin yellow R	yellow	orange-red	10.1–12.0	—

You may wonder why an indicator's pH range, such as that for phenolphthalein, is not equally distributed around its pK_a value. The explanation is simple. Figure 9.2.7 presents an idealized view in which our sensitivity to the indicator's two colors is equal. For some indicators only the weak acid or the weak base is colored. For other indicators both the weak acid and the weak base are colored, but one form is easier to see. In either case, the indicator's pH range is skewed in the direction of the indicator's less colored form. Thus, phenolphthalein's pH range is skewed in the direction of its colorless form, shifting the pH range to values lower than those suggested by Figure 9.2.7 .

The relatively broad range of pHs over which an indicator changes color places additional limitations on its ability to signal a titration's end point. To minimize a determinate titration error, the indicator's entire pH range must fall within the rapid change in pH near the equivalence point. For example, in Figure 9.2.8 we see that phenolphthalein is an appropriate indicator for the titration of 50.0 mL of 0.050 M acetic acid with 0.10 M NaOH. Bromothymol blue, on the other hand, is an inappropriate indicator because its change in color begins well before the initial sharp rise in pH, and, as a result, spans a relatively large range of volumes. The early change in color increases the probability of obtaining an inaccurate result, and the range of possible end point volumes increases the probability of obtaining imprecise results.

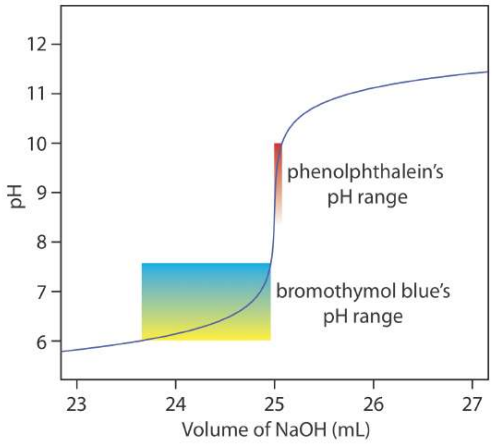


Figure 9.2.8 . Portion of the titration curve for 50.0 mL of 0.050 M CH_3COOH with 0.10 M NaOH, highlighting the region that contains the equivalence point. The end point transitions for the indicators phenolphthalein and bromothymol blue are superimposed on the titration curve.

? EXERCISE 9.2.5

Suggest a suitable indicator for the titration of 25.0 mL of 0.125 M NH_3 with 0.0625 M NaOH. You constructed a titration curve for this titration in Exercise 9.2.2 and Exercise 9.2.3 .

Answer

The pH at the equivalence point is 5.31 (see Exercise 9.2.2) and the sharp part of the titration curve extends from a pH of approximately 7 to a pH of approximately 4. Of the indicators in Table 9.2.3 , methyl red is the best choice because its pK_a value of 5.0 is closest to the equivalence point's pH and because the pH range of 4.2–6.3 for its change in color will not produce a significant titration error.

FINDING THE END POINT BY MONITORING PH

An alternative approach for locating a titration's end point is to monitor the titration's progress using a sensor whose signal is a function of the analyte's concentration. The result is a plot of the entire titration curve, which we can use to locate the end point with a minimal error.

A pH electrode is the obvious sensor for monitoring an acid–base titration and the result is a ***potentiometric titration curve***. For example, Figure 9.2.9 a shows a small portion of the potentiometric titration curve for the titration of 50.0 mL of 0.050 M CH_3COOH with 0.10 M NaOH, which focuses on the region that contains the equivalence point. The simplest method for finding the end point is to locate the titration curve's inflection point, which is shown by the arrow. This is also the least accurate method, particularly if the titration curve has a shallow slope at the equivalence point.

See Chapter 11 for more details about pH electrodes.

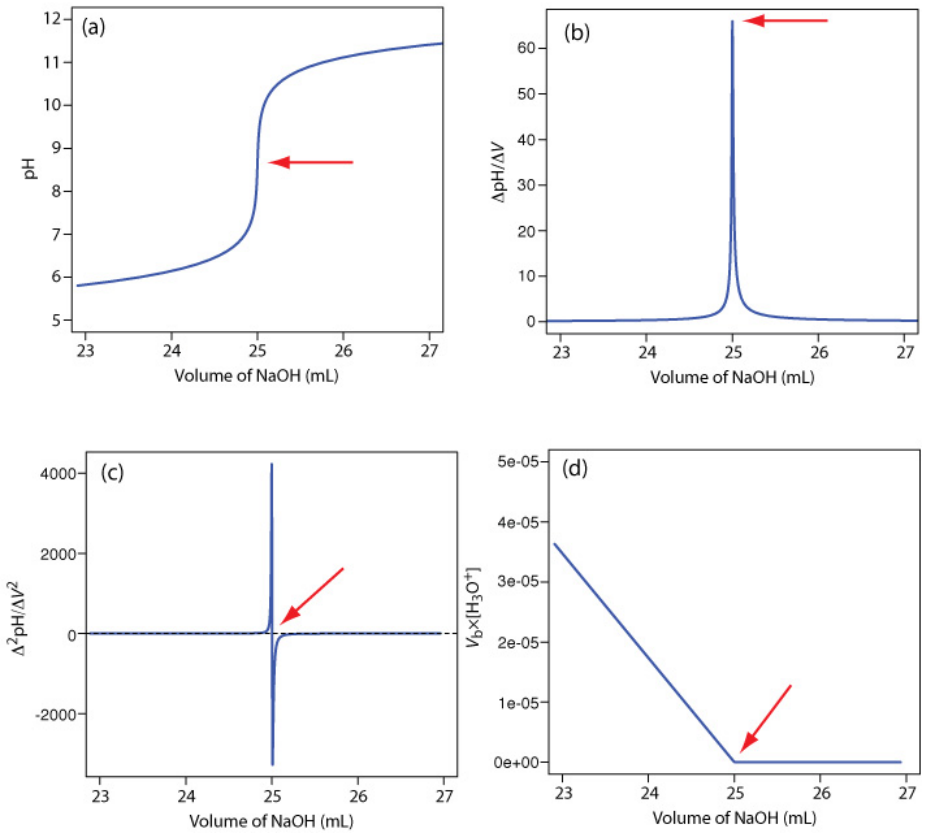


Figure 9.2.9 . Titration curves for the titration of 50.0 mL of 0.050 M CH_3COOH with 0.10 M NaOH: (a) normal titration curve; (b) first derivative titration curve; (c) second derivative titration curve; (d) Gran plot. The red arrows show the location of each titration's end point.

Another method for locating the end point is to plot the first derivative of the titration curve, which gives its slope at each point along the *x*-axis. Examine Figure 9.2.9 a and consider how the titration curve's slope changes as we approach, reach, and pass the equivalence point. Because the slope reaches its maximum value at the inflection point, the first derivative shows a spike at the equivalence point (Figure 9.2.9 b). The second derivative of a titration curve can be more useful than the first derivative because the equivalence point intersects the volume axis. Figure 9.2.9 c shows the resulting titration curve.

Suppose we have the following three points on our titration curve:

volume (mL)	pH
23.65	6.00
23.91	6.10
24.13	6.20

Mathematically, we can approximate the first derivative as $\Delta\text{pH}/\Delta V$, where ΔpH is the change in pH between successive additions of titrant. Using the first two points, the first derivative is

$$\frac{\Delta\text{pH}}{\Delta V} = \frac{6.10 - 6.00}{23.91 - 23.65} = 0.385$$

which we assign to the average of the two volumes, or 23.78 mL. For the second and third points, the first derivative is 0.455 and the average volume is 24.02 mL.

volume (mL)	ΔpH
23.78	0.385
24.02	0.455

We can approximate the second derivative as $\Delta(\Delta\text{pH}/\Delta V)/\Delta V$, or $\Delta^2\text{pH}/\Delta V^2$. Using the two points from our calculation of the first derivative, the second derivative is

$$\frac{\Delta^2\text{pH}}{\Delta V^2} = \frac{0.455 - 0.385}{24.02 - 23.78} = 0.292$$

which we assign to the average of the two volumes, or 23.90 mL. Note that calculating the first derivative comes at the expense of losing one piece of information (three points become two points), and calculating the second derivative comes at the expense of losing two pieces of information.

Derivative methods are particularly useful when titrating a sample that contains more than one analyte. If we rely on indicators to locate the end points, then we usually must complete separate titrations for each analyte so that we can see the change in color for each end point. If we record the titration curve, however, then a single titration is sufficient. The precision with which we can locate the end point also makes derivative methods attractive for an analyte that has a poorly defined normal titration curve.

Derivative methods work well only if we record sufficient data during the rapid increase in pH near the equivalence point. This usually is not a problem if we use an automatic titrator, such as the one seen earlier in Figure 9.1.5. Because the pH changes so rapidly near the equivalence point—a change of several pH units over a span of several drops of titrant is not unusual—a manual titration does not provide enough data for a useful derivative titration curve. A manual titration does contain an abundance of data during the more gently rising portions of the titration curve before and after the equivalence point. This data also contains information about the titration curve's equivalence point.

Consider again the titration of acetic acid, CH_3COOH, with NaOH. At any point during the titration acetic acid is in equilibrium with H_3O^+ and CH_3COO^-

$$\text{CH}_3\text{COOH}(aq) + \text{H}_2\text{O}(l) \rightleftharpoons \text{H}_3\text{O}^+(aq) + \text{CH}_3\text{COO}^-(aq)$$

for which the equilibrium constant is

$$K_a = \frac{\left[\text{H}_3\text{O}^+\right]\left[\text{CH}_3\text{COO}^-\right]}{\left[\text{CH}_3\text{COOH}\right]}$$

Before the equivalence point the concentrations of CH_3COOH and CH_3COO^- are

$$\left[\text{CH}_3\text{COOH}\right] = \frac{(\text{mol CH}_3\text{COOH})_{\text{initial}} - (\text{mol NaOH})_{\text{added}}}{\text{total volume}} = \frac{M_aV_a - M_bV_b}{V_a + V_b}$$

$$\left[\text{CH}_3\text{COO}^-\right] = \frac{(\text{mol NaOH})_{\text{added}}}{\text{total volume}} = \frac{M_bV_b}{V_a + V_b}$$

Substituting these equations into the K_a expression and rearranging leaves us with

$$K_\text{a} = \frac{\left[\text{H}_3\text{O}^+\right](M_bV_b)\,/\,(V_a + V_b)}{\{M_aV_a - M_bV_b\}\,/\,(V_a + V_b)}$$

$$K_aM_aV_a - K_aM_bV_b = \left[\text{H}_3\text{O}^+\right](M_bV_b)$$

$$\frac{K_a M_a V_a}{M_b} - K_a V_b = \left[\mathrm{H_3O^+}\right] V_b$$

Finally, recognizing that the equivalence point volume is

$$V_{eq} = \frac{M_a V_a}{M_b}$$

leaves us with the following equation.

$$\left[\mathrm{H_3O^+}\right] \times V_b = K_\mathrm{a} V_{eq} - K_\mathrm{a} V_b$$

For volumes of titrant before the equivalence point, a plot of $V_b \times \left[\mathrm{H_3O^+}\right]$ versus V_b is a straight-line with an *x*-intercept of V_{eq} and a slope of $-K_\mathrm{a}$. Figure 9.2.9 d shows a typical result. This method of data analysis, which converts a portion of a titration curve into a straight-line, is a ***Gran plot***.

> Values of K_a determined by this method may have a substantial error if the effect of activity is ignored. See Chapter 6.9 for a discussion of activity.

FINDING THE END POINT BY MONITORING TEMPERATURE

The reaction between an acid and a base is exothermic. Heat generated by the reaction is absorbed by the titrand, which increases its temperature. Monitoring the titrand's temperature as we add the titrant provides us with another method for recording a titration curve and identifying the titration's end point (Figure 9.2.10).

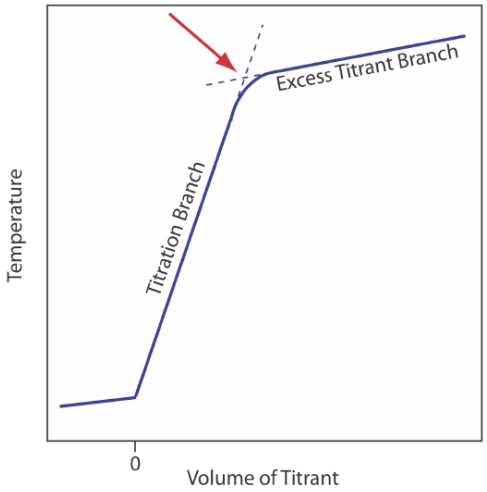


Figure 9.2.10 . Typical thermometric titration curve. The endpoint, shown by the red arrow, is found by extrapolating the titration branch and the excess titration branch.

Before we add the titrant, any change in the titrand's temperature is the result of warming or cooling as it equilibrates with the surroundings. Adding titrant initiates the exothermic acid–base reaction and increases the titrand's temperature. This part of a thermometric titration curve is called the titration branch. The temperature continues to rise with each addition of titrant until we reach the equivalence point. After the equivalence point, any change in temperature is due to the titrant's enthalpy of dilution and the difference between the temperatures of the titrant and titrand. Ideally, the equivalence point is a distinct intersection of the titration branch and the excess titrant branch. As shown in Figure 9.2.10 , however, a thermometric titration curve usually shows curvature near the equivalence point due to an incomplete neutralization reaction or to the excessive dilution of the titrand and the titrant during the titration. The latter problem is minimized by using a titrant that is 10–100 times more concentrated than the analyte, although this results in a very small end point volume and a larger relative error. If necessary, the end point is found by extrapolation.

Although not a common method for monitoring an acid–base titration, a thermometric titration has one distinct advantage over the direct or indirect monitoring of pH. As discussed earlier, the use of an indicator or the monitoring of pH is limited by the magnitude of the relevant equilibrium constants. For example, titrating boric acid, H_3BO_3, with NaOH does not provide a sharp end point when monitoring pH because boric acid's K_a of 5.8×10^{-10} is too small (Figure 9.2.11 a). Because boric acid's enthalpy of neutralization is fairly large, –42.7 kJ/mole, its thermometric titration curve provides a useful endpoint (Figure 9.2.11 b).

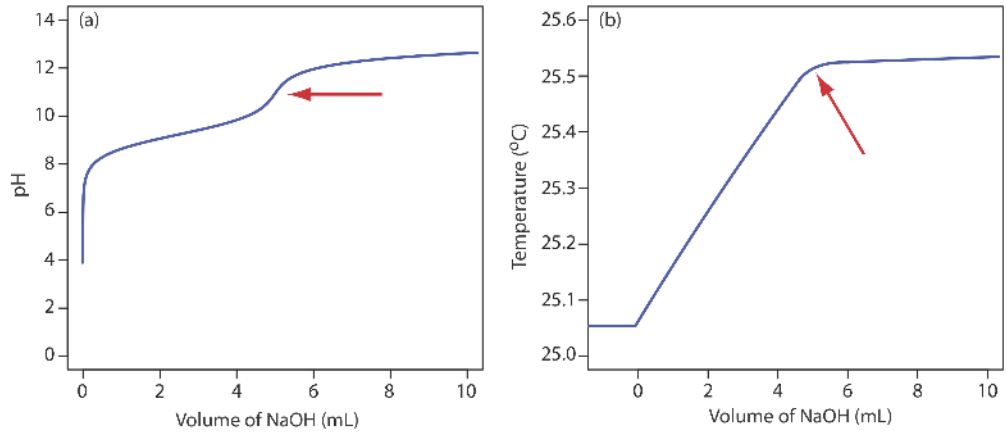


Figure 9.2.11 . Titration curves for the titration of 50.0 mL of 0.050 M H_3BO_3 with 0.50 M NaOH obtained by monitoring (a) pH and (b) temperature. The red arrows show the end points for the titrations.

TITRATIONS IN NONAQUEOUS SOLVENTS

Thus far we have assumed that the titrant and the titrand are aqueous solutions. Although water is the most common solvent for acid–base titrimetry, switching to a nonaqueous solvent can improve a titration's feasibility.

For an amphoteric solvent, SH, the autoprotolysis constant, K_s, relates the concentration of its protonated form, SH_2^+, to its deprotonated form, S^-

$$2SH \rightleftharpoons SH_2^+ + S^-$$
$$K_s = \left[SH_2^+\right]\left[S^-\right]$$

and the solvent's pH and pOH are

$$pH = -\log\left[SH_2^+\right]$$
$$pOH = -\log\left[S^-\right]$$

> You should recognize that K_w is just specific form of K_s when the solvent is water.

The most important limitation imposed by K_s is the change in pH during a titration. To understand why this is true, let's consider the titration of 50.0 mL of 1.0×10^{-4} M HCl using 1.0×10^{-4} M NaOH as the titrant. Before the equivalence point, the pH is determined by the untitrated strong acid. For example, when the volume of NaOH is 90% of V_{eq}, the concentration of H_3O^+ is

$$\left[H_3O^+\right] = \frac{M_aV_a - M_bV_b}{V_a + V_b} = \frac{\left(1.0 \times 10^{-4}\ \text{M}\right)\left(50.0\ \text{mL}\right) - \left(1.0 \times 10^{-4}\ \text{M}\right)\left(45.0\ \text{mL}\right)}{50.0\ \text{mL} + 45.0\ \text{mL}} = 5.3 \times 10^{-6}\ \text{M}$$

and the pH is 5.3. When the volume of NaOH is 110% of V_{eq}, the concentration of OH^- is

$$\left[OH^-\right] = \frac{M_bV_b - M_aV_a}{V_a + V_b} = \frac{\left(1.0 \times 10^{-4}\ \text{M}\right)\left(55.0\ \text{mL}\right) - \left(1.0 \times 10^{-4}\ \text{M}\right)\left(50.0\ \text{mL}\right)}{55.0\ \text{mL} + 50.0\ \text{mL}} = 4.8 \times 10^{-6}\ \text{M}$$

and the pOH is 5.3. The titrand's pH is

$$pH = pK_w - pOH = 14.0 - 5.3 = 8.7$$

and the change in the titrand's pH as the titration goes from 90% to 110% of V_{eq} is

$$\Delta pH = 8.7 - 5.3 = 3.4$$

If we carry out the same titration in a nonaqueous amphiprotic solvent that has a K_s of 1.0×10^{-20} , the pH after adding 45.0 mL of NaOH is still 5.3. However, the pH after adding 55.0 mL of NaOH is

$$pH = pK_s - pOH = 20.0 - 5.3 = 14.7$$

In this case the change in pH

$$\Delta pH = 14.7 - 5.3 = 9.4$$

is significantly greater than that obtained when the titration is carried out in water. Figure 9.2.12 shows the titration curves in both the aqueous and the nonaqueous solvents.

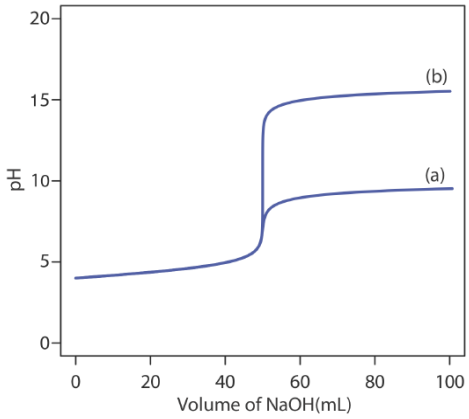


Figure 9.2.12 . Titration curves for 50.0 mL of 1.0×10^{-4} M HCl using 1.0×10^{-4} M NaOH in (a) water, $K_w = 1.0 \times 10^{-14}$, and (b) a nonaqueous amphiprotic solvent, $K_s = 1.0 \times 10^{-20}$.

Another parameter that affects the feasibility of an acid–base titration is the titrand's dissociation constant. Here, too, the solvent plays an important role. The strength of an acid or a base is a relative measure of how easy it is to transfer a proton from the acid to the solvent or from the solvent to the base. For example, HF, with a K_a of 6.8×10^{-4}, is a better proton donor than CH_3COOH, for which K_a is 1.75×10^{-5}.

The strongest acid that can exist in water is the hydronium ion, H_3O^+. HCl and HNO_3 are strong acids because they are better proton donors than H_3O^+ and essentially donate all their protons to H_2O, leveling their acid strength to that of H_3O^+. In a different solvent HCl and HNO_3 may not behave as strong acids.

If we place acetic acid in water the dissociation reaction

$$CH_3COOH(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + CH_3COO^-(aq)$$

does not proceed to a significant extent because CH_3COO^- is a stronger base than H_2O and H_3O^+ is a stronger acid than CH_3COOH. If we place acetic acid in a solvent that is a stronger base than water, such as ammonia, then the reaction

$$CH_3COOH + NH_3 \rightleftharpoons NH_4^+ + CH_3COO^-$$

proceeds to a greater extent. In fact, both HCl and CH_3COOH are strong acids in ammonia.

All other things being equal, the strength of a weak acid increases if we place it in a solvent that is more basic than water, and the strength of a weak base increases if we place it in a solvent that is more acidic than water. In some cases, however, the opposite effect is observed. For example, the pK_b for NH_3 is 4.75 in water and it is 6.40 in the more acidic glacial acetic acid. In contradiction to our expectations, NH_3 is a weaker base in the more acidic solvent. A full description of the solvent's effect on the pK_a of weak acid or the pK_b of a weak base is beyond the scope of this text. You should be aware, however, that a titration that is not feasible in water may be feasible in a different solvent.

REPRESENTATIVE METHOD 9.2.1: DETERMINATION OF PROTEIN IN BREAD

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical acid–base titrimetric method. Although each method is unique, the following description of the determination of protein in bread provides an instructive example of a typical procedure. The description here is based on Method 13.86 as published in *Official Methods of Analysis*, 8th Ed., Association of Official Agricultural Chemists: Washington, D. C., 1955.

Description of the Methods

This method is based on a determination of %w/w nitrogen using the Kjeldahl method. The protein in a sample of bread is oxidized to NH_4^+ using hot concentrated H_2SO_4. After making the solution alkaline, which converts NH_4^+ to NH_3, the ammonia is distilled into a flask that contains a known amount of HCl. The amount of unreacted HCl is determined by a back titration using a standard strong base titrant. Because different cereal proteins contain similar amounts of nitrogen—on average there are 5.7 g protein for every gram of nitrogen—we multiply the experimentally determined %w/w N by a factor of 5.7 gives the %w/w protein in the sample.

Procedure

Transfer a 2.0-g sample of bread, which previously has been air-dried and ground into a powder, to a suitable digestion flask along with 0.7 g of a HgO catalyst, 10 g of K_2SO_4, and 25 mL of concentrated H_2SO_4. Bring the solution to a boil. Continue boiling until the solution turns clear and then boil for at least an additional 30 minutes. After cooling the solution below room temperature, remove the Hg^{2+} catalyst by

adding 200 mL of H_2O and 25 mL of 4% w/v K_2S. Add a few Zn granules to serve as boiling stones and 25 g of NaOH. Quickly connect the flask to a distillation apparatus and distill the NH_3 into a collecting flask that contains a known amount of standardized HCl. The tip of the condenser must be placed below the surface of the strong acid. After the distillation is complete, titrate the excess strong acid with a standard solution of NaOH using methyl red as an indicator (Figure 9.2.13).

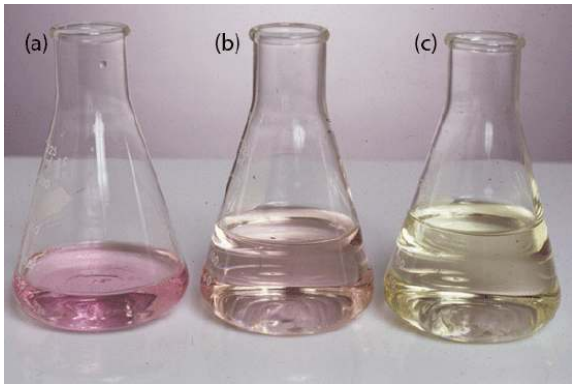


Figure 9.2.13 . Methyl red's endpoint for the titration of a strong acid with a strong base; the indicator is: (a) red prior to the end point; (b) orange at the end point; and (c) yellow after the end point.

Questions

1. Oxidizing the protein converts all of its nitrogen to NH_4^+. Why is the amount of nitrogen not determined by directly titrating the NH_4^+ with a strong base?

There are two reasons for not directly titrating the ammonium ion. First, because NH_4^+ is a very weak acid (its K_a is 5.6×10^{-10}), its titration with NaOH has a poorly-defined end point. Second, even if we can determine the end point with acceptable accuracy and precision, the solution also contains a substantial concentration of unreacted H_2SO_4. The presence of two acids that differ greatly in concentration makes for a difficult analysis. If the titrant's concentration is similar to that of H_2SO_4, then the equivalence point volume for the titration of NH_4^+ is too small to measure reliably. On the other hand, if the titrant's concentration is similar to that of NH_4^+, the volume needed to neutralize the H_2SO_4 is unreasonably large.

2. Ammonia is a volatile compound as evidenced by the strong smell of even dilute solutions. This volatility is a potential source of determinate error. Is this determinate error negative or positive?

Any loss of NH_3 is loss of nitrogen and, therefore, a loss of protein. The result is a negative determinate error.

3. Identify the steps in this procedure that minimize the determinate error from the possible loss of NH_3.

Three specific steps minimize the loss of ammonia: (1) the solution is cooled below room temperature before we add NaOH; (2) after we add NaOH, the digestion flask is quickly connected to the distillation apparatus; and (3) we place the condenser's tip below the surface of the HCl to ensure that the NH_3 reacts with the HCl before it is lost through volatilization.

4. How does K_2S remove Hg^{2+}, and why is its removal important?

Adding sulfide precipitates Hg^{2+} as HgS. This is important because NH_3 forms stable complexes with many metal ions, including Hg^{2+}. Any NH_3 that reacts with Hg^{2+} is not collected during distillation, providing another source of determinate error.

QUANTITATIVE APPLICATIONS

Although many quantitative applications of acid–base titrimetry have been replaced by other analytical methods, a few important applications continue to find use. In this section we review the general application of acid–base titrimetry to the analysis of inorganic and organic compounds, with an emphasis on applications in environmental and clinical analysis. First, however, we discuss the selection and standardization of acidic and basic titrants.

SELECTING AND STANDARDIZING A TITRANT

The most common strong acid titrants are HCl, $HClO_4$, and H_2SO_4. Solutions of these titrants usually are prepared by diluting a commercially available concentrated stock solution. Because the concentration of a concentrated acid is known only approximately, the titrant's concentration is determined by standardizing against one of the primary standard weak bases listed in Table 9.2.4 .

> The nominal concentrations of the concentrated stock solutions are 12.1 M HCl, 11.7 M $HClO_4$, and 18.0 M H_2SO_4. The actual concentrations of these acids are given as %w/v and vary slightly from lot-to-lot.

Table 9.2.4 . Selected Primary Standards for Standardizing Strong Acid and Strong Base Titrants

titrant type	primary standard	titration reaction	comment
strong acid	Na_2CO_3	$Na_2CO_3 + 2H_3O^+ \rightarrow H_2CO_3 + 2Na^+ + 2H_2O$	a
strong acid	$(HOCH_2)3CNH_2$	$(HOCH_2)_3CNH_2 + H_3O^+ \longrightarrow (HOCH_2)_3CNH_3^+ + H_2O$	b
strong acid	$Na2B_4O_7$	$Na_2B_4O_7 + 2H_3O^+ + 3H_2O \rightarrow 2Na^+ + 4H_3BO_3$	
strong base	$KHC_8H_4O_4$	$KHC_8H_4O_4 + OH^- \rightarrow K^+ + C_8H_4O_4^- + H_2O$	c
strong base	C_6H_5COOH	$C_6H_5COOH + OH^- \rightarrow C_6H_5COO^- + H_2O$	d
strong base	$KH(IO_3)_2$	$KH(IO_3)_2 + OH^- \rightarrow K^+ + 2IO_3^- + H_2O$	

(a) The end point for this titration is improved by titrating to the second equivalence point, boiling the solution to expel CO2, and retitrating to the second equivalence point. The reaction in this case is

$$Na_2CO_3 + 2H_3O^+ \rightarrow CO_2 + 2Na^+ + 3H_2O$$

(b) *Tris*-(hydroxymethyl)aminomethane often goes by the shorter name of TRIS or THAM.
(c) Potassium hydrogen phthalate often goes by the shorter name of KHP.
(d) Because it is not very soluble in water, dissolve benzoic acid in a small amount of ethanol before diluting with water.

The most common strong base titrant is NaOH, which is available both as an impure solid and as an approximately 50% w/v solution. Solutions of NaOH are standardized against any of the primary weak acid standards listed in Table 9.3.[4] .

Using NaOH as a titrant is complicated by potential contamination from the following reaction between dissolved CO_2 and OH^-.

$$CO_2(aq) + 2OH^-(aq) \rightarrow CO_3^{2-}(aq) + H_2O(l) \tag{9.3.7}$$

Any solution in contact with the atmosphere contains a small amount of CO_2*(aq)* from the equilibrium

$$CO_2(g) \rightleftharpoons CO_2(aq)$$

During the titration, NaOH reacts both with the titrand and with CO_2, which increases the volume of NaOH needed to reach the titration's end point. This is not a problem if the end point pH is less than 6. Below this pH the CO_3^{2-} from reaction 9.3.7 reacts with H_3O^+ to form carbonic acid.

$$CO_3^{2-}(aq) + 2H_3O^+(aq) \rightarrow 2H_2O(l) + H_2CO_3(aq). \tag{9.3.8}$$

Combining reaction 9.3.7 and reaction 9.3.8 gives an overall reaction that does not include OH^-.

$$CO_2(aq) + H_2O(l) \longrightarrow H_2CO_3(aq)$$

Under these conditions the presence of CO_2 does not affect the quantity of OH^- used in the titration and is not a source of determinate error.

If the end point pH is between 6 and 10, however, the neutralization of CO_3^{2-} requires one proton

$$CO_3^{2-}(aq) + H_3O^+(aq) \rightarrow H_2O(l) + HCO_3^-(aq)$$

and the net reaction between CO_2 and OH^- is

$$CO_2(aq) + OH^-(aq) \rightarrow HCO_3^-(aq)$$

Under these conditions some OH^- is consumed in neutralizing CO_2, which results in a determinate error. We can avoid the determinate error if we use the same end point pH for both the standardization of NaOH and the analysis of our analyte, although this is not always practical.

Solid NaOH is always contaminated with carbonate due to its contact with the atmosphere, and we cannot use it to prepare a carbonate-free solution of NaOH. Solutions of carbonate-free NaOH are prepared from 50% w/v NaOH because Na_2CO_3 is insoluble in concentrated NaOH. When CO_2 is absorbed, Na_2CO_3 precipitates and settles to the bottom of the container, which allow access to the carbonate-free NaOH. When pre- paring a solution of NaOH, be sure to use water that is free from dissolved CO_2. Briefly boiling the water expels CO_2; after it cools, the water is used to prepare carbonate-free solutions of NaOH. A solution of carbonate-free NaOH is relatively stable if we limit its contact with the atmosphere. Standard solutions of sodium hydroxide are not stored in glass bottles as NaOH reacts with glass to form silicate; instead, store such solutions in polyethylene bottles.

INORGANIC ANALYSIS

Acid–base titrimetry is a standard method for the quantitative analysis of many inorganic acids and bases. A standard solution of NaOH is used to determine the concentration of inorganic acids, such as H_3PO_4 or H_3AsO_4, and inorganic bases, such as Na_2CO_3 are analyzed using a standard solution of HCl.

If an inorganic acid or base that is too weak to be analyzed by an aqueous acid–base titration, it may be possible to complete the analysis by adjusting the solvent or by an indirect analysis. For example, when analyzing boric acid, H_3BO_3, by titrating with NaOH, accuracy is limited by boric acid's small acid dissociation constant of 5.8×10^{-10} . Boric acid's K_a value increases to 1.5×10^{-4} in the presence of mannitol, because it forms a stable complex with the borate ion, which results is a sharper end point and a more accurate titration. Similarly, the analysis of ammonium salts is limited by the ammonium ion' small acid dissociation constant of 5.7×10^{-10} . We can determine NH_4^+ indirectly by using a strong base to convert it to NH_3, which is removed by distillation and titrated with HCl. Because NH_3 is a stronger weak base than NH_4^+ is a weak acid (its K_b is 1.58×10^{-5}), the titration has a sharper end point.

We can analyze a neutral inorganic analyte if we can first convert it into an acid or a base. For example, we can determine the concentration of NO_3^- by reducing it to NH_3 in a strongly alkaline solution using Devarda's alloy, a mixture of 50% w/w Cu, 45% w/w Al, and 5% w/w Zn.

$$3NO_3^-(aq) + 8Al(s) + 5OH^-(aq) + 2H_2O(l) \rightarrow 8AlO_2^-(aq) + 3NH_3(aq)$$

The NH_3 is removed by distillation and titrated with HCl. Alternatively, we can titrate NO_3^- as a weak base by placing it in an acidic nonaqueous solvent, such as anhydrous acetic acid, and using $HClO_4$ as a titrant.

Acid–base titrimetry continues to be listed as a standard method for the determination of alkalinity, acidity, and free CO_2 in waters and wastewaters. ***Alkalinity*** is a measure of a sample's capacity to neutralize acids. The most important sources of alkalinity are OH^-, HCO_3^-, and CO_3^{2-}, although other weak bases, such as phosphate, may contribute to the overall alkalinity. Total alkalinity is determined by titrating to a fixed end point pH of 4.5 (or to the bromocresol green end point) using a standard solution of HCl or H_2SO_4. Results are reported as mg $CaCO_3$/L.

> Although a variety of strong bases and weak bases may contribute to a sample's alkalinity, a single titration cannot distinguish between the possible sources. Reporting the total alkalinity as if $CaCO_3$ is the only source provides a means for comparing the acid-neutralizing capacities of different samples.

When the sources of alkalinity are limited to OH^-, HCO_3^-, and CO_3^{2-}, separate titrations to a pH of 4.5 (or the bromocresol green end point) and a pH of 8.3 (or the phenolphthalein end point) allow us to determine which species are present and their respective concentrations. Titration curves for OH^-, HCO_3^-, and $CO_3^{2-}$are shown in Figure 9.2.14 . For a solution that contains OH^- alkalinity only, the volume of strong acid needed to reach each of the two end points is identical (Figure 9.2.14 a). When the only source of alkalinity is CO_3^{2-}, the volume of strong acid needed to reach the end point at a pH of 4.5 is exactly twice that needed to reach the end point at a pH of 8.3 (Figure 9.2.14 b). If a solution contains HCO_3^- alkalinity only, the volume of strong acid needed to reach the end point at a pH of 8.3 is zero, but that for the pH 4.5 end point is greater than zero (Figure 9.2.14 c).

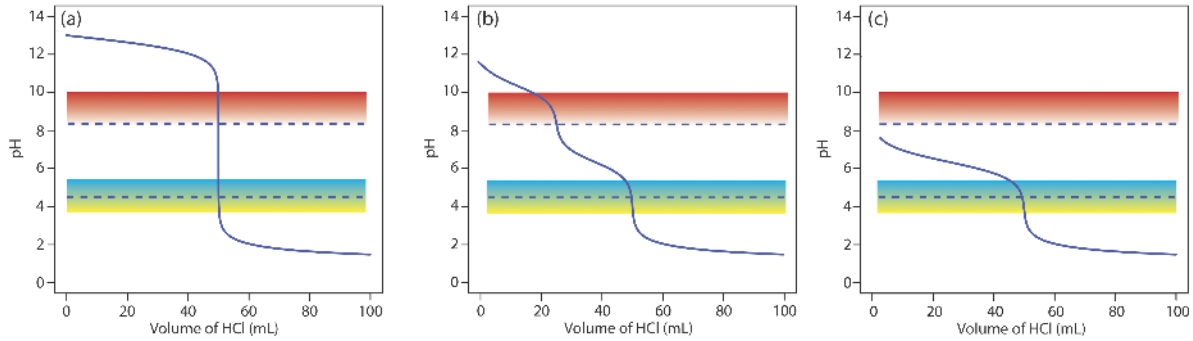


Figure 9.2.14 . Titration curves for 50.0 mL of (a) 0.10 M NaOH, (b) 0.050 M Na_2CO_3, and (c) 0.10 M $NaHCO_3$ using 0.10 M HCl as a titrant. The dashed lines indicate the fixed pH end points of 8.3 and 4.5. The color gradients show the phenolphthalein (red-to-colorless) and the bromocresol green (blue-to-green) endpoints. When titrating to the phenolphthalein endpoint, the titration continues until the last trace of red is lost.

A mixture of OH^- and CO_3^{2-} or a mixture of HCO_3^- and CO_3^{2-} also is possible. Consider, for example, a mixture of OH^- and CO_3^{2-}. The volume of strong acid to titrate OH^- is the same whether we titrate to a pH of 8.3 or a pH of 4.5. Titrating CO_3^{2-} to a pH of 4.5, however, requires twice as much strong acid as titrating to a pH of 8.3. Consequently, when we titrate a mixture of these two ions, the volume of strong acid needed to reach a pH of 4.5 is less than twice that needed to reach a pH of 8.3. For a mixture of HCO_3^- and CO_3^{2-} the volume of strong acid needed to reach a pH of 4.5 is more than twice that needed to reach a pH of 8.3. Table 9.2.5 summarizes the relationship between the sources of alkalinity and the volumes of titrant needed to reach the two end points.

> A mixture of OH^- and HCO_3^- is unstable with respect to the formation of CO_3^{2-}. Problem 15 in the end-of-chapter problems asks you to explain why this is true.

Table 9.2.5 . Relationship Between End Point Volumes and Sources of Alkalinity

source of alkalinity	relationship between end point volumes
OH^-	$V_{pH\ 4.5} = V_{pH\ 8.3}$
CO_3^{2-}	$V_{pH\ 4.5} = 2 \times V_{pH\ 8.3}$
HCO_3^-	$V_{pH\ 4.5} > 0; V_{pH\ 8.3} = 0$
OH^- and CO_3^{2-}	$V_{pH\ 4.5} < 2 \times V_{pH\ 8.3}$
CO_3^{2-} and HCO_3^-	$V_{pH\ 4.5} > 2 \times V_{pH\ 8.3}$

Acidity is a measure of a water sample's capacity to neutralize base and is divided into strong acid and weak acid acidity. Strong acid acidity from inorganic acids such as HCl, HNO_3, and H_2SO_4 is common in industrial effluents and in acid mine drainage. Weak acid acidity usually is dominated by the formation of H_2CO_3 from dissolved CO_2, but also includes contributions from hydrolyzable metal ions such as Fe^{3+}, Al^{3+}, and Mn^{2+}. In addition, weak acid acidity may include a contribution from organic acids.

Acidity is determined by titrating with a standard solution of NaOH to a fixed pH of 3.7 (or the bromothymol blue end point) and to a fixed pH of 8.3 (or the phenolphthalein end point). Titrating to a pH of 3.7 provides a measure of strong acid acidity, and titrating to a pH of 8.3 provides a measure of total acidity. Weak acid acidity is the difference between the total acidity and the strong acid acidity. Results are expressed as the amount of $CaCO_3$ that can be neutralized by the sample's acidity. An alternative approach for determining strong acid and weak acid acidity is to obtain a potentiometric titration curve and use a Gran plot to determine the two equivalence points. This approach has been used, for example, to determine the forms of acidity in atmospheric aerosols [Ferek, R. J.; Lazrus, A. L.; Haagenson, P. L.; Winchester, J. W. *Environ. Sci. Technol.* **1983**, *17*, 315–324].

> As is the case with alkalinity, acidity is reported as mg $CaCO_3$/L.

Water in contact with either the atmosphere or with carbonate-bearing sediments contains free CO_2 in equilibrium with $CO_2(g)$ and with aqueous H_2CO_3, HCO_3^- and CO_3^{2-}. The concentration of free CO_2 is determined by titrating with a standard solution of NaOH to the phenolphthalein end point, or to a pH of 8.3, with results reported as mg CO_2/L. This analysis essentially is the same as that for the determination of total acidity and is used only for water samples that do not contain strong acid acidity.

> Free CO_2 is the same thing as $CO_2(aq)$.

ORGANIC ANALYSIS

Acid–base titrimetry continues to have a small, but important role for the analysis of organic compounds in pharmaceutical, biochemical, agricultur- al, and environmental laboratories. Perhaps the most widely employed acid–base titration is the ***Kjeldahl analysis*** for organic nitrogen. Examples of analytes determined by a Kjeldahl analysis include caffeine and saccharin in pharmaceutical products, proteins in foods, and the analysis of nitrogen in fertilizers, sludges, and sediments. Any nitrogen present in a –3 oxidation state is oxidized quantitatively to NH_4^+. Because some aromatic heterocyclic compounds, such as pyridine, are difficult to oxidize, a catalyst is used to ensure a quantitative oxidation. Nitrogen in other oxidation states, such as nitro and azo nitrogens, are oxidized to N_2, which results in a negative determinate error. Including a reducing agent, such as salicylic acid, converts this nitrogen to a –3 oxidation state, eliminating this source of error. Table 9.2.6 provides additional examples in which an element is converted quantitatively into a titratable acid or base.

Table 9.2.6 . Selected Elemental Analyses Based on an Acid–Base Titration

element	convert to...	reaction producing titratable species	titration details
N	NH_3 (g)	NH3 (aq) + **HCl** (aq) → NH_4^+ (aq) + Cl^- (aq)	add HCl in excess and back titrate with NaOH
S	SO_2(g)	SO_3 (g) + H_2O_2 (aq) → **H_2SO_4** (aq)	titrate H_2SO_4 with NaOH
C	CO_2 (g)	CO_2 (g) + **$Ba(OH)_2$** (aq) → $BaCO_3$ (s) + H_2O (l)	add excess $Ba(OH)_2$ and back titrate with HCl
Cl	**HCl** (g)	—	titrate HCl with NaOH
F	SiF_4 (g)	$3SiF_4$ (aq) + $2H_2O$ (l) → **$2H_3SiF_6$** (aq) + SiO2 (s)	titrate H_2SiF_6 with NaOH
the species that is titrated is shown in **bold**			

Several organic functional groups are weak acids or weak bases. Carboxylic (–COOH), sulfonic ($–SO_3H$) and phenolic ($–C_6H_5OH$) functional groups are weak acids that are titrated successfully in either aqueous or non-aqueous solvents. Sodium hydroxide is the titrant of choice for aqueous solutions. Nonaqueous titrations often are carried out in a basic solvent, such as ethylenediamine, using tetrabutylammonium hydroxide, $(C_4H_9)_4NOH$, as the titrant. Aliphatic and aromatic amines are weak bases that are titrated using HCl in aqueous solutions, or $HClO_4$ in glacial acetic acid. Other functional groups are analyzed indirectly following a reaction that produces or consumes an acid or base. Typical examples are shown in Table 9.2.7 .

Table 9.2.7 . Selected Acid–Base Titrimetric Methods for Organic Functional Groups Based on the Production or Consumption of Acid or Base

functional group	reaction producing titratable species	titration details
ester	RCOOR' (aq) + **OH^-** (aq) → $RCOO^-$ (aq) + HOR' (aq)	titrate OH^- with HCl
carbonyl	R_2CO (aq) + NH4OH•HCl (aq) → R_2CNOH (aq) + **HCl** (aq) + H2O (l)	titrate HCl with NaOH
alcohol	[1]: $(CH_3CO)_2O$ + ROH → CH_3COOR + **CH_3COOH** [2]: $(CH_3CO)_2)$ + H_2O → 2**CH_3COOH**	titrate CH_3COOH with NaOH; a blank titration of acetic anhydride, $(CH_3CO)_2O$, corrects for the contribution of reaction [2]

the species that is titrated is shown in **bold**
for alcohols, reaction [1] is carried out in pyridine to prevent the hydrolysis of acetic anhydride by water. After reaction [1] is complete, water is added to covert any unreacted acetic anhydride to acetic acid (reaction [2])

Many pharmaceutical compounds are weak acids or weak bases that are analyzed by an aqueous or a nonaqueous acid–base titration; examples include salicylic acid, phenobarbital, caffeine, and sulfanilamide. Amino acids and proteins are analyzed in glacial acetic acid using $HClO_4$ as the titrant. For example, a procedure for determining the amount of nutritionally available protein uses an acid–base titration of lysine residues [(a) Molnár-Perl, I.; Pintée-Szakács, M. *Anal. Chim. Acta* **1987**, *202*, 159–166; (b) Barbosa, J.; Bosch, E.; Cortina, J. L.; Rosés, M. *Anal. Chim. Acta* **1992**, *256*, 177–181].

QUANTITATIVE CALCULATIONS

The quantitative relationship between the titrand and the titrant is determined by the titration reaction's stoichiometry. If the titrand is polyprotic, then we must know to which equivalence point we are titrating. The following example illustrates how we can use a ladder diagram to determine a titration reaction's stoichiometry.

EXAMPLE 9.2.2

A 50.00-mL sample of a citrus drink requires 17.62 mL of 0.04166 M NaOH to reach the phenolphthalein end point. Express the sample's acidity as grams of citric acid, $C_6H_8O_7$, per 100 mL.

Solution

Because citric acid is a triprotic weak acid, we first must determine if the phenolphthalein end point corresponds to the first, second, or third equivalence point. Citric acid's ladder diagram is shown in Figure 9.2.15 a. Based on this ladder diagram, the first equivalence point is between a pH of 3.13 and a pH of 4.76, the second equivalence point is between a pH of 4.76 and a pH of 6.40, and the third equivalence point is greater than a pH of 6.40. Because phenolphthalein's end point pH is 8.3–10.0 (see Table 9.2.3), the titration must proceed to the third equivalence point and the titration reaction is

$$C_6H_8O_7(aq) + 3OH^-(aq) \longrightarrow C_6H_5O_7^{3-}(aq) + 3H_2O(l)$$

To reach the equivalence point, each mole of citric acid consumes three moles of NaOH; thus

$$(0.04166\ \text{M NaOH})(0.01762\ \text{L NaOH}) = 7.3405 \times 10^{-4}\ \text{mol NaOH}$$

$$7.3405 \times 10^{-4}\ \text{mol NaOH} \times \frac{1\ \text{mol}\ C_6H_8O_7}{3\ \text{mol NaOH}} = 2.4468 \times 10^{-4}\ \text{mol}\ C_6H_8O_7$$

$$2.4468 \times 10^{-4}\ \text{mol}\ C_6H_8O_7 \times \frac{192.1\ \text{g}\ C_6H_8O_7}{\text{mol}\ C_6H_8O_7} = 0.04700\ \text{g}\ C_6H_8O_7$$

Because this is the amount of citric acid in a 50.00 mL sample, the concentration of citric acid in the citrus drink is 0.09400 g/100 mL. The complete titration curve is shown in Figure 9.2.15 b.

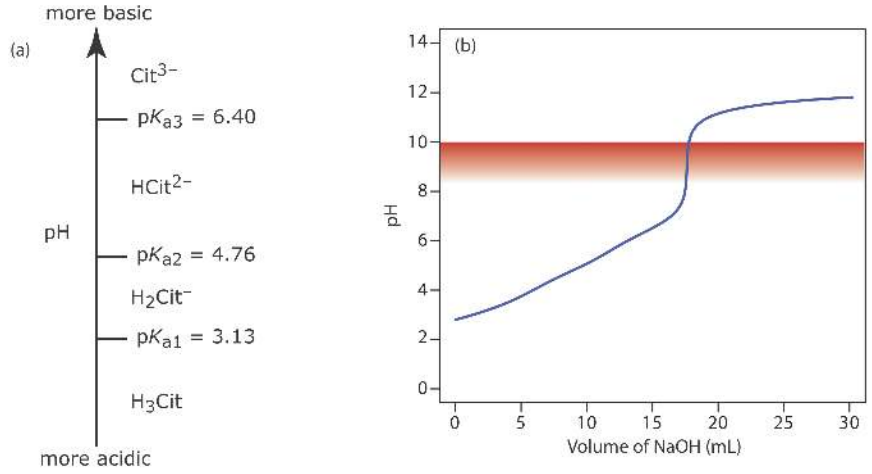


Figure 9.2.15 . (a) Ladder diagram for citric acid; (b) Titration curve for the sample in Example 9.2.2 showing phenolphthalein's pH transition region.

? EXERCISE 9.2.6

Your company recently received a shipment of salicylic acid, $C_7H_6O_3$, for use in the production of acetylsalicylic acid (aspirin). You can accept the shipment only if the salicylic acid is more than 99% pure. To evaluate the shipment's purity, you dissolve a 0.4208-g sample in water and titrate to the phenolphthalein end point, using 21.92 mL of 0.1354 M NaOH. Report the shipment's purity as %w/w $C_7H_6O_3$. Salicylic acid is a diprotic weak acid with pK_a values of 2.97 and 13.74.

Answer

Because salicylic acid is a diprotic weak acid, we must first determine to which equivalence point it is being titrated. Using salicylic acid's pK_a values as a guide, the pH at the first equivalence point is between 2.97 and 13.74, and the second equivalence points is at a pH greater than 13.74. From Table 9.2.3 , phenolphthalein's end point is in the pH range 8.3–10.0. The titration, therefore, is to the first equivalence point for which the moles of NaOH equal the moles of salicylic acid; thus

$$(0.1354\ \text{M})(0.02192\ \text{L}) = 2.968 \times 10^{-3}\ \text{mol NaOH}$$

$$2.968 \times 10^{-3}\ \text{mol NaOH} \times \frac{1\ \text{mol}\ C_7H_6O_3}{\text{mol NaOH}} \times \frac{138.12\ \text{g}\ C_7H_6O_3}{\text{mol}\ C_7H_6O_3} = 0.4099\ \text{g}\ C_7H_6O_3$$

$$\frac{0.4099\ \text{g}\ C_7H_6O_3}{0.4208\ \text{g sample}} \times 100 = 97.41\ \%\text{w/w}\ C_7H_6O_3$$

Because the purity of the sample is less than 99%, we reject the shipment.

In an indirect analysis the analyte participates in one or more preliminary reactions, one of which produces or consumes acid or base. Despite the additional complexity, the calculations are straightforward.

✔ EXAMPLE 9.2.3

The purity of a pharmaceutical preparation of sulfanilamide, $C_6H_4N_2O_2S$, is determined by oxidizing the sulfur to SO_2 and bubbling it through H_2O_2 to produce H_2SO_4. The acid is titrated to the bromothymol blue end point using a standard solution of NaOH. Calculate the purity of the preparation given that a 0.5136-g sample requires 48.13 mL of 0.1251 M NaOH.

Solution

The bromothymol blue end point has a pH range of 6.0–7.6. Sulfuric acid is a diprotic acid, with a pK_{a2} of 1.99 (the first K_a value is very large and the acid dissociation reaction goes to completion, which is why H_2SO4 is a strong acid). The titration, therefore, proceeds to the second equivalence point and the titration reaction is

$$H_2SO_4(aq) + 2OH^-(aq) \longrightarrow 2H_2O(l) + SO_4^{2-}(aq)$$

Using the titration results, there are

$$(0.1251\ \text{M NaOH})(0.04813\ \text{L NaOH}) = 6.021 \times 10^{-3}\ \text{mol NaOH}$$

$$6.012 \times 10^{-3}\ \text{mol NaOH} \times \frac{1\ \text{mol}\ H_2SO_4}{2\ \text{mol NaOH}} = 3.010 \times 10^{-3}\ \text{mol}\ H_2SO_4$$

$$3.010 \times 10^{-3}\ \text{mol}\ H_2SO_4 \times \frac{1\ \text{mol S}}{\text{mol}\ H_2SO_4} \times \frac{1\ \text{mol}\ C_6H_4N_2O_2S}{\text{mol S}} \times \frac{168.17\ \text{g}\ C_6H_4N_2O_2S}{\text{mol}\ C_6H_4N_2O_2S} = 0.5062\ \text{g}\ C_6H_4N_2O_2S$$

produced when the SO_2 is bubbled through H_2O_2. Because all the sulfur in H_2SO_4 comes from the sulfanilamide, we can use a conservation of mass to determine the amount of sulfanilamide in the sample.

$$\frac{0.5062\ \text{g}\ C_6H_4N_2O_2S}{0.5136\ \text{g sample}} \times 100 = 98.56\ \%\text{w/w}\ C_6H_4N_2O_2S$$

? EXERCISE 9.2.7

The concentration of NO_2 in air is determined by passing the sample through a solution of H_2O_2, which oxidizes NO_2 to HNO_3, and titrating the HNO_3 with NaOH. What is the concentration of NO_2, in mg/L, if a 5.0 L sample of air requires 9.14 mL of 0.01012 M NaOH to reach the methyl red end point

Answer

The moles of HNO_3 produced by pulling the sample through H_2O_2 is

$$(0.01012\ \text{M})(0.00914\ \text{L}) \times \frac{1\ \text{mol}\ HNO_3}{\text{mol NaOH}} = 9.25 \times 10^{-5}\ \text{mol}\ HNO_3$$

A conservation of mass on nitrogen requires that each mole of NO_2 produces one mole of HNO_3; thus, the mass of NO_2 in the sample is

$$9.25 \times 10^{-5}\ \text{mol}\ HNO_3 \times \frac{1\ \text{mol}\ NO_2}{\text{mol}\ HNO_3} \times \frac{46.01\ \text{g}\ NO_2}{\text{mol}\ NO_2} = 4.26 \times 10^{-3}\ \text{g}\ NO_2$$

and the concentration of NO_2 is

$$\frac{4.26 \times 10^{-3}\ \text{g}\ NO_2}{5\ \text{L air}} \times \frac{1000\ \text{mg}}{\text{g}} = 0.852\ \text{mg}\ NO_2\ \text{L air}$$

For a back titration we must consider two acid–base reactions. Again, the calculations are straightforward.

✓ EXAMPLE 9.2.4

The amount of protein in a sample of cheese is determined by a Kjeldahl analysis for nitrogen. After digesting a 0.9814-g sample of cheese, the nitrogen is oxidized to NH_4^+, converted to NH_3 with NaOH, and the NH_3 distilled into a collection flask that contains 50.00 mL of 0.1047 M HCl. The excess HCl is back titrated with 0.1183 M NaOH, requiring 22.84 mL to reach the bromothymol blue end point. Report the %w/w protein in the cheese assuming there are 6.38 grams of protein for every gram of nitrogen in most dairy products.

Solution

The HCl in the collection flask reacts with two bases

$$HCl(aq) + NH_3(aq) \rightarrow NH_4^+(aq) + Cl^-(aq)$$

$$HCl(aq) + OH^-(aq) \rightarrow H_2O(l) + Cl^-(aq)$$

The collection flask originally contains

$$(0.1047\ \text{M HCl})(0.05000\ \text{L HCl}) = 5.235 \times 10^{-3}\text{mol HCl}$$

of which

$$(0.1183\ \text{M NaOH})(0.02284\ \text{L NaOH}) \times \frac{1\ \text{mol HCl}}{\text{mol NaOH}} = 2.702 \times 10^{-3}\ \text{mol HCl}$$

react with NaOH. The difference between the total moles of HCl and the moles of HCl that react with NaOH is the moles of HCl that react with NH_3.

$$5.235 \times 10^{-3}\ \text{mol HCl} - 2.702 \times 10^{-3}\ \text{mol HCl} = 2.533 \times 10^{-3}\ \text{mol HCl}$$

Because all the nitrogen in NH_3 comes from the sample of cheese, we use a conservation of mass to determine the grams of nitrogen in the sample.

$$2.533 \times 10^{-3} \text{ mol HCl} \times \frac{1 \text{ mol NH}_3}{\text{mol HCl}} \times \frac{14.01 \text{ g N}}{\text{mol NH}_3} = 0.03549 \text{ g N}$$

The mass of protein, therefore, is

$$0.03549 \text{ g N} \times \frac{6.38 \text{ g protein}}{\text{g N}} = 0.2264 \text{ g protein}$$

and the % w/w protein is

$$\frac{0.2264 \text{ g protein}}{0.9814 \text{ g sample}} \times 100 = 23.1 \text{ \%w/w protein}$$

EXERCISE 9.2.8

Limestone consists mainly of $CaCO_3$, with traces of iron oxides and other metal oxides. To determine the purity of a limestone, a 0.5413-g sample is dissolved using 10.00 mL of 1.396 M HCl. After heating to expel CO_2, the excess HCl was titrated to the phenolphthalein end point, requiring 39.96 mL of 0.1004 M NaOH. Report the sample's purity as %w/w $CaCO_3$.

Answer

The total moles of HCl used in this analysis is

$$(1.396 \text{ M})(0.01000 \text{ L}) = 1.396 \times 10^{-2} \text{ mol HCl}$$

Of the total moles of HCl

$$(0.1004 \text{ M NaOH})(0.03996 \text{ L}) \times \frac{1 \text{ mol HCl}}{\text{mol NaOH}} = 4.012 \times 10^{-3} \text{ mol HCl}$$

are consumed in the back titration with NaOH, which means that

$$1.396 \times 10^{-2} \text{ mol HCl} - 4.012 \times 10^{-3} \text{ mol HCl} = 9.95 \times 10^{-3} \text{ mol HCl}$$

react with the $CaCO_3$. Because CO_3^{2-} is dibasic, each mole of $CaCO_3$ consumes two moles of HCl; thus

$$9.95 \times 10^{-3} \text{ mol HCl} \times \frac{1 \text{ mol CaCO}_3}{2 \text{ mol HCl}} \times \frac{100.09 \text{ g CaCO}_3}{\text{mol CaCO}_3} = 0.498 \text{ g CaCO}_3$$

$$\frac{0.498 \text{ g CaCO}_3}{0.5143 \text{ g sample}} \times 100 = 96.8 \text{ \%w/w CaCO}_3$$

Earlier we noted that we can use an acid–base titration to analyze a mixture of acids or bases by titrating to more than one equivalence point. The concentration of each analyte is determined by accounting for its contribution to each equivalence point.

EXAMPLE 9.2.5

The alkalinity of natural waters usually is controlled by OH^-, HCO_3^-, and CO_3^{2-}, present singularly or in combination. Titrating a 100.0-mL sample to a pH of 8.3 requires 18.67 mL of 0.02812 M HCl. A second 100.0-mL aliquot requires 48.12 mL of the same titrant to reach a pH of 4.5. Identify the sources of alkalinity and their concentrations in milligrams per liter.

Solution

Because the volume of titrant to reach a pH of 4.5 is more than twice that needed to reach a pH of 8.3, we know from Table 9.2.5 , that the sample's alkalinity is controlled by CO_3^{2-} and HCO_3^-. Titrating to a pH of 8.3 neutralizes CO_3^{2-} to HCO_3^-

$$CO_3^{2-}(aq) + HCl(aq) \rightarrow HCO_3^-(aq) + Cl^-(aq)$$

but there is no reaction between the titrant and HCO_3^- (see Figure 9.2.14). The concentration of CO_3^{2-} in the sample, therefore, is

$$(0.02812\ \text{M HCl})(0.01867\ \text{L HCl}) \times \frac{1\ \text{mol}\ CO_3^{2-}}{\text{mol HCl}} = 5.250 \times 10^{-4}\ \text{mol}\ CO_3^{2-}$$

$$\frac{5.250 \times 10^{-4}\ \text{mol}\ CO_3^{2-}}{0.1000\ \text{L}} \times \frac{60.01\ \text{g}\ CO_3^{2-}}{\text{mol}\ CO_3^{2-}} \times \frac{1000\ \text{mg}}{\text{g}} = 315.1\ \text{mg/L}$$

Titrating to a pH of 4.5 neutralizes CO_3^{2-} to H_2CO_3 and neutralizes HCO_3^- to H_2CO_3 (see Figure 9.2.14).

$$CO_3^{2-}(aq) + 2HCl(aq) \rightarrow H_2CO_3(aq) + 2Cl^-(aq)$$
$$HCO_3^-(aq) + HCl(aq) \rightarrow H_2CO_3(aq) + Cl^-(aq)$$

Because we know how many moles of CO_3^{2-} are in the sample, we can calculate the volume of HCl it consumes.

$$5.250 \times 10^{-4}\ \text{mol}\ CO_3^{2-} \times \frac{2\ \text{mol HCl}}{\text{mol}\ CO_3^{2-}} \times \frac{1\ \text{L HCl}}{0.02812\ \text{mol HCl}} \times \frac{1000\ \text{mL}}{\text{L}} = 37.34\ \text{mL HCl}$$

This leaves 48.12 mL–37.34 mL, or 10.78 mL of HCl to react with HCO_3^-. The amount of HCO_3^- in the sample is

$$(0.02812\ \text{M HCl})(0.01078\ \text{L HCl}) \times \frac{1\ \text{mol}\ HCO_3^-}{\text{mol HCl}} = 3.031 \times 10^{-4}\ \text{mol}\ HCO_3^-$$

The sample contains 315.1 mg CO_3^{2-}/L and 185.0 mg HCO_3^-/L

? EXERCISE 9.2.9

Samples that contain a mixture of the monoprotic weak acids 2–methylanilinium chloride ($C_7H_{10}NCl$, pK_a = 4.447) and 3–nitrophenol ($C_6H_5NO_3$, pK_a = 8.39) can be analyzed by titrating with NaOH. A 2.006-g sample requires 19.65 mL of 0.200 M NaOH to reach the bromocresol purple end point and 48.41 mL of 0.200 M NaOH to reach the phenolphthalein end point. Report the %w/w of each compound in the sample.

Answer

Of the two analytes, 2-methylanilinium is the stronger acid and is the first to react with the titrant. Titrating to the bromocresol purple end point, therefore, provides information about the amount of 2-methylanilinium in the sample.

$$(0.200\ \text{M NaOH})(0.01965\ \text{L}) \times \frac{1\ \text{mol}\ C_7H_{10}NCl}{\text{mol NaOH}} \times \frac{143.61\ \text{g}\ C_7H_{10}NCl}{\text{mol}\ C_7H_{10}NCl} = 0.564\ \text{g}\ C_7H_{10}NCl$$

$$\frac{0.564\ \text{g}\ C_7H_{10}NCl}{2.006\ \text{g sample}} \times 100 = 28.1\ \%\text{w/w}\ C_7H_{10}NCl$$

Titrating from the bromocresol purple end point to the phenolphthalein end point, a total of 48.41 mL – 19.65 mL = 28.76 mL, gives the amount of NaOH that reacts with 3-nitrophenol. The amount of 3-nitrophenol in the sample, therefore, is

$$(0.200\ \text{M NaOH})(0.02876\ \text{L}) \times \frac{1\ \text{mol}\ C_6H_5NO_3}{\text{mol NaOH}} \times \frac{139.11\ \text{g}\ C_6H_5NO_3}{\text{mol}\ C_6H_5NO_3} = 0.800\ \text{g}\ C_6H_5NO_3$$

$$\frac{0.800\ \text{g}\ C_6H_5NO_3}{2.006\ \text{g sample}} \times 100 = 39.8\ \%\text{w/w}\ C_6H_5NO_3$$

QUALITATIVE APPLICATIONS

Example 9.5 shows how we can use an acid–base titration to determine the forms of alkalinity in waters and their concentrations. We can extend this approach to other systems. For example, if we titrate a sample to the methyl orange end point and the phenolphthalein end point using either a strong acid or a strong base, we can determine which of the following species are present and their concentrations: H_3PO_4, $H_2PO_4^-$, HPO_4^{2-}, PO_4^{3-}, HCl, and NaOH. As outlined in Table 9.2.8 , each species or mixture of species has a unique relationship between the volumes of titrant needed to reach these two end points. Note that mixtures containing three or more these species are not possible.

Use a ladder diagram to convince yourself that mixtures containing three or more of these species are unstable.

Table 9.2.8 . Relationship Between End Point Volumes for Mixtures of Phosphate Species with HCl and NaOH

solution composition	relationship between end point volumes with strong base titrant	relationship between end point volumes with strong acid titrant
H_3PO_4	$V_{PH} = 2 \times V_{MO}$	—
$H_2PO_4^-$	$V_{PH} > 0; V_{MO} = 0$	—
HPO_4^{2-}	—	$V_{MO} > 0; V_{PH} = 0$
PO_4^{3-}	—	$V_{MO} = 2 \times V_{PH}$
HCl	$V_{PH} = V_{MO}$	—
NaOH	—	$V_{MO} = V_{PH}$
HCl and H_3PO_4	$V_{PH} < 2 \times V_{MO}$	—
H_3PO_4 and $H_2PO_4^-$	$V_{PH} > 2 \times V_{MO}$	—
$H_2PO_4^-$ and HPO_4^{2-}	$V_{PH} > 0; V_{MO} = 0$	$V_{MO} > 0; V_{PH} = 0$
HPO_4^{2-} and PO_4^{3-}	—	$V_{MO} > 2 \times V_{PH}$
PO_4^{3-} and NaOH	—	$V_{MO} < 2 \times V_{PH}$

V_{PH} and V_{MO} are, respectively, the volume of titrant at the phenolphthalein and methyl orange end points
when no information is provided, the volume at each end point is zero

CHARACTERIZATION APPLICATIONS

In addition to a quantitative analysis and a qualitative analysis, we also can use an acid–base titration to characterize the chemical and physical properties of matter. Two useful characterization applications are the determination of a compound's equivalent weight and the determination of its acid dissociation constant or its base dissociation constant.

EQUIVALENT WEIGHTS

Suppose we titrate a sample of an impure weak acid to a well-defined end point using a monoprotic strong base as the titrant. If we assume the titration involves the transfer of *n* protons, then the moles of titrant needed to reach the end point is

$$\text{moles titrant} = \frac{n \text{ moles titrant}}{\text{moles analyte}} \times \text{moles analyte}$$

If we know the analyte's identity, we can use this equation to determine the amount of analyte in the sample

$$\text{grams analyte} = \text{moles titrant} \times \frac{1 \text{ mole analyte}}{n \text{ moles analyte}} \times FW \text{ analyte}$$

where *FW* is the analyte's formula weight.

But what if we do not know the analyte's identify? If we titrate a pure sample of the analyte, we can obtain some useful information that may help us establish its identity. Because we do not know the number of protons that are titrated, we let $n = 1$ and replace the analyte's formula weight with its equivalent weight (*EW*)

$$\text{grams analyte} = \text{moles titrant} \times \frac{1 \text{ equivalent analyte}}{1 \text{ mole analyte}} = EW \text{ analyte}$$

where

$$FW = n \times EW$$

✔ EXAMPLE 9.2.6

A 0.2521-g sample of an unknown weak acid is titrated with 0.1005 M NaOH, requiring 42.68 mL to reach the phenolphthalein end point. Determine the compound's equivalent weight. Which of the following compounds is most likely to be the unknown weak acid?

acid	formula	formula weight (g/mol)	type
ascorbic acid	$C_8H_8O_6$	176.1	monoprotic
malonic acid	$C_3H_4O_4$	104.1	diprotic
succinic acid	C_4H_6O4	118.1	diprotic
citric acid	$C_6H_8O_7$	192.1	triprotic

Solution

The moles of NaOH needed to reach the end point is

$$(0.1005 \text{ M NaOH})(0.04268 \text{ L NaOH}) = 4.289 \times 10^{-3} \text{ mol NaOH}$$

The equivalents of weak acid are the same as the moles of NaOH used in the titration; thus, he analyte's equivalent weight is

$$EW = \frac{0.2521\ \text{g}}{4.289 \times 10^{-3}\ \text{equivalents}} = 58.78\ \text{g/equivalent}$$

The possible formula weights for the weak acid are 58.78 g/mol (n = 1), 117.6 g/mol (n = 2), and 176.3 g/mol (n = 3). If the analyte is a monoprotic weak acid, then its formula weight is 58.78 g/mol, eliminating ascorbic acid as a possibility. If it is a diprotic weak acid, then the analyte's formula weight is either 58.78 g/mol or 117.6 g/mol, depending on whether the weak acid was titrated to its first or its second equivalence point. Succinic acid, with a formula weight of 118.1 g/mole is a possibility, but malonic acid is not. If the analyte is a triprotic weak acid, then its formula weight is 58.78 g/mol, 117.6 g/mol, or 176.3 g/mol. None of these values is close to the formula weight for citric acid, eliminating it as a possibility. Only succinic acid provides a possible match.

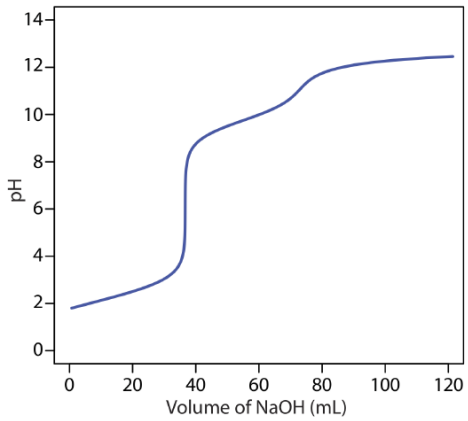


Figure 9.2.16 . Titration curve for Exercise 9.2.10 .

? EXERCISE 9.2.10

Figure 9.2.16 shows the potentiometric titration curve for the titration of a 0.500-g sample an unknown weak acid. The titrant is 0.1032 M NaOH. What is the weak acid's equivalent weight?

Answer

The first of the two visible end points is approximately 37 mL of NaOH. The analyte's equivalent weight, therefore, is

$$(0.1032\ \text{M NaOH})(0.037\ \text{L}) \times \frac{1\ \text{equivalent}}{\text{mol NaOH}} = 3.8 \times 10^{-3}\ \text{equivalents}$$

$$EW = \frac{0.5000\ \text{g}}{3.8 \times 10^{-3}\ \text{equivalents}} = 1.3 \times 10^{2}\ \text{g/equivalent}$$

EQUILIBRIUM CONSTANTS

Another application of acid–base titrimetry is the determination of a weak acid's or a weak base's dissociation constant. Consider, for example, a solution of acetic acid, CH_3COOH, for which the dissociation constant is

$$K_a = \frac{[H_3O^+]\,[CH_3COO^-]}{[CH_3COOH]}$$

When the concentrations of CH_3COOH and CH_3COO^- are equal, the K_a expression reduces to $K_a = [H_3O^+]$, or pH = pK_a. If we titrate a solution of acetic acid with NaOH, the pH equals the pK_a when the volume of NaOH is approximately $1/2V_{eq}$. As shown in Figure 9.2.17 , a potentiometric titration curve provides a reasonable estimate of acetic acid's pK_a.

Recall that pH = pK_a is a step on a ladder diagram, which divides the pH axis into two regions, one where the weak acid is the predominate species, and one where its conjugate weak base is the predominate species.

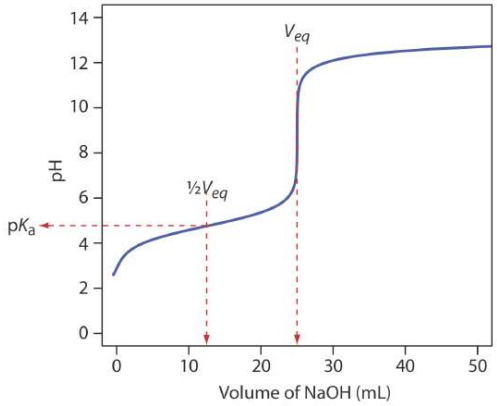


Figure 9.2.17 . Estimating acetic acid's pK_a using its potentiometric titration curve.

This method provides a reasonable estimate for a weak acid's pK_a if the acid is neither too strong nor too weak. These limitations are easy to appreciate if we consider two limiting cases. For the first limiting case, let's assume the weak acid, HA, is more than 50% dissociated before the titration begins (a relatively large K_a value); in this case the concentration of HA before the equivalence point is always less than the concentration of A^- and there is no point on the titration curve where [HA] = [A^-]. At the other extreme, if the acid is too weak, then less than 50% of the weak acid reacts with the titrant at the equivalence point. In this case the concentration of HA before the equivalence point is always greater than that of A^-. Determining the pK_a by the half-equivalence point method overestimates its value if the acid is too strong and underestimates its value if the acid is too weak.

? EXERCISE 9.2.11

Use the potentiometric titration curve in Figure 9.2.16 to estimate the pK_a values for the weak acid in Exercise 9.2.10 .

Answer

At $1/2V_{eq}$, or approximately 18.5 mL, the pH is approximately 2.2; thus, we estimate that the analyte's pK_a is 2.2.

A second approach for determining a weak acid's pK_a is to use a Gran plot. For example, earlier in this chapter we derived the following equation for the titration of a weak acid with a strong base.

$$\left[H_3O^+\right] \times V_b = K_a V_{eq} - K_a V_b$$

A plot of $[H_3O^+] \times V_b$ versus V_b for volumes less than the equivalence point yields a straight line with a slope of $-K_a$. Other linearizations have been developed that use the entire titration curve or that require no assumptions [(a) Gonzalez, A. G.; Asuero, A. G. *Anal. Chim. Acta* **1992**, *256*, 29–33; (b) Papanastasiou, G.; Ziogas, I.; Kokkindis, G. *Anal. Chim. Acta* **1993**, *277*, 119–135]. This approach to determining an acidity constant has been used to study the acid–base properties of humic acids, which are naturally occurring, large molecular weight organic acids with multiple acidic sites. In one study a humic acid was found to have six titratable sites, three which were identified as carboxylic acids, two which were believed to be secondary or tertiary amines, and one which was identified as a phenolic group [Alexio, L. M.; Godinho, O. E. S.; da Costa, W. F. *Anal. Chim. Acta* **1992**, *257*, 35–39].

Values of K_a determined by this method may have a substantial error if the effect of activity is ignored. See Chapter 6.9 for a discussion of activity.

EVALUATION OF ACID–BASE TITRIMETRY

SCALE OF OPERATION

In an acid–base titration, the volume of titrant needed to reach the equivalence point is proportional to the moles of titrand. Because the pH of the titrand or the titrant is a function of its concentration, the change in pH at the equivalence point—and thus the feasibility of an acid–base titration—depends on their respective concentrations. Figure 9.2.18 , for example, shows a series of titration curves for the titration of several concentrations of HCl with equimolar solutions NaOH. For titrand and titrant concentrations smaller than 10^{-3} M, the change in pH at the end point is too small to provide an accurate and a precise result.

Acid–base titrimetry is an example of a total analysis technique in which the signal is proportional to the absolute amount of analyte. See Chapter 3 for a discussion of the difference between total analysis techniques and concentration techniques.

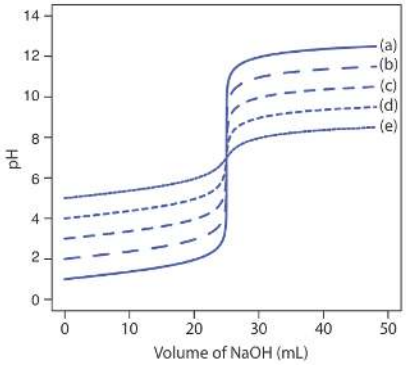


Figure 9.2.18 . Titration curves for 25.0 mL of (a) 10^{-1} M HCl, (b) 10^{-2} M HCl, (c) 10^{-3} M HCl, (d) 10^{-4} M HCl, and (e) 10^{-5} M HCl. In each case the titrant is an equimolar solution of NaOH.

A minimum concentration of 10^{-3} M places limits on the smallest amount of analyte we can analyze successfully. For example, suppose our analyte has a formula weight of 120 g/mol. To successfully monitor the titration's end point using an indicator or a pH probe, the titrand needs an initial volume of approximately 25 mL. If we assume the analyte's formula weight is 120 g/mol, then each sample must contain at least 3 mg of analyte. For this reason, acid–base titrations generally are limited to major and minor analytes. We can extend the analysis of gases to trace analytes by pulling a large volume of the gas through a suitable collection solution.

> We need a volume of titrand sufficient to cover the tip of the pH probe or to allow for an easy observation of the indicator's color. A volume of 25 mL is not an unreasonable estimate of the minimum volume.

One goal of analytical chemistry is to extend analyses to smaller samples. Here we describe two interesting approaches to titrating μL and pL samples. In one experimental design (Figure 9.2.19), samples of 20–100 μL are held by capillary action between a flat-surface pH electrode and a stainless steel sample stage [Steele, A.; Hieftje, G. M. *Anal. Chem.* **1984**, *56*, 2884–2888]. The titrant is added using the oscillations of a piezoelectric ceramic device to move an angled glass rod in and out of a tube connected to a reservoir that contains the titrant. Each time the glass tube is withdrawn an approximately 2 nL microdroplet of titrant is released. The microdroplets are allowed to fall onto the sample, with mixing accomplished by spinning the sample stage at 120 rpm. A total of 450 microdroplets, with a combined volume of 0.81–0.84 μL, is dispensed between each pH measurement. In this fashion a titration curve is constructed. This method has been used to titrate solutions of 0.1 M HCl and 0.1 M CH_3COOH with 0.1 M NaOH. Absolute errors ranged from a minimum of +0.1% to a maximum of –4.1%, with relative standard deviations from 0.15% to 4.7%. Samples as small as 20 μL were titrated successfully.

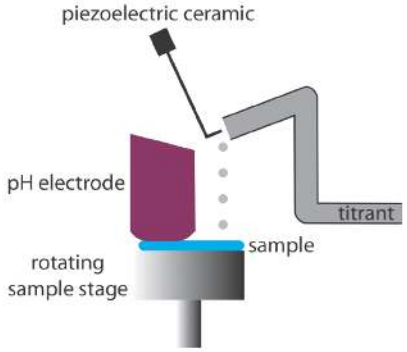


Figure 9.2.19 . Experimental design for a microdroplet titration apparatus.

Another approach carries out the acid–base titration in a single drop of solution [(a) Gratzl, M.; Yi, C. *Anal. Chem.* **1993**, *65*, 2085–2088; (b) Yi, C.; Gratzl, M. *Anal. Chem.* **1994**, *66*, 1976–1982; (c) Hui, K. Y.; Gratzl, M. *Anal. Chem.* **1997**, *69*, 695–698; (d) Yi, C.; Huang, D.; Gratzl, M. *Anal. Chem.* **1996**, *68*, 1580–1584; (e) Xie, H.; Gratzl, M. *Anal. Chem.* **1996**, *68*, 3665–3669]. The titrant is delivered using a microburet fashioned from a glass capillary micropipet (Figure 9.2.20). The microburet has a 1-2 μm tip filled with an agar gel membrane. The tip of the microburet is placed within a drop of the sample solution, which is suspended in heptane, and the titrant is allowed to diffuse into the sample. The titration's progress is monitored using an acid–base indicator and the time needed to reach the end point is measured. The rate of the titrant's diffusion from the microburet is determined by a prior calibration. Once calibrated the end point time is converted to an end point volume. Samples usually consist of picoliter volumes (10^{-12} liters), with the smallest sample being 0.7 pL. The precision of the titrations is about 2%.

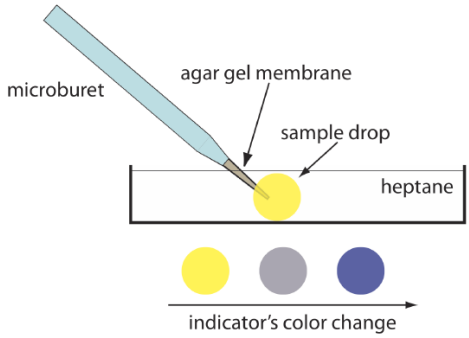


Figure 9.2.20 . Experimental set-up for a diffusional microtitration. The indicator is a mixture of bromothymol blue and bromocresol purple.

Titrations conducted with microliter or picoliter sample volumes require a smaller absolute amount of analyte. For example, diffusional titrations have been conducted on as little as 29 femtomoles (10^{-15} moles) of nitric acid. Nevertheless, the analyte must be present in the sample at a major or minor level for the titration to give accurate and precise results.

ACCURACY

When working with a macro–major or a macro–minor sample, an acid–base titration can achieve a relative error of 0.1–0.2%. The principal limitation to accuracy is the difference between the end point and the equivalence point.

PRECISION

An acid–base titration's relative precision depends primarily on the precision with which we can measure the end point volume and the precision in detecting the end point. Under optimum conditions, an acid–base titration has a relative precision of 0.1–0.2%. We can improve the relative precision by using the largest possible buret and by ensuring we use most of its capacity in reaching the end point. A smaller volume buret is a better choice when using costly reagents, when waste disposal is a concern, or when we must complete the titration quickly to avoid competing chemical reactions. An automatic titrator is particularly useful for titrations that require small volumes of titrant because it provides significantly better precision (typically about ±0.05% of the buret's volume).

The precision of detecting the end point depends on how it is measured and the slope of the titration curve at the end point. With an indicator the precision of the end point signal usually is ±0.03–0.10 mL. Potentiometric end points usually are more precise.

SENSITIVITY

For an acid–base titration we can write the following general analytical equation to express the titrant's volume in terms of the amount of titrand

$$\text{volume of titrant } = k \times \text{ moles of titrand}$$

where *k*, the sensitivity, is determined by the stoichiometry between the titrand and the titrant. Consider, for example, the determination of sulfurous acid, H_2SO_3, by titrating with NaOH to the first equivalence point

$$H_2SO_3(aq) + OH^-(aq) \rightarrow H_2O(l) + HSO_3^-(aq)$$

At the equivalence point the relationship between the moles of NaOH and the moles of H_2SO_3 is

$$\text{mol NaOH} = \text{mol } H_2SO_3$$

Substituting the titrant's molarity and volume for the moles of NaOH and rearranging

$$M_{NaOH} \times V_{NNOH} = \text{mol } H_2SO_3$$

$$V_{NaOH} = \frac{1}{M_{NaOH}} \times \text{mol } H_2SO_3$$

we find that *k* is

$$k = \frac{1}{M_{NaOH}}$$

There are two ways in which we can improve a titration's sensitivity. The first, and most obvious, is to decrease the titrant's concentration because it is inversely proportional to the sensitivity, *k*. The second approach, which applies only if the titrand is multiprotic, is to titrate to a later equivalence point. If we titrate H_2SO_3 to its second equivalence point

$$H_2SO_3(aq) + 2OH^-(aq) \rightarrow 2H_2O(l) + SO_3^{2-}(aq)$$

then each mole of H_2SO_3 consumes two moles of NaOH

$$\text{mol NaOH} = 2 \times \text{mol } H_2SO_3$$

and the sensitivity becomes

$$k = \frac{2}{M_{\text{NaOH}}}$$

In practice, however, any improvement in sensitivity is offset by a decrease in the end point's precision if a larger volume of titrant requires us to refill the buret. For this reason, standard acid–base titrimetric procedures are written to ensure that a titration uses 60–100% of the buret's volume.

SELECTIVITY

Acid–base titrants are not selective. A strong base titrant, for example, reacts with all acids in a sample, regardless of their individual strengths. If the titrand contains an analyte and an interferent, then selectivity depends on their relative acid strengths. Let's consider two limiting situations.

If the analyte is a stronger acid than the interferent, then the titrant will react with the analyte before it begins reacting with the interferent. The feasibility of the analysis depends on whether the titrant's reaction with the interferent affects the accurate location of the analyte's equivalence point. If the acid dissociation constants are substantially different, the end point for the analyte can be determined accurately. Conversely, if the acid dissociation constants for the analyte and interferent are similar, then there may not be an accurate end point for the analyte. In the latter case a quantitative analysis for the analyte is not possible.

In the second limiting situation the analyte is a weaker acid than the interferent. In this case the volume of titrant needed to reach the analyte's equivalence point is determined by the concentration of both the analyte and the interferent. To account for the interferent's contribution to the end point, an end point for the interferent must be available. Again, if the acid dissociation constants for the analyte and interferent are significantly different, then the analyte's determination is possible. If the acid dissociation constants are similar, however, there is only a single equivalence point and we cannot separate the analyte's and the interferent's contributions to the equivalence point volume.

TIME, COST, AND EQUIPMENT

Acid–base titrations require less time than most gravimetric procedures, but more time than many instrumental methods of analysis, particularly when analyzing many samples. With an automatic titrator, however, concerns about analysis time are less significant. When performing a titration manually our equipment needs—a buret and, perhaps, a pH meter—are few in number, inexpensive, routinely available, and easy to maintain. Automatic titrators are available for between $3000 and $10 000.

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9.4: COMPLEXATION TITRATIONS

The earliest examples of metal–ligand ***complexation titrations*** are Liebig's determinations, in the 1850s, of cyanide and chloride using, respectively, Ag^+ and Hg^{2+} as the titrant. Practical analytical applications of complexation titrimetry were slow to develop because many metals and ligands form a series of metal–ligand complexes. Liebig's titration of CN^- with Ag^+ was successful because they form a single, stable complex of $Ag(CN)_2^-$, which results in a single, easily identified end point. Other metal–ligand complexes, such as CdI_4^{2-}, are not analytically useful because they form a series of metal–ligand complexes (CdI^+, $CdI_2(aq)$, CdI_3^- and CdI_4^{2-}) that produce a sequence of poorly defined end points.

> Recall that an acid–base titration curve for a diprotic weak acid has a single end point if its two K_a values are not sufficiently different. See Figure 9.2.6 for an example.

In 1945, Schwarzenbach introduced aminocarboxylic acids as multidentate ligands. The most widely used of these new ligands—ethylenediaminetetraacetic acid, or EDTA—forms a strong 1:1 complex with many metal ions. The availability of a ligand that gives a single, easily identified end point made complexation titrimetry a practical analytical method.

CHEMISTRY AND PROPERTIES OF EDTA

Ethylenediaminetetraacetic acid, or EDTA, is an aminocarboxylic acid. EDTA, the structure of which is shown in Figure 9.3.1 a in its fully deprotonated form, is a Lewis acid with six binding sites—the four negatively charged carboxylate groups and the two tertiary amino groups—that can donate up to six pairs of electrons to a metal ion. The resulting metal–ligand complex, in which EDTA forms a cage-like structure around the metal ion (Figure 9.3.1 b), is very stable. The actual number of coordination sites depends on the size of the metal ion, however, all metal–EDTA complexes have a 1:1 stoichiometry.

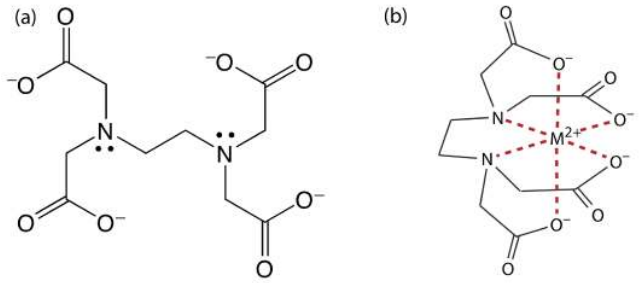


Figure 9.3.1 . Structures of (a) EDTA, in its fully deprotonated form, and (b) in a six-coordinate metal–EDTA complex with a divalent metal ion.

METAL–EDTA FORMATION CONSTANTS

To illustrate the formation of a metal–EDTA complex, let's consider the reaction between Cd^{2+} and EDTA

$$Cd^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons CdY^{2-}(aq) \tag{9.4.1}$$

where Y^{4-} is a shorthand notation for the fully deprotonated form of EDTA shown in Figure 9.3.1 a. Because the reaction's formation constant

$$K_f = \frac{[CdY^{2-}]}{[Cd^{2+}]\,[Y^{4-}]} = 2.9 \times 10^{16} \tag{9.4.2}$$

is large, its equilibrium position lies far to the right. Formation constants for other metal–EDTA complexes are found in Appendix 12.

EDTA IS A WEAK ACID

In addition to its properties as a ligand, EDTA is also a weak acid. The fully protonated form of EDTA, H_6Y^{2+}, is a hexaprotic weak acid with successive pK_a values of

$$pK_{a1} = 0.0 \quad pK_{a2} = 1.5 \quad pK_{a3} = 2.0$$

$$pK_{a4} = 2.66 \quad pK_{a5} = 6.16 \quad pK_{a6} = 10.24$$

The first four values are for the carboxylic acid protons and the last two values are for the ammonium protons. Figure 9.3.2 shows a ladder diagram for EDTA. The specific form of EDTA in reaction 9.4.1 is the predominate species only when the pH is more basic than 10.24.

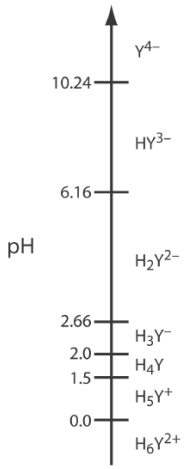


Figure 9.3.2 . Ladder diagram for EDTA.

CONDITIONAL METAL–LIGAND FORMATION CONSTANTS

The formation constant for CdY^{2-} in Equation 9.4.2 assumes that EDTA is present as Y^{4-}. Because EDTA has many forms, when we prepare a solution of EDTA we know it total concentration, C_{EDTA}, not the concentration of a specific form, such as Y^{4-}. To use Equation 9.4.2, we need to rewrite it in terms of C_{EDTA}.

At any pH a mass balance on EDTA requires that its total concentration equal the combined concentrations of each of its forms.

$$C_{EDTA} = \left[H_6Y^{2+}\right] + \left[H_5Y^{+}\right] + \left[H_4Y\right] + \left[H_3Y^{-}\right] + \left[H_2Y^{2-}\right] + \left[HY^{3-}\right] + \left[Y^{4-}\right]$$

To correct the formation constant for EDTA's acid–base properties we need to calculate the fraction, $\alpha_{Y^{4-}}$, of EDTA that is present as Y^{4-}.

$$\alpha_{Y^{4-}} = \frac{\left[Y^{4-}\right]}{C_{EDTA}} \tag{9.4.3}$$

Table 9.3.1 provides values of $\alpha_{Y^{4-}}$ for selected pH levels. Solving Equation 9.4.3 for $[Y^{4-}]$ and substituting into Equation 9.4.2 for the CdY^{2-} formation constant

$$K_f = \frac{\left[CdY^{2-}\right]}{\left[Cd^{2+}\right](\alpha_{Y^{4-}})C_{EDTA}}$$

and rearranging gives

$$K_f' = K_f \times \alpha_{Y^{4-}} = \frac{\left[CdY^{2-}\right]}{\left[Cd^{2+}\right]C_{EDTA}} \tag{9.4.4}$$

where K_f' is a pH-dependent ***conditional formation constant***. As shown in Table 9.3.2 , the conditional formation constant for CdY^{2-} becomes smaller and the complex becomes less stable at more acidic pHs.

Table 9.3.1 . Values of $\alpha_{Y^{4-}}$ for EDTA at Selected pH Levels

pH	$\alpha_{Y^{4-}}$	pH	$\alpha_{Y^{4-}}$
1	1.94×10^{-18}	8	5.68×10^{-3}
2	3.47×10^{-14}	9	5.47×10^{-2}
3	2.66×10^{-11}	10	0.367
4	3.80×10^{-9}	11	0.853
5	3.73×10^{-7}	12	0.983
6	2.37×10^{-5}	13	0.988
7	5.06×10^{-4}	14	1.00

Table 9.3.2 . Conditional Formation Constants for CdY^{2-}

pH	K'_f	pH	K'_f
1	5.6×10^{-2}	8	1.6×10^{14}
2	1.0×10^{3}	9	1.6×10^{15}
3	7.7×10^{5}	10	1.1×10^{16}
4	1.1×10^{8}	11	2.5×10^{16}
5	1.1×10^{10}	12	2.9×10^{16}
6	6.9×10^{11}	13	2.9×10^{16}
7	1.5×10^{13}	14	2.9×10^{16}

EDTA COMPETES WITH OTHER LIGANDS

To maintain a constant pH during a complexation titration we usually add a buffering agent. If one of the buffer's components is a ligand that binds with Cd^{2+}, then EDTA must compete with the ligand for Cd^{2+}. For example, an NH_4^+/NH_3 buffer includes NH_3, which forms several stable Cd^{2+}–NH_3 complexes. Because EDTA forms a stronger complex with Cd^{2+} than does NH_3, it displaces NH_3; however, the stability of the Cd^{2+}–EDTA complex decreases.

We can account for the effect of an ***auxiliary complexing agent***, such as NH_3, in the same way we accounted for the effect of pH. Before adding EDTA, the mass balance on Cd^{2+}, C_{Cd}, is

$$C_{Cd} = \left[Cd^{2+}\right] + \left[Cd(NH_3)^{2+}\right] + \left[Cd(NH_3)_2^{2+}\right] + \left[Cd(NH_3)_3^{2+}\right] + \left[Cd(NH_3)_4^{2+}\right]$$

and the fraction of uncomplexed Cd^{2+}, $\alpha_{Cd^{2+}}$, is

$$\alpha_{Cd^{2+}} = \frac{\left[Cd^{2+}\right]}{C_{Cd}} \tag{9.4.5}$$

> The value of $\alpha_{Cd^{2+}}$ depends on the concentration of NH_3. Contrast this with $\alpha_{Y^{4-}}$, which depends on pH.

Solving Equation 9.4.5 for $[Cd^{2+}]$ and substituting into Equation 9.4.4 gives

$$K'_f = K_f \times \alpha_{Y^{4-}} = \frac{[CdY^{2-}]}{\alpha_{Cd^{2+}} C_{Cd} C_{EDTA}}$$

Because the concentration of NH_3 in a buffer essentially is constant, we can rewrite this equation

$$K''_f = K_f \times \alpha_{Y^{4-}} \times \alpha_{Cd^{2+}} = \frac{[CdY^{2-}]}{C_{Cd} C_{EDTA}} \tag{9.4.6}$$

to give a conditional formation constant, K''_f, that accounts for both pH and the auxiliary complexing agent's concentration. Table 9.3.3 provides values of $\alpha_{M^{2+}}$ for several metal ion when NH_3 is the complexing agent.

Table 9.3.3 . Values of $\alpha_{M^{2+}}$ for Selected Concentrations of Ammonia

$[NH_3]$ (M)	$\alpha_{Ca^{2+}}$	$\alpha_{Cd^{2+}}$	$\alpha_{Co^{2+}}$	$\alpha_{Cu^{2+}}$	$\alpha_{Mg^{2+}}$	$\alpha_{Ni^{2+}}$	$\alpha_{Zn^{2+}}$
1	5.50×10^{-1}	6.09×10^{-8}	1.00×10^{-6}	3.79×10^{-14}	1.76×10^{-1}	9.20×10^{-10}	3.95×10^{-10}
0.5	7.36×10^{-1}	1.05×10^{-6}	2.22×10^{-5}	6.86×10^{-13}	4.13×10^{-1}	3.44×10^{-8}	6.27×10^{-9}
0.1	9.39×10^{-1}	3.51×10^{-4}	6.64×10^{-3}	4.63×10^{-10}	8.48×10^{-1}	5.12×10^{-5}	3.68×10^{-6}
0.05	9.69×10^{-1}	2.72×10^{-3}	3.54×10^{-2}	7.17×10^{-9}	9.22×10^{-1}	6.37×10^{-4}	5.45×10^{-5}
0.01	9.94×10^{-1}	8.81×10^{-2}	3.55×10^{-1}	3.22×10^{-6}	9.84×10^{-1}	4.32×10^{-2}	1.82×10^{-2}
0.005	9.97×10^{-1}	2.27×10^{-1}	5.68×10^{-1}	3.62×10^{-5}	9.92×10^{-1}	1.36×10^{-1}	1.27×10^{-1}
0.001	9.99×10^{-1}	6.09×10^{-1}	8.84×10^{-1}	4.15×10^{-4}	9.98×10^{-1}	5.76×10^{-1}	7.48×10^{-1}

COMPLEXOMETRIC EDTA TITRATION CURVES

Now that we know something about EDTA's chemical properties, we are ready to evaluate its usefulness as a titrant. To do so we need to know the shape of a complexometric titration curve. In chapter 9.2 we learned that an acid–base titration curve shows how the titrand's pH changes as we add titrant. The analogous result for a complexation titration shows the change in pM, where M is the metal ion's concentration, as a function of the volume of EDTA. In this section we will learn how to calculate a titration curve using the equilibrium calculations from Chapter 6. We also will learn how to sketch a good approximation of any complexation titration curve using a limited number of simple calculations.

pM = –log[M^{2+}]

CALCULATING THE TITRATION CURVE

Let's calculate the titration curve for 50.0 mL of 5.00×10^{-3} M Cd^{2+} using a titrant of 0.0100 M EDTA. Furthermore, let's assume the titrand is buffered to a pH of 10 using a buffer that is 0.0100 M in NH_3.

Because the pH is 10, some of the EDTA is present in forms other than Y^{4-}. In addition, EDTA will compete with NH_3 for the Cd^{2+}. To evaluate the titration curve, therefore, we first need to calculate the conditional formation constant for CdY^{2-}. From Table 9.3.1 and Table 9.3.3 we find that $\alpha_{Y^{4-}}$ is 0.367 at a pH of 10, and that $\alpha_{Cd^{2+}}$ is 0.0881 when the concentration of NH_3 is 0.0100 M. Using these values, the conditional formation constant is

$$K_f'' = K_f \times \alpha_{Y^{4-}} \times \alpha_{Cd^{2+}} = \left(2.9 \times 10^{16}\right)(0.367)(0.0881) = 9.4 \times 10^{14}$$

Because K_f'' is so large, we can treat the titration reaction

$$Cd^{2+}(aq) + Y^{4-}(aq) \longrightarrow CdY^{2-}(aq)$$

as if it proceeds to completion.

The next task is to determine the volume of EDTA needed to reach the equivalence point. At the equivalence point we know that the moles of EDTA added must equal the moles of Cd^{2+} in our sample; thus

$$\text{mol EDTA} = M_{EDTA} \times V_{EDTA} = M_{Cd} \times V_{Cd} = \text{mol } Cd^{2+}$$

Substituting in known values, we find that it requires

$$V_{eq} = V_{EDTA} = \frac{M_{Cd} V_{Cd}}{M_{EDTA}} = \frac{\left(5.00 \times 10^{-3}\text{ M}\right)(50.0\text{ mL})}{0.0100\text{ M}} = 25.0\text{ mL}$$

of EDTA to reach the equivalence point.

Before the equivalence point, Cd^{2+} is present in excess and pCd is determined by the concentration of unreacted Cd^{2+}. Because not all unreacted Cd^{2+} is free—some is complexed with NH_3—we must account for the presence of NH_3. For example, after adding 5.0 mL of EDTA, the total concentration of Cd^{2+} is

$$C_{Cd} = \frac{(\text{mol } Cd^{2+})_{\text{initial}} - (\text{mol EDTA})_{\text{added}}}{\text{total volume}} = \frac{M_{Cd} V_{Cd} - M_{EDTA} V_{EDTA}}{V_{Cd} + V_{EDTA}}$$

$$C_{Cd} = \frac{\left(5.00 \times 10^{-3}\text{ M}\right)(50.0\text{ mL}) - (0.0100\text{ M})(5.0\text{ mL})}{50.0\text{ mL} + 5.0\text{ mL}}$$

$$C_{Cd} = 3.64 \times 10^{-3}\text{ M}$$

To calculate the concentration of free Cd^{2+} we use Equation 9.4.5

$$\left[Cd^{2+}\right] = \alpha_{Cd^{2+}} \times C_{Cd} = (0.0881)\left(3.64 \times 10^{-3}\text{ M}\right) = 3.21 \times 10^{-4}\text{ M}$$

which gives a pCd of

$$\text{pCd} = -\log\left[Cd^{2+}\right] = -\log\left(3.21 \times 10^{-4}\right) = 3.49$$

At the equivalence point all Cd^{2+} initially in the titrand is now present as CdY^{2-}. The concentration of Cd^{2+}, therefore, is determined by the dissociation of the CdY^{2-} complex. First, we calculate the concentration of CdY^{2-}.

$$\left[CdY^{2-}\right] = \frac{\left(\text{mol } Cd^{2+}\right)_{\text{initial}}}{\text{total volume}} = \frac{M_{Cd} V_{Cd}}{V_{Cd} + V_{EDTA}}$$

$$\left[CdY^{2-}\right] = \frac{\left(5.00 \times 10^{-3}\text{ M}\right)(50.0\text{ mL})}{50.0\text{ mL} + 25.0\text{ mL}} = 3.33 \times 10^{-3}\text{ M}$$

Next, we solve for the concentration of Cd^{2+} in equilibrium with CdY^{2-}.

$$K_f'' = \frac{\left[CdY^{2-}\right]}{C_{Cd} C_{EDTA}} = \frac{3.33 \times 10^{-3} - x}{(x)(x)} = 9.5 \times 10^{14}$$

$$x = C_{Cd} = 1.87 \times 10^{-9}\text{ M}$$

In calculating that [CdY^{2-}] at the equivalence point is 3.33×10^{-3} M, we assumed the reaction between Cd^{2+} and EDTA went to completion. Here we let the system relax back to equilibrium, increasing C_{Cd} and C_{EDTA} from 0 to *x*, and decreasing the concentration of CdY^{2-} by *x*.

Once again, to find the concentration of uncomplexed Cd we must account for the presence of NH_3; thus

$$\left[Cd^{2+}\right] = \alpha_{Cd^{2+}} \times C_{Cd} = (0.0881)\left(1.87 \times 10^{-9}\ \text{M}\right) = 1.64 \times 10^{-10}\ \text{M}$$

and pCd is 9.78 at the equivalence point.

After the equivalence point, EDTA is in excess and the concentration of Cd^{2+} is determined by the dissociation of the CdY^{2-} complex. First, we calculate the concentrations of CdY^{2-} and of unreacted EDTA. For example, after adding 30.0 mL of EDTA the concentration of CdY^{2-} is

$$\left[CdY^{2-}\right] = \frac{\left(\text{mol}Cd^{2+}\right)_{\text{initial}}}{\text{total volume}} = \frac{M_{Cd}V_{Cd}}{V_{Cd} + V_{EDTA}}$$

$$\left[CdY^{2-}\right] = \frac{\left(5.00 \times 10^{-3}\ \text{M}\right)(50.0\ \text{mL})}{50.0\ \text{mL} + 30.0\ \text{mL}} = 3.12 \times 10^{-3}\ \text{M}$$

and the concentration of EDTA is

$$C_{EDTA} = \frac{(\text{mol EDTA})_{\text{added}} - (\text{mol Cd}^{2+})_{\text{initial}}}{\text{total volume}} = \frac{M_{EDTA}V_{EDTA} - M_{Cd}V_{Cd}}{V_{Cd} + V_{EDTA}}$$

$$C_{EDTA} = \frac{(0.0100\ \text{M})(30.0\ \text{mL}) - (5.00 \times 10^{-3}\ \text{M})(50.0\ \text{mL})}{50.0\ \text{mL} + 30.0\ \text{mL}}$$

$$C_{EDTA} = 6.25 \times 10^{-4}\ \text{M}$$

Substituting into Equation 9.4.6 and solving for [Cd^{2+}] gives

$$\frac{\left[CdY^{2-}\right]}{C_{Cd}C_{EDTA}} = \frac{3.12 \times 10^{-3}\ \text{M}}{C_{Cd}\left(6.25 \times 10^{-4}\ \text{M}\right)} = 9.5 \times 10^{14}$$

$$C_{Cd} = 5.27 \times 10^{-15}\ \text{M}$$

$$\left[Cd^{2+}\right] = \alpha_{Cd^{2+}} \times C_{Cd} = (0.0881)(5.27 \times 10^{-15}\ \text{M}) = 4.64 \times 10^{-16}\ \text{M}$$

a pCd of 15.33. Table 9.3.4 and Figure 9.3.3 show additional results for this titration.

After the equilibrium point we know the equilibrium concentrations of CdY^{2-} and of EDTA in all its forms, C_{EDTA}. We can solve for C_{Cd} using K_f'' and then calculate [Cd^{2+}] using $\alpha_{Cd^{2+}}$. Because we used the same conditional formation constant, K_f'', for other calculations in this section, this is the approach used here as well. There is a second method for calculating [Cd^{2+}] after the equivalence point. Because the calculation uses only [CdY^{2-}] and C_{EDTA}, we can use K_f' instead of K_f''; thus

$$\frac{\left[CdY^{2-}\right]}{\left[Cd^{2+}\right]C_{EDTA}} = \alpha_{Y^{4-}} \times K_f$$

$$\frac{3.13 \times 10^{-3}\ \text{M}}{\left[Cd^{2+}\right]\left(6.25 \times 10^{-4}\right)} = (0.367)\left(2.9 \times 10^{16}\right)$$

Solving gives [Cd^{2+}] = 4.71×10^{-16} M and a pCd of 15.33. We will use this approach when we learn how to sketch a complexometric titration curve.

Table 9.3.4 . Titration of 50.0 mL of 5.00×10^{-3} M Cd^{2+} with 0.0100 M EDTA at a pH of 10 and in the Presence of 0.0100 M NH_3

volume of EDTA (mL)	pCd	volume of EDTA (mL)	pCd
0.00	3.36	27.0	14.95
5.00	3.49	30.0	15.33
10.0	3.66	35.0	15.61
15.0	3.87	40.0	15.76
20.0	4.20	45.0	15.86
23.0	4.62	50.0	15.94
25.0	9.78		

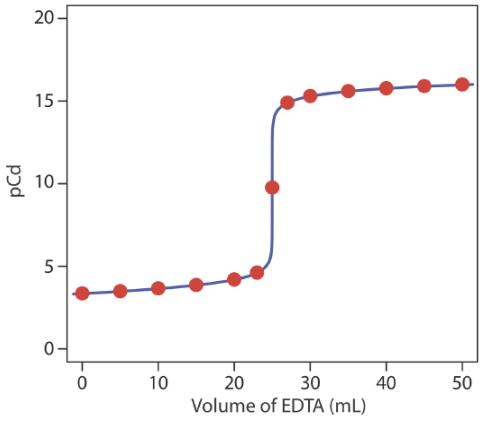


Figure 9.3.3 . Titration curve for the titration of 50.0 mL of 5.00×10^{-3} M Cd^{2+} with 0.0100 M EDTA at a pH of 10 and in the presence of 0.0100 M NH_3. The red points correspond to the data in Table 9.3.4 . The blue line shows the complete titration curve.

? EXERCISE 9.3.1

Calculate titration curves for the titration of 50.0 mL of 5.00×10^{-3} M Cd^{2+} with 0.0100 M EDTA (a) at a pH of 10 and (b) at a pH of 7. Neither titration includes an auxiliary complexing agent. Compare your results with Figure 9.3.3 and comment on the effect of pH on the titration of Cd^{2+} with EDTA.

Answer

Let's begin with the calculations at a pH of 10 where some of the EDTA is present in forms other than Y^{4-}. To evaluate the titration curve, therefore, we need the conditional formation constant for CdY^{2-}, which, from Table 9.3.2 is $K'_f = 1.1 \times 10^{16}$. Note that the conditional formation constant is larger in the absence of an auxiliary complexing agent.

The titration's equivalence point requires

$$V_{eq} = V_{\text{EDTA}} = \frac{M_{\text{Cd}} V_{\text{Cd}}}{M_{\text{EDTA}}} = \frac{\left(5.00 \times 10^{-3}\ \text{M}\right)\left(50.0\ \text{mL}\right)}{\left(0.0100\ \text{M}\right)} = 25.0\ \text{mL}$$

of EDTA.

Before the equivalence point, Cd^{2+} is present in excess and pCd is determined by the concentration of unreacted Cd^{2+}. For example, after adding 5.00 mL of EDTA, the total concentration of Cd^{2+} is

$$\left[Cd^{2+}\right] = \frac{\left(5.00 \times 10^{-3}\ \text{M}\right)\left(50.0\ \text{mL}\right) - \left(0.0100\ \text{M}\right)\left(5.00\ \text{mL}\right)}{50.0\ \text{mL} + 5.00\ \text{mL}}$$

which gives $[Cd^{2+}]$ as 3.64×10^{-3} and pCd as 2.43.

At the equivalence point all Cd^{2+} initially in the titrand is now present as CdY^{2-}. The concentration of Cd^{2+}, therefore, is determined by the dissociation of the CdY^{2-} complex. First, we calculate the concentration of CdY^{2-}.

$$\left[CdY^{2-}\right] = \frac{\left(5.00 \times 10^{-3}\ \text{M}\right)\left(50.0\ \text{mL}\right)}{50.0\ \text{mL} + 25.00\ \text{mL}} = 3.33 \times 10^{-3}\ \text{M}$$

Next, we solve for the concentration of Cd^{2+} in equilibrium with CdY^{2-}.

$$K_f' = \frac{\left[CdY^{2-}\right]}{\left[Cd^{2+}\right] C_{EDTA}} = \frac{3.33 \times 10^{-3} - x}{(x)(x)} = 1.1 \times 10^{16}$$

Solving gives $[Cd^{2+}]$ as 5.50×10^{-10} M or a pCd of 9.26 at the equivalence point.

After the equivalence point, EDTA is in excess and the concentration of Cd^{2+} is determined by the dissociation of the CdY^{2-} complex. First, we calculate the concentrations of CdY^{2-} and of unreacted EDTA. For example, after adding 30.0 mL of EDTA

$$\left[CdY^{2-}\right] = \frac{\left(5.00 \times 10^{-3}\ \text{M}\right)(50.0\ \text{mL})}{50.0\ \text{mL} + 30.00\ \text{mL}} = 3.12 \times 10^{-3}\ \text{M}$$

$$C_{EDTA} = \frac{(0.0100\ \text{M})(30.00\ \text{mL}) - \left(5.00 \times 10^{-3}\ \text{M}\right)(50.0\ \text{mL})}{50.0\ \text{mL} + 30.00\ \text{mL}}$$

$$C_{EDTA} = 6.25 \times 10^{-4}\ \text{M}$$

Substituting into the equation for the conditional formation constant

$$K_f' = \frac{\left[CdY^{2-}\right]}{\left[Cd^{2+}\right] C_{EDTA}} = \frac{3.12 \times 10^{-3}\ \text{M}}{(\text{x})\left(6.25 \times 10^{-4}\ \text{M}\right)} = 1.1 \times 10^{16}$$

and solving for $[Cd^{2+}]$ gives 4.54×10^{-16} M or a pCd of 15.34.

The calculations at a pH of 7 are identical, except the conditional formation constant for CdY^{2-} is 1.5×10^{13} instead of 1.1×10^{16}. The following table summarizes results for these two titrations as well as the results from Table 9.3.4 for the titration of Cd^{2+} at a pH of 10 in the presence of 0.0100 M NH_3 as an auxiliary complexing agent.

Volume of EDTA (mL)	pCd at pH 10	pCd at pH 10 w/ 0.0100 M NH_3	pCd at pH 7
0	2.30	3.36	2.30
5.00	2.43	3.49	2.43
10.0	2.60	3.66	2.60
15.0	2.81	3.87	2.81
20.0	3.15	4.20	3.15
23.0	3.56	4.62	3.56
25.0	9.26	9.77	7.83
27.0	14.94	14.95	12.08
30.0	15.34	15.33	12.48
35.0	15.61	15.61	12.78
40.0	15.76	15.76	12.95
45.0	15.86	15.86	13.08
50.0	15.94	15.94	13.18

Examining these results allows us to draw several conclusions. First, in the absence of an auxiliary complexing agent the titration curve before the equivalence point is independent of pH (compare columns 2 and 4). Second, for any pH, the titration curve after the equivalence point is the same regardless of whether an auxiliary complexing agent is present (compare columns 2 and 3). Third, the largest change in pH through the equivalence point occurs at higher pHs and in the absence of an auxiliary complexing agent. For example, from 23.0 mL to 27.0 mL of EDTA the change in pCd is 11.38 at a pH of 10, 10.33 at a pH of 10 in the presence of 0.0100 M NH_3, and 8.52 at a pH of 7.

SKETCHING AN EDTA TITRATION CURVE

To evaluate the relationship between a titration's equivalence point and its end point, we need to construct only a reasonable approximation of the exact titration curve. In this section we demonstrate a simple method for sketching a complexation titration curve. Our goal is to sketch the titration curve quickly, using as few calculations as possible. Let's use the titration of 50.0 mL of 5.00×10^{-3} M Cd^{2+} with 0.0100 M EDTA in the presence of 0.0100 M NH_3 to illustrate our approach. This is the same example we used in developing the calculations for a complexation titration curve. You can review the results of that calculation in Table 9.3.4 and Figure 9.3.3 .

We begin by calculating the titration's equivalence point volume, which, as we determined earlier, is 25.0 mL. Next, we draw our axes, placing pCd on the *y*-axis and the titrant's volume on the *x*-axis. To indicate the equivalence point's volume, we draw a vertical line that intersects the *x*-axis at 25.0 mL of EDTA. Figure 9.3.4 a shows the result of the first step in our sketch.

Before the equivalence point, Cd^{2+} is present in excess and pCd is determined by the concentration of unreacted Cd^{2+}. Because not all unreacted Cd^{2+} is free—some is complexed with NH_3—we must account for the presence of NH_3. The calculations are straightforward, as

we saw earlier. Figure 9.3.4 b shows the pCd after adding 5.00 mL and 10.0 mL of EDTA.

The third step in sketching our titration curve is to add two points after the equivalence point. Here the concentration of Cd^{2+} is controlled by the dissociation of the Cd^{2+}–EDTA complex. Beginning with the conditional formation constant

$$K_f' = \frac{[CdY^{2-}]}{[Cd^{2+}]\,C_{EDTA}} = \alpha_{Y^{4-}} \times K_f = (0.367)\left(2.9 \times 10^{16}\right) = 1.1 \times 10^{16}$$

we take the log of each side and rearrange, arriving at

$$\log K_f' = -\log[Cd^{2+}] + \log \frac{[CdY^{2-}]}{C_{EDTA}}$$

$$pCd = \log K_f' + \log \frac{C_{EDTA}}{[CdY^{2-}]}$$

> Recall that we can use either of our two possible conditional formation constants, K_f' or K_f'', to determine the composition of the system at equilibrium.

Note that after the equivalence point, the titrand is a metal–ligand complexation buffer, with pCd determined by C_{EDTA} and $[CdY^{2-}]$. The buffer is at its lower limit of $pCd = \log K_f' - 1$ when

$$\frac{C_{EDTA}}{[CdY^{2-}]} = \frac{(\text{mole EDTA})_{added} - (\text{mol } Cd^{2+})_{initial}}{(\text{mol } Cd^{2+})_{initial}} = \frac{1}{10}$$

Making appropriate substitutions and solving, we find that

$$\frac{M_{EDTA}V_{EDTA} - M_{Cd}V_{Cd}}{M_{Cd}V_{Cd}} = \frac{1}{10}$$

$$M_{EDTA}V_{EDTA} - M_{Cd}V_{Cd} = 0.1 \times M_{Cd}V_{Cd}$$

$$V_{EDTA} = \frac{1.1 \times M_{Cd}V_{Cd}}{M_{EDTA}} = 1.1 \times V_{eq}$$

Thus, when the titration reaches 110% of the equivalence point volume, pCd is $\log K_f' - 1$. A similar calculation should convince you that pCd is $\log K_f' + 1$ when the volume of EDTA is $2 \times V_{eq}$.

Figure 9.3.4 c shows the third step in our sketch. First, we add a ladder diagram for the CdY^{2-} complex, including its buffer range, using its $\log K_f'$ value of 16.04. Next, we add two points, one for pCd at 110% of V_{eq} (a pCd of 15.04 at 27.5 mL) and one for pCd at 200% of V_{eq} (a pCd of 16.04 at 50.0 mL).

Next, we draw a straight line through each pair of points, extending each line through the vertical line that indicates the equivalence point's volume (Figure 9.3.4 d). Finally, we complete our sketch by drawing a smooth curve that connects the three straight-line segments (Figure 9.3.4 e). A comparison of our sketch to the exact titration curve (Figure 9.3.4 f) shows that they are in close agreement.

> Our treatment here is general and applies to any complexation titration using EDTA as a titrant.

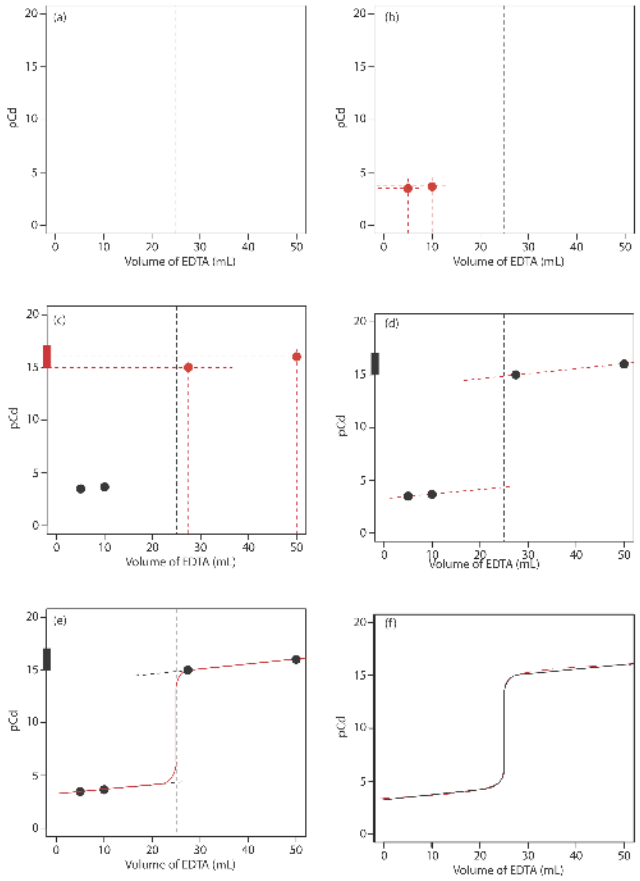


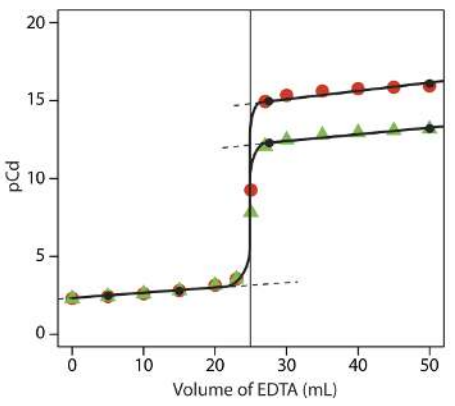
Figure 9.3.4 . Illustrations showing the steps in sketching an approximate titration curve for the titration of 50.0 mL of 5.00×10^{-3} M Cd^{2+} with 0.0100 M EDTA in the presence of 0.0100 M NH_3: (a) locating the equivalence point volume; (b) plotting two points before the equivalence point; (c) plotting two points after the equivalence point; (d) preliminary approximation of titration curve using straight-lines; (e) final approximation of titration curve using a smooth curve; (f) comparison of approximate titration curve (solid black line) and exact titration curve (dashed red line). See the text for additional details.

? EXERCISE 9.3.2

Sketch titration curves for the titration of 50.0 mL of 5.00×10^{-3} M Cd^{2+} with 0.0100 M EDTA (a) at a pH of 10 and (b) at a pH of 7. Compare your sketches to the calculated titration curves from Exercise 9.3.1 .

Answer

The figure below shows a sketch of the titration curves. The two black points before the equivalence point (V_{EDTA} = 5 mL, pCd= 2.43 and V_{EDTA} = 15 mL, pCd= 2.81) are the same for both pHs and taken from the results of Exercise 9.3.1 . The two black points after the equivalence point for a pH of 7 (V_{EDTA} = 27.5 mL, pCd= 12.2 and V_{EDTA} = 50 mL, pCd= 13.2) are plotted using the log K'_f of 13.2 for CdY^{2-}. The two points after the equivalence point for a pH of 10 (V_{EDTA} = 27.5 mL, pCd= 15.0 andV_{EDTA} = 50 mL, pCd= 16.0) are plotted using the log K'_f of 16.0 for CdY^{2-}. The points in red are the calculations from Exercise 9.3.1 for a pH of 10, and the points in green are the calculations from Exercise 9.3.1 for a pH of 7.



SELECTING AND EVALUATING THE ENDPOINT

The equivalence point of a complexation titration occurs when we react stoichiometrically equivalent amounts of the titrand and titrant. As is the case for an acid–base titration, we estimate the equivalence point for a complexation titration using an experimental end point. A variety of methods are available for locating the end point, including indicators and sensors that respond to a change in the solution conditions.

FINDING THE END POINT WITH AN INDICATOR

Most indicators for complexation titrations are organic dyes—known as ***metallochromic indicators***—that form stable complexes with metal ions. The indicator, In^{m-}, is added to the titrand's solution where it forms a stable complex with the metal ion, MIn^{n-}. As we add EDTA it reacts first with free metal ions, and then displaces the indicator from MIn^{n-}.

$$MIn^{n-}(aq) + Y^{4-}(aq) \rightarrow MY^{2-}(aq) + In^{m-}(aq)$$

If MIn^{n-} and In^{m-} have different colors, then the change in color signals the end point.

The accuracy of an indicator's end point depends on the strength of the metal–indicator complex relative to the strength of the metal–EDTA complex. If the metal–indicator complex is too strong, the change in color occurs after the equivalence point. If the metal–indicator complex is too weak, however, the end point occurs before we reach the equivalence point.

Most metallochromic indicators also are weak acids. One consequence of this is that the conditional formation constant for the metal–indicator complex depends on the titrand's pH. This provides some control over an indicator's titration error because we can adjust the strength of a metal–indicator complex by adjusted the pH at which we carry out the titration. Unfortunately, because the indicator is a weak acid, the color of the uncomplexed indicator also may change with pH. Figure 9.3.5 , for example, shows the color of the indicator calmagite as a function of pH and pMg, where H_2In^-, HIn^{2-}, and In^{3-} are different forms of the uncomplexed indicator, and $MgIn^-$ is the Mg^{2+}–calmagite complex. Because the color of calmagite's metal–indicator complex is red, its use as a metallochromic indicator has a practical pH range of approximately 8.5–11 where the uncomplexed indicator, HIn^{2-}, has a blue color.

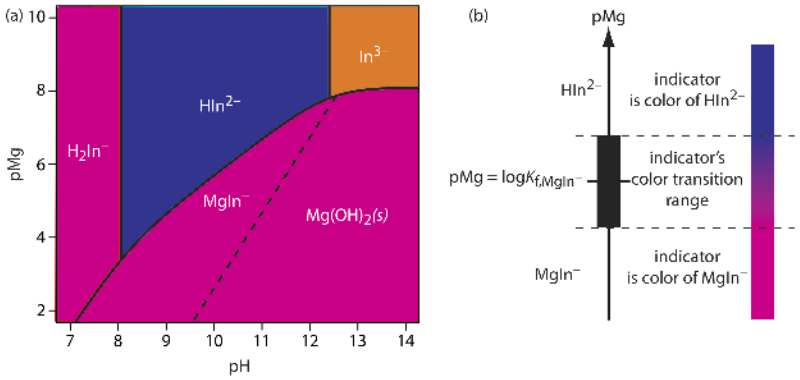


Figure 9.3.5 . (a) Predominance diagram for the metallochromic indicator calmagite showing the most important forms and colors of calmagite as a function of pH and pMg, where H_2In^-, HIn^{2-}, and In^{3-} are uncomplexed forms of calmagite, and $MgIn^-$ is its complex with Mg^{2+}. Conditions to the right of the dashed line, where Mg^{2+} precipitates as $Mg(OH)_2$, are not analytically useful for a complexation titration. A red to blue end point is possible if we maintain the titrand's pH in the range 8.5–11. (b) Diagram showing the relationship between the concentration of Mg^{2+} (as pMg) and the indicator's color. The ladder diagram defines pMg values where $MgIn^-$ and HIn^{2-} are predominate species. The indicator changes color when pMg is between $\log K_f - 1$ and $\log K_f + 1$. This figure is essentially a two-variable ladder diagram. The solid lines are equivalent to a step on a conventional ladder diagram, indicating conditions where two (or three) species are equal in concentration.

Table 9.3.5 provides examples of metallochromic indicators and the metal ions and pH conditions for which they are useful. Even if a suitable indicator does not exist, it often is possible to complete an EDTA titration by introducing a small amount of a secondary metal–EDTA complex if the secondary metal ion forms a stronger complex with the indicator and a weaker complex with EDTA than the analyte. For example, calmagite has a poor end point when titrating Ca^{2+} with EDTA. Adding a small amount of Mg^{2+}–EDTA to the titrand gives a sharper end point. Because Ca^{2+} forms a stronger complex with EDTA, it displaces Mg^{2+}, which then forms the red-colored Mg^{2+}–calmagite complex. At the titration's end point, EDTA displaces Mg^{2+} from the Mg^{2+}–calmagite complex, signaling the end point by the presence of the uncomplexed indicator's blue form.

Table 9.3.5 . Selected Metallochromic Indicators

indicator	pH range	metal ions	indicator	pH range	metal ions
calmagite	8.5–11	Ba, *Ca*, Mg, Zn	eriochrome Black T	7.5–10.5	Ba, *Ca*, Mg, Zn
eriochrome Blue Black R	8–12	*Ca*, Mg, Zn, Cu	PAN	2–11	Cd, Cu, Zn
murexide	6–13	Ca, Ni, Cu	salicylic acid	2–3	Fe
all metal ions carry a +2 charge expect for iron, which is +3 metal ions in *italic* font have poor end points					

FINDING THE END POINT BY MONITORING ABSORBANCE

An important limitation when using a metallochromic indicator is that we must be able to see the indicator's change in color at the end point. This may be difficult if the solution is already colored. For example, when titrating Cu^{2+} with EDTA, ammonia is used to adjust the titrand's pH. The intensely colored $Cu(NH_3)_2^{4+}$ complex obscures the indicator's color, making an accurate determination of the end point difficult. Other absorbing species present within the sample matrix may also interfere. This often is a problem when analyzing clinical samples, such as blood, or environmental samples, such as natural waters.

If at least one species in a complexation titration absorbs electromagnet- ic radiation, then we can identify the end point by monitoring the titrand's absorbance at a carefully selected wavelength. For example, we can identify the end point for a titration of Cu^{2+} with EDTA in the presence of NH_3 by monitoring the titrand's absorbance at a wavelength of 745 nm, where the $Cu(NH_3)_2^{4+}$ complex absorbs strongly. At the beginning of the titration the absorbance is at a maximum. As we add EDTA, however, the reaction

$$Cu(NH_3)_4^{2+}(aq) + Y^{4-} \rightleftharpoons CuY^{2-}(aq) + 4NH_3(aq)$$

decreases the concentration of $Cu(NH_3)_2^{4+}$ and decreases the absorbance until we reach the equivalence point. After the equivalence point the absorbance essentially remains unchanged. The resulting spectrophotometric titration curve is shown in Figure 9.3.6 a. Note that the titration curve's *y*-axis is not the measured absorbance, A_{meas}, but a corrected absorbance, A_{corr}

$$A_{corr} = A_{meas} \times \frac{V_{EDTA} + V_{Cu}}{V_{Cu}}$$

where V_{EDTA} and V_{Cu} are, respectively, the volumes of EDTA and Cu. Correcting the absorbance for the titrand's dilution ensures that the spectrophotometric titration curve consists of linear segments that we can extrapolate to find the end point. Other common spectrophotometric titration curves are shown in Figures 9.3.6 b-f.

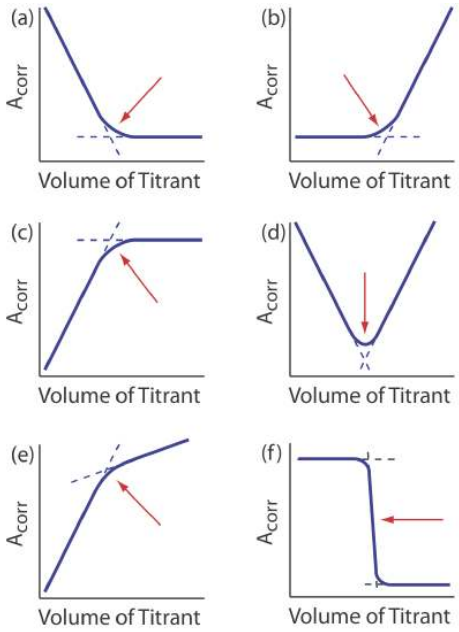


Figure 9.3.6 . Examples of spectrophotometric titration curves: (a) only the titrand absorbs; (b) only the titrant absorbs; (c) only the product of the titration reaction absorbs; (d) both the titrand and the titrant absorb; (e) both the titration reaction's product and the titrant absorb; (f) only the indicator absorbs. The red arrows indicate the end points for each titration curve.

REPRESENTATIVE METHOD 9.3.1: DETERMINATION OF HARDNESS OF WATER AND WASTEWATER

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical complexation titrimetric method. Although each method is unique, the following description of the determination of the hardness of water provides an instructive example of a typical procedure. The description here is based on Method 2340C as published in *Standard Methods for the Examination of Water and Wastewater*, 20th Ed., American Public Health Association: Washington, D. C., 1998.

Description of the Method

The operational definition of water hardness is the total concentration of cations in a sample that can form an insoluble complex with soap. Although most divalent and trivalent metal ions contribute to hardness, the two most important metal ions are Ca^{2+} and Mg^{2+}. Hardness is determined by titrating with EDTA at a buffered pH of 10. Calmagite is used as an indicator. Hardness is reported as mg $CaCO_3$/L.

Procedure

Select a volume of sample that requires less than 15 mL of titrant to keep the analysis time under 5 minutes and, if necessary, dilute the sample to 50 mL with distilled water. Adjust the sample's pH by adding 1–2 mL of a pH 10 buffer that contains a small amount of Mg^{2+}–EDTA. Add 1–2 drops of indicator and titrate with a standard solution of EDTA until the red-to-blue end point is reached (Figure 9.3.7).

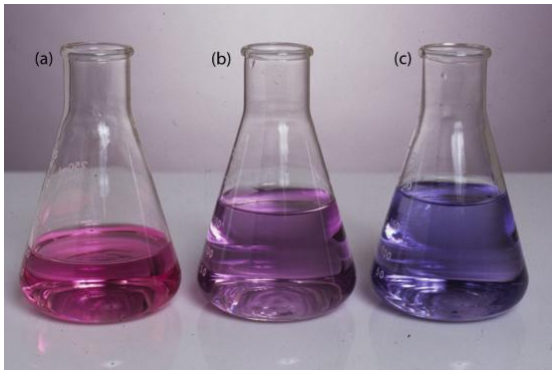


Figure 9.3.7 . End point for the titration of hardness with EDTA using calmagite as an indicator; the indicator is: (a) red prior to the end point due to the presence of the Mg^{2+}–indicator complex; (b) purple at the titration's end point; and (c) blue after the end point due to the presence of uncomplexed indicator.

Questions

1. Why is the sample buffered to a pH of 10? What problems might you expect at a higher pH or a lower pH?

Of the two primary cations that contribute to hardness, Mg^{2+} forms the weaker complex with EDTA and is the last cation to react with the titrant. Calmagite is a useful indicator because it gives a distinct end point when titrating Mg^{2+} (see Table 9.3.5). Because of calmagite's

acid–base properties, the range of pMg values over which the indicator changes color depends on the titrand's pH (Figure 9.3.5). Figure 9.3.8 shows the titration curve for a 50-mL solution of 10^{-3} M Mg^{2+} with 10^{-2} M EDTA at pHs of 9, 10, and 11. Superimposed on each titration curve is the range of conditions for which the average analyst will observe the end point. At a pH of 9 an early end point is possible, which results in a negative determinate error. A late end point and a positive determinate error are possible if the pH is 11.

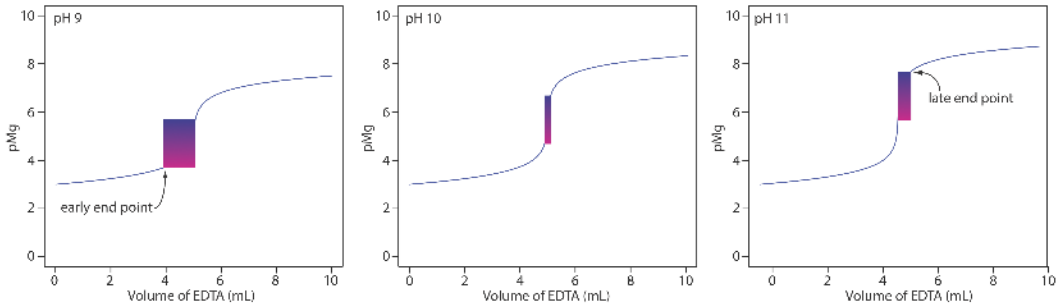


Figure 9.3.8 . Titration curves for 50 mL of 10^{-3} M Mg^{2+} with 10^{-3} M EDTA at pHs 9, 10, and 11 using calmagite as an indicator. The range of pMg and volume of EDTA over which the indicator changes color is shown for each titration curve.

2. Why is a small amount of the Mg^{2+}–EDTA complex added to the buffer?

The titration's end point is signaled by the indicator calmagite. The indicator's end point with Mg^{2+} is distinct, but its change in color when titrating Ca^{2+} does not provide a good end point (see Table 9.3.5). If the sample does not contain any Mg^{2+} as a source of hardness, then the titration's end point is poorly defined, which leads to an inaccurate and imprecise result. Adding a small amount of Mg^{2+}–EDTA to the buffer ensures that the titrand includes at least some Mg^{2+}. Because Ca^{2+} forms a stronger complex with EDTA, it displaces Mg^{2+} from the Mg^{2+}–EDTA complex, freeing the Mg^{2+} to bind with the indicator. This displacement is stoichiometric, so the total concentration of hardness cations remains unchanged. The displacement by EDTA of Mg^{2+} from the Mg^{2+}–indicator complex signals the titration's end point.

3. Why does the procedure specify that the titration take no longer than 5 minutes?

A time limitation suggests there is a kinetically-controlled interference, possibly arising from a competing chemical reaction. In this case the interference is the possible precipitation of $CaCO_3$ at a pH of 10.

QUANTITATIVE APPLICATIONS

Although many quantitative applications of complexation titrimetry have been replaced by other analytical methods, a few important applications continue to find relevance. In the section we review the general application of complexation titrimetry with an emphasis on applications from the analysis of water and wastewater. First, however, we discuss the selection and standardization of complexation titrants.

SELECTION AND STANDARDIZATION OF TITRANTS

EDTA is a versatile titrant that can be used to analyze virtually all metal ions. Although EDTA is the usual titrant when the titrand is a metal ion, it cannot be used to titrate anions, for which Ag^+ or Hg^{2+} are suitable titrants.

Solutions of EDTA are prepared from its soluble disodium salt, $Na_2H_2Y{\bullet}2H_2O$, and standardized by titrating against a solution made from the primary standard $CaCO_3$. Solutions of Ag^+ and Hg^{2+} are prepared using $AgNO_3$ and $Hg(NO_3)_2$, both of which are secondary standards. Standardization is accomplished by titrating against a solution prepared from primary standard grade NaCl.

INORGANIC ANALYTES

Complexation titrimetry continues to be listed as a standard method for the determination of hardness, Ca^{2+}, CN^-, and Cl^- in waters and wastewaters. The evaluation of hardness was described earlier in Representative Method 9.3.1. The determination of Ca^{2+} is complicated by the presence of Mg^{2+}, which also reacts with EDTA. To prevent an interference the pH is adjusted to 12–13, which precipitates Mg^{2+} as $Mg(OH)_2$. Titrating with EDTA using murexide or Eriochrome Blue Black R as the indicator gives the concentration of Ca^{2+}.

Cyanide is determined at concentrations greater than 1 mg/L by making the sample alkaline with NaOH and titrating with a standard solution of $AgNO_3$ to form the soluble $Ag(CN)_2^-$ complex. The end point is determined using *p*-dimethylaminobenzalrhodamine as an indicator, with the solution turning from a yellow to a salmon color in the presence of excess Ag^+.

Chloride is determined by titrating with $Hg(NO_3)_2$, forming $HgCl_2(aq)$. The sample is acidified to a pH of 2.3–3.8 and diphenylcarbazone, which forms a colored complex with excess Hg^{2+}, serves as the indicator. The pH indicator xylene cyanol FF is added to ensure that the pH is within the desired range. The initial solution is a greenish blue, and the titration is carried out to a purple end point.

QUANTITATIVE CALCULATIONS

The quantitative relationship between the titrand and the titrant is determined by the titration reaction's stoichiometry. For a titration using EDTA, the stoichiometry is always 1:1.

EXAMPLE 9.3.1

The concentration of a solution of EDTA is determined by standardizing against a solution of Ca^{2+} prepared using a primary standard of $CaCO_3$. A 0.4071-g sample of $CaCO_3$ is transferred to a 500-mL volumetric flask, dissolved using a minimum of 6 M HCl, and diluted to volume. After transferring a 50.00-mL portion of this solution to a 250-mL Erlenmeyer flask, the pH is adjusted by adding 5 mL of a pH 10 NH_3–NH_4Cl buffer that contains a small amount of Mg^{2+}–EDTA. After adding calmagite as an indicator, the solution is titrated with the EDTA, requiring 42.63 mL to reach the end point. Report the molar concentration of EDTA in the titrant.

Solution

The primary standard of Ca^{2+} has a concentration of

$$\frac{0.4071\text{ g CaCO}_3}{0.5000\text{ L}} \times \frac{1\text{ mol Ca}^{2+}}{100.09\text{ g CaCO}_3} = 8.135 \times 10^{-3}\text{ M Ca}^{2+}$$

The moles of Ca^{2+} in the titrand is

$$8.135 \times 10^{-3}\text{ M Ca}^{2+} \times 0.05000\text{ L} = 4.068 \times 10^{-4}\text{ mol Ca}^{2+}$$

which means that 4.068×10^{-4} moles of EDTA are used in the titration. The molarity of EDTA in the titrant is

$$\frac{4.068 \times 10^{-4}\text{ mol Ca}^{2+}}{0.04263\text{ L}} = 9.543 \times 10^{-3}\text{ M EDTA}$$

EXERCISE 9.3.3

A 100.0-mL sample is analyzed for hardness using the procedure outlined in Representative Method 9.3.1, requiring 23.63 mL of 0.0109 M EDTA. Report the sample's hardness as mg $CaCO_3$/L.

Answer

In an analysis for hardness we treat the sample as if Ca^{2+} is the only metal ion that reacts with EDTA. The grams of Ca^{2+} in the sample, therefore, are

$$(0.0109\text{ M EDTA})(0.02363\text{ L}) \times \frac{1\text{ mol Ca}^{2+}}{\text{mol EDTA}} = 2.58 \times 10^{-4}\text{ mol Ca}^{2+}$$

$$2.58 \times 10^{-4}\text{ mol Ca}^{2+} \times \frac{1\text{ mol CaCO}_3}{\text{mol Ca}^{2+}} \times \frac{100.09\text{ g CaCO}_3}{\text{mol CaCO}_3} = 0.0258\text{ g CaCO}_3$$

and the sample's hardness is

$$\frac{0.0258\text{ g CaCO}_3}{0.1000\text{ L}} \times \frac{1000\text{ mg}}{\text{g}} = 258\text{ g CaCO}_3\text{/L}$$

As shown in the following example, we can extended this calculation to complexation reactions that use other titrants.

EXAMPLE 9.3.2

The concentration of Cl^- in a 100.0-mL sample of water from a freshwater aquifer is tested for the encroachment of sea water by titrating with 0.0516 M $Hg(NO_3)_2$. The sample is acidified and titrated to the diphenylcarbazone end point, requiring 6.18 mL of the titrant. Report the concentration of Cl^-, in mg/L, in the aquifer.

Solution

The reaction between Cl^- and Hg^{2+} produces a metal–ligand complex of $HgCl_2$*(aq)*. Each mole of Hg^{2}+ reacts with 2 moles of Cl^-; thus

$$\frac{0.0516\text{ mol Hg(NO}_3)_2}{\text{L}} \times 0.00618\text{ L} \times \frac{2\text{ mol Cl}^-}{\text{mol Hg(NO}_3)_2} \times \frac{35.453\text{ g Cl}^-}{\text{mol Cl}^-} = 0.0226\text{ g Cl}^-$$

are in the sample. The concentration of Cl^- in the sample is

$$\frac{0.0226\text{ g Cl}^-}{0.1000\text{ L}} \times \frac{1000\text{ mg}}{\text{g}} = 226\text{ mg/L}$$

EXERCISE 9.3.4

A 0.4482-g sample of impure NaCN is titrated with 0.1018 M $AgNO_3$, requiring 39.68 mL to reach the end point. Report the purity of the sample as %w/w NaCN.

Answer

The titration of CN^- with Ag^+ produces the metal-ligand complex $Ag(CN)_2^-$; thus, each mole of $AgNO_3$ reacts with two moles of NaCN. The grams of NaCN in the sample is

$$(0.1018\text{ M AgNO}_3)(0.03968\text{ L}) \times \frac{2\text{ mol NaCN}}{\text{mol AgNO}_3} \times \frac{49.01\text{ g NaCN}}{\text{mol NaCN}} = 0.3959\text{ g NaCN}$$

and the purity of the sample is

$$\frac{0.3959\text{ g NaCN}}{0.4482\text{ g sample}} \times 100 = 88.33\%\text{ w/w NaCN}$$

Finally, complex titrations involving multiple analytes or back titrations are possible.

EXAMPLE 9.3.3

An alloy of chromel that contains Ni, Fe, and Cr is analyzed by a complexation titration using EDTA as the titrant. A 0.7176-g sample of the alloy is dissolved in HNO_3 and diluted to 250 mL in a volumetric flask. A 50.00-mL aliquot of the sample, treated with pyrophosphate to mask the Fe and Cr, requires 26.14 mL of 0.05831 M EDTA to reach the murexide end point. A second 50.00-mL aliquot is treated with hexamethylenetetramine to mask the Cr. Titrating with 0.05831 M EDTA requires 35.43 mL to reach the murexide end point. Finally, a third 50.00-mL aliquot is treated with 50.00 mL of 0.05831 M EDTA, and back titrated to the murexide end point with 6.21 mL of 0.06316 M Cu^{2+}. Report the weight percents of Ni, Fe, and Cr in the alloy.

Solution

The stoichiometry between EDTA and each metal ion is 1:1. For each of the three titrations, therefore, we can write an equation that relates the moles of EDTA to the moles of metal ions that are titrated.

titration 1: mol Ni = mol EDTA
titration 2: mol Ni +mol Fe = mol EDTA
titration 3: mol Ni + mol Fe + mol Cr + mol Cu = mol EDTA

We use the first titration to determine the moles of Ni in our 50.00-mL portion of the dissolved alloy. The titration uses

$$\frac{0.05831\text{ mol EDTA}}{\text{L}} \times 0.02614\text{ L} = 1.524 \times 10^{-3}\text{ mol EDTA}$$

which means the sample contains 1.524×10^{-3} mol Ni.

Having determined the moles of EDTA that react with Ni, we use the second titration to determine the amount of Fe in the sample. The second titration uses

$$\frac{0.05831\text{ mol EDTA}}{\text{L}} \times 0.03543\text{ L} = 2.066 \times 10^{-3}\text{ mol EDTA}$$

of which 1.524×10^{-3} mol are used to titrate Ni. This leaves 5.42×10^{-4} mol of EDTA to react with Fe; thus, the sample contains 5.42×10^{-4} mol of Fe.

Finally, we can use the third titration to determine the amount of Cr in the alloy. The third titration uses

$$\frac{0.05831\text{ mol EDTA}}{\text{L}} \times 0.0500\text{ L} = 3.926 \times 10^{-3}\text{ mol EDTA}$$

of which 1.524×10^{-3} mol are used to titrate Ni and 5.42×10^{-4} mol are used to titrate Fe. This leaves 8.50×10^{-4} mol of EDTA to react with Cu and Cr. The amount of EDTA that reacts with Cu is

$$\frac{0.06316\text{ mol Cu}^{2+}}{\text{L}} \times 0.006211\text{ L} \times \frac{1\text{ mol EDTA}}{\text{mol Cu}^{2+}} = 3.92 \times 10^{-4}\text{ mol EDTA}$$

leaving 4.58×10^{-4} mol of EDTA to react with Cr. The sample, therefore, contains 4.58×10^{-4} mol of Cr.

Having determined the moles of Ni, Fe, and Cr in a 50.00-mL portion of the dissolved alloy, we can calculate the %w/w of each analyte in the alloy.

$$\frac{1.524 \times 10^{-3} \text{ mol Ni}}{50.00 \text{ mL}} \times \frac{58.69 \text{ g Ni}}{\text{mol Ni}} = 0.4472 \text{ g Ni}$$

$$\frac{0.4472 \text{ g Ni}}{0.7176 \text{ g sample}} \times 100 = 62.32\% \text{ w/w Ni}$$

$$\frac{5.42 \times 10^{-4} \text{ mol Fe}}{50.00 \text{ mL}} \times \frac{55.845 \text{ g Fe}}{\text{mol Fe}} = 0.151 \text{ g Fe}$$

$$\frac{0.151 \text{ g Fe}}{0.7176 \text{ g sample}} \times 100 = 21.0\% \text{ w/w Fe}$$

$$\frac{4.58 \times 10^{-4} \text{ mol Cr}}{50.00 \text{ mL}} \times \frac{51.996 \text{ g Cr}}{\text{mol Cr}} = 0.119 \text{ g Cr}$$

$$\frac{0.119 \text{ g Cr}}{0.7176 \text{ g sample}} \times 100 = 16.6\% \text{ w/w Cr}$$

EXERCISE 9.3.5

An indirect complexation titration with EDTA can be used to determine the concentration of sulfate, SO_4^{2-}, in a sample. A 0.1557-g sample is dissolved in water and any sulfate present is precipitated as $BaSO_4$ by adding $Ba(NO_3)_2$. After filtering and rinsing the precipitate, it is dissolved in 25.00 mL of 0.02011 M EDTA. The excess EDTA is titrated with 0.01113 M Mg^{2+}, requiring 4.23 mL to reach the end point. Calculate the %w/w Na_2SO_4 in the sample.

Answer

The total moles of EDTA used in this analysis is

$$(0.02011 \text{ M EDTA})(0.02500 \text{ L}) = 5.028 \times 10^{-4} \text{ mol EDTA}$$

Of this,

$$(0.01113 \text{ M } Mg^{2+})(0.00423 \text{ L}) \times \frac{1 \text{ mol EDTA}}{\text{mol } Mg^{2+}} = 4.708 \times 10^{-5} \text{ mol EDTA}$$

are consumed in the back titration with Mg^{2+}, which means that

$$5.028 \times 10^{-4} \text{ mol EDTA} - 4.708 \times 10^{-5} \text{ mol EDTA} = 4.557 \times 10^{-4} \text{ mol EDTA}$$

react with the $BaSO_4$. Each mole of $BaSO_4$ reacts with one mole of EDTA; thus

$$4.557 \times 10^{-4} \text{ mol EDTA} \times \frac{1 \text{ mol } BaSO_4}{\text{mol EDTA}} \times \frac{1 \text{ mol } Na_2SO_4}{\text{mol } BaSO_4} \times \frac{142.04 \text{ g } Na_2SO_4}{\text{mol } Na_2SO_4} = 0.06473 \text{ g } Na_2SO_4$$

$$\frac{0.06473 \text{ g } Na_2SO_4}{0.1557 \text{ g sample}} \times 100 = 41.57\% \text{ w/w } Na_2SO_4$$

EVALUATION OF COMPLEXATION TITRIMETRY

The scale of operations, accuracy, precision, sensitivity, time, and cost of a complexation titration are similar to those described earlier for acid–base titrations. Complexation titrations, however, are more selective. Although EDTA forms strong complexes with most metal ion, by carefully controlling the titrand's pH we can analyze samples that contain two or more analytes. The reason we can use pH to provide selectivity is shown in Figure 9.3.9 a. A titration of Ca^{2+} at a pH of 9 has a distinct break in the titration curve because the conditional formation constant for CaY^{2-} of 2.6×10^9 is large enough to ensure that the reaction of Ca^{2+} and EDTA goes to completion. At a pH of 3, however, the conditional formation constant of 1.23 is so small that very little Ca^{2+} reacts with the EDTA. Suppose we need to analyze a mixture of Ni^{2+} and Ca^{2+}. Both analytes react with EDTA, but their conditional formation constants differ significantly. If we adjust the pH to 3 we can titrate Ni^{2+} with EDTA without titrating Ca^{2+} (Figure 9.3.9 b). When the titration is complete, we adjust the titrand's pH to 9 and titrate the Ca^{2+} with EDTA.

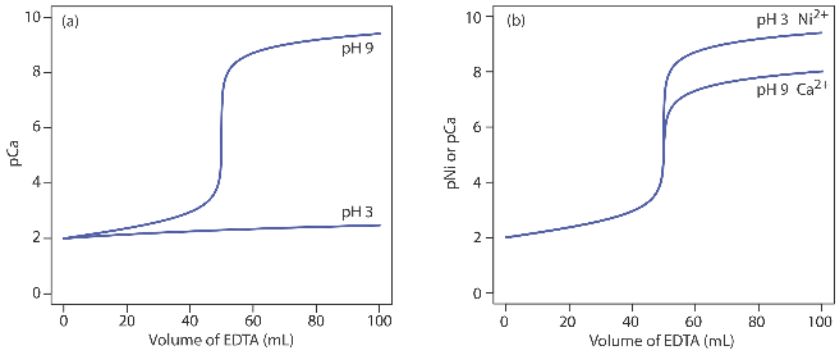


Figure 9.3.9 . Titration curves illustrating how we can use the titrand's pH to control EDTA's selectivity. (a) Titration of 50.0 mL of 0.010 M Ca^{2+} at a pH of 3 and a pH of 9 using 0.010 M EDTA. At a pH of 3 the CaY^{2-} complex is too weak to titrate successfully. (b) Titration of a 50.0 mL mixture of 0.010 M Ca^{2+} and 0.010 M Ni^{2+} at a pH of 3 and at a pH of 9 using 0.010 M EDTA. At a pH of 3 EDTA reacts only with Ni^{2+}. When the titration is complete, raising the pH to 9 allows for the titration of Ca^{2+}.

A spectrophotometric titration is a particularly useful approach for analyzing a mixture of analytes. For example, as shown in Figure 9.3.10 , we can determine the concentration of a two metal ions if there is a difference between the absorbance of the two metal-ligand complexes.

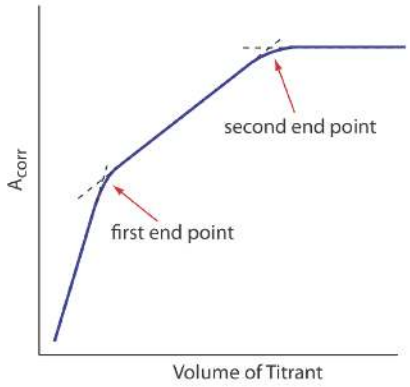


Figure 9.3.10 . Spectrophotometric titration curve for the complexation titration of a mixture of two analytes. The red arrows indicate the end points for each analyte.

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9.5: PROBLEMS

Some of the problems that follow require one or more equilibrium constants or standard state potentials. For your convenience, here are hyperlinks to the appendices containing these constants:

Appendix 10: Solubility Products

Appendix 11: Acid Dissociation Constants

Appendix 12: Metal-Ligand Formation Constants

Appendix 13: Standard State Reduction Potentials

1. Calculate or sketch titration curves for the following acid–base titrations.

(a) 25.0 mL of 0.100 M NaOH with 0.0500 M HCl

(b) 50.0 mL of 0.0500 M HCOOH with 0.100 M NaOH

(c) 50.0 mL of 0.100 M NH_3 with 0.100 M HCl

(d) 50.0 mL of 0.0500 M ethylenediamine with 0.100 M HCl

(e) 50.0 mL of 0.0400 M citric acid with 0.120 M NaOH

(f) 50.0 mL of 0.0400 M H_3PO_4 with 0.120 M NaOH

2. Locate the equivalence point(s) for each titration curve in problem 1 and, where feasible, calculate the pH at the equivalence point. What is the stoichiometric relationship between the moles of acid and the moles of base for each of these equivalence points?

3. Suggest an appropriate visual indicator for each of the titrations in problem 1.

4. To sketch the titration curve for a weak acid we approximate the pH at 10% of the equivalence point volume as $pK_a - 1$, and the pH at 90% of the equivalence point volume as $pK_a + 1$. Show that these assumptions are reasonable.

5. Tartaric acid, $H_2C_4H_4O_6$, is a diprotic weak acid with a pK_{a1} of 3.0 and a pK_{a2} of 4.4. Suppose you have a sample of impure tartaric acid (purity > 80%), and that you plan to determine its purity by titrating with a solution of 0.1 M NaOH using an indicator to signal the end point. Describe how you will carry out the analysis, paying particular attention to how much sample to use, the desired pH range for the indicator, and how you will calculate the %w/w tartaric acid. Assume your buret has a maximum capacity of 50 mL.

6. The following data for the titration of a monoprotic weak acid with a strong base were collected using an automatic titrator. Prepare normal, first derivative, second derivative, and Gran plot titration curves for this data, and locate the equivalence point for each.

volume of NaOH (mL)	pH	volume of NaOH (mL)	pH
0.25	3.0	49.95	7.8
0.86	3.2	49.97	8.0
1.63	3.4	49.98	8.2
2.72	3.6	49.99	8.4
4.29	3.8	50.00	8.7
6.54	4.0	50.01	9.1
9.67	4.2	50.02	9.4
13.79	4.4	50.04	9.6
18.83	4.6	50.06	9.8
24.47	4.8	50.10	10.0
30.15	5.0	50.16	10.2
35.33	5.2	50.25	10.4
39.62	5.4	50.40	10.6
42.91	5.6	50.63	10.8
45.28	5.8	51.01	11.0
46.91	6.0	51.61	11.2
48.01	6.2	52.58	11.4
48.72	6.4	54.15	11.6
49.19	6.6	56.73	11.8
49.48	6.8	61.11	12.0
49.67	7.0	68.83	12.2
49.79	7.2	83.54	12.4
49.87	7.4	116.14	12.6
49.92	7.6		

7. Schwartz published the following simulated data for the titration of a 1.02×10^{-4} M solution of a monoprotic weak acid (pK_a = 8.16) with 1.004×10^{-3} M NaOH [Schwartz, L. M. *J. Chem. Educ.* **1992**, *69*, 879–883]. The simulation assumes that a 50-mL pipet is used to transfer a portion of the weak acid solution to the titration vessel. A calibration of the pipet shows that it delivers a volume of only 49.94 mL. Prepare normal, first derivative, second derivative, and Gran plot titration curves for this data, and determine the equivalence point for each. How do these equivalence points compare to the expected equivalence point? Comment on the utility of each titration curve for the analysis of very dilute solutions of very weak acids.

mL of NaOH	pH	mL of NaOH	pH
0.03	6.212	4.79	8.858
0.09	6.504	4.99	8.926
0.29	6.936	5.21	8.994
0.72	7.367	5.41	9.056
1.06	7.567	5.61	9.118
1.32	7.685	5.85	9.180
1.53	7.776	6.05	9.231
1.76	7.863	6.28	9.283
1.97	7.938	6.47	9.327
2.18	8.009	6.71	9.374
2.38	8.077	6.92	9.414
2.60	8.146	7.15	9.451
2.79	8.208	7.36	9.484
3.01	8.273	7.56	9.514
3.19	8.332	7.79	9.545
3.41	8.398	7.99	9.572
3.60	8.458	8.21	9.599
3.80	8.521	8.44	9.624
3.99	8.584	8.64	9.645
4.18	8.650	8.84	9.666
4.40	8.720	9.07	9.688
4.57	8.784	9.27	9.706

8. Calculate or sketch the titration curve for a 50.0 mL solution of a 0.100 M monoprotic weak acid (pK_a = 8.0) with 0.1 M strong base in a nonaqueous solvent with $K_s = 10^{-20}$. You may assume that the change in solvent does not affect the weak acid's pK_a. Compare your titration curve to the titration curve when water is the solvent.

9. The titration of a mixture of *p*-nitrophenol (pK_a = 7.0) and *m*-nitrophenol (pK_a = 8.3) is followed spectrophotometrically. Neither acid absorbs at a wavelength of 545 nm, but their respective conjugate bases do absorb at this wavelength. The *m*-nitrophenolate ion has a greater absorbance than an equimolar solution of the *p*-nitrophenolate ion. Sketch the spectrophotometric titration curve for a 50.00-mL mixture consisting of 0.0500 M *p*-nitrophenol and 0.0500 M *m*-nitrophenol with 0.100 M NaOH. Compare your result to the expected potentiometric titration curves.

10. A quantitative analysis for aniline ($C_6H_5NH_2$, $K_b = 3.94 \times 10^{-10}$) is carried out by an acid–base titration using glacial acetic acid as the solvent and $HClO_4$ as the titrant. A known volume of sample that contains 3–4 mmol of aniline is transferred to a 250-mL Erlenmeyer flask and diluted to approximately 75 mL with glacial acetic acid. Two drops of a methyl violet indicator are added, and the solution is titrated with previously standardized 0.1000 M $HClO_4$ (prepared in glacial acetic acid using anhydrous HClO4) until the end point is reached. Results are reported as parts per million aniline.

(a) Explain why this titration is conducted using glacial acetic acid as the solvent instead of using water.

(b) One problem with using glacial acetic acid as solvent is its relatively high coefficient of thermal expansion of 0.11%/^{o}C. For example, 100.00 mL of glacial acetic acid at 25°C occupies 100.22 mL at 27°C. What is the effect on the reported concentration of aniline if the standardization of $HClO_4$ is conducted at a temperature that is lower than that for the analysis of the unknown?

(c) The procedure calls for a sample that contains 3–4 mmoles of aniline. Why is this requirement necessary?

Some of the problems that follow require one or more equilibrium constants or standard state potentials. For your convenience, here are hyperlinks to the appendices containing these constants:

Appendix 10: Solubility Products

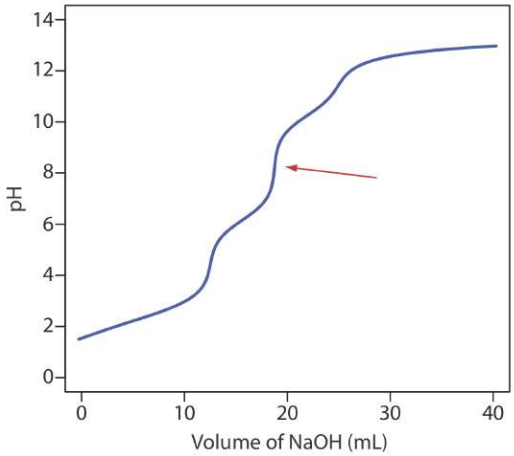
Appendix 11: Acid Dissociation Constants

Appendix 12: Metal-Ligand Formation Constants

11. Using a ladder diagram, explain why the presence of dissolved CO_2 leads to a determinate error for the standardization of NaOH if the end point's pH is between 6–10, but no determinate error if the end point's pH is less than 6.

12. A water sample's acidity is determined by titrating to fixed end point pHs of 3.7 and 8.3, with the former providing a measure of the concentration of strong acid and the later a measure of the combined concentrations of strong acid and weak acid. Sketch a titration curve for a mixture of 0.10 M HCl and 0.10 M H_2CO_3 with 0.20 M strong base, and use it to justify the choice of these end points.

13. Ethylenediaminetetraacetic acid, H_4Y, is a weak acid with successive acid dissociation constants of 0.010, 2.19×10^{-3}, 6.92×10^{-7}, and 5.75×10^{-11}. The figure below shows a titration curve for H_4Y with NaOH. What is the stoichiometric relationship between H_4Y and NaOH at the equivalence point marked with the red arrow?



14. A Gran plot method has been described for the quantitative analysis of a mixture that consists of a strong acid and a monoprotic weak acid [(a) Boiani, J. A. *J. Chem. Educ.* **1986**, *63*, 724–726; (b) Castillo, C. A.; Jaramillo, A. *J. Chem. Educ.* **1989**, *66*, 341]. A 50.00-mL mixture of HCl and CH_3COOH is transferred to an Erlenmeyer flask and titrated by using a digital pipet to add successive 1.00-mL aliquots of 0.09186 M NaOH. The progress of the titration is monitored by recording the pH after each addition of titrant. Using the two papers listed above as a reference, prepare a Gran plot for the following data and determine the concentrations of HCl and CH_3COOH.

mL of NaOH	pH	mL of NaOH	pH	mL of NaOH	pH
1.00	1.83	24.00	4.45	47.00	12.14
2.00	1.86	25.00	4.53	48.00	12.17
3.00	1.89	26.00	4.61	49.00	12.20
4.00	1.92	27.00	4.69	50.00	12.23
5.00	1.95	28.00	4.76	51.00	12.26
6.00	1.99	29.00	4.84	52.00	12.28
7.00	2.03	30.00	4.93	53.00	12.30
8.00	2.10	31.00	5.02	54.00	12.32
9.00	2.18	32.00	5.13	55.00	12.34
10.00	2.31	33.00	5.23	56.00	12.36
11.00	2.51	34.00	5.37	57.00	12.38
12.00	2.81	35.00	5.52	58.00	12.39
13.00	3.16	36.00	5.75	59.00	12.40
14.00	3.36	37.00	6.14	60.00	12.42
15.00	3.54	38.00	10.30	61.00	12.43
16.00	3.69	39.00	11.31	62.00	12.44
17.00	3.81	40.00	11.58	63.00	12.45
18.00	3.93	41.00	11.74	64.00	12.47
19.00	4.02	42.00	11.85	65.00	12.48
20.00	4.14	43.00	11.93	66.00	12.49
21.00	4.22	44.00	12.00	67.00	12.50
22.00	4.30	45.00	12.05	68.00	12.51
23.00	4.38	46.00	12.10	69.00	12.52

15. Explain why it is not possible for a sample of water to simultaneously have OH^- and HCO_3^- as sources of alkalinity.

16. For each of the samples a–e, determine the sources of alkalinity (OH^-, HCO_3^-, CO_3^{2-}) and their respective concentrations in parts per million In each case a 25.00-mL sample is titrated with 0.1198 M HCl to the bromocresol green and the phenolphthalein end points.

sample	volume of HCl (mL) to phenolphthalein end point	volume of HCl (mL) to the bromocresol green end point
a	21.36	21.38
b	5.67	21.13
c	0.00	14.28
d	17.12	34.26
e	21.36	25.69

17. A sample may contain any of the following: HCl, NaOH, H_3PO_4, $H_2PO_4^-$, HPO_4^{2-}, or PO_4^{3-}. The composition of a sample is determined by titrating a 25.00-mL portion with 0.1198 M HCl or 0.1198 M NaOH to the phenolphthalein and to the methyl orange end points. For each of the following samples, determine which species are present and their respective molar concentrations.

sample	titrant	volume (mL) to phenophthalein end point	volume (mL) to methyl orange end point
a	HCl	11.54	35.29
b	NaOH	19.79	9.89
c	HCl	22.76	22.78
d	NaOH	39.42	17.48

18. The protein in a 1.2846-g sample of an oat cereal is determined by a Kjeldahl analysis. The sample is digested with H_2SO_4, the resulting solution made basic with NaOH, and the NH_3 distilled into 50.00 mL of 0.09552 M HCl. The excess HCl is back titrated using 37.84 mL of 0.05992 M NaOH. Given that the proteins in grains average 17.54% w/w N, report the %w/w protein in the sample.

19. The concentration of SO_2 in air is determined by bubbling a sample of air through a trap that contains H_2O_2. Oxidation of SO_2 by H_2O_2 results in the formation of H_2SO_4, which is then determined by titrat-ing with NaOH. In a typical analysis, a sample of air is passed through the peroxide trap at a rate of 12.5 L/min for 60 min and required 10.08 mL of 0.0244 M NaOH to reach the phenolphthalein end point. Calculate the μL/L SO_2 in the sample of air. The density of SO_2 at the temperature of the air sample is 2.86 mg/mL.

20. The concentration of CO_2 in air is determined by an indirect acid–base titration. A sample of air is bubbled through a solution that contains an excess of $Ba(OH)_2$, precipitating $BaCO_3$. The excess $Ba(OH)_2$ is back titrated with HCl. In a typical analysis a 3.5-L sample of air is bubbled through 50.00 mL of 0.0200 M $Ba(OH)_2$. Back titrating with 0.0316 M HCl requires 38.58 mL to reach the end point. Determine the ppm CO_2 in the sample of air given that the density of CO_2 at the temperature of the sample is 1.98 g/L.

Some of the problems that follow require one or more equilibrium constants or standard state potentials. For your convenience, here are hyperlinks to the appendices containing these constants:

Appendix 10: Solubility Products

Appendix 11: Acid Dissociation Constants

Appendix 12: Metal-Ligand Formation Constants

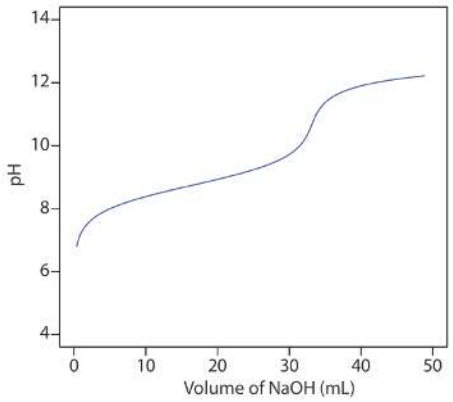
Appendix 13: Standard State Reduction Potentials

21. The purity of a synthetic preparation of methylethyl ketone, C_4H_8O, is determined by reacting it with hydroxylamine hydrochloride, liberating HCl (see reaction in Table 9.2.7). In a typical analysis a 3.00-mL sample is diluted to 50.00 mL and treated with an excess of hydroxylamine hydrochloride. The liberated HCl is titrated with 0.9989 M NaOH, requiring 32.68 mL to reach the end point. Report the percent purity of the sample given that the density of methylethyl ketone is 0.805 g/mL.

22. Animal fats and vegetable oils are triesters formed from the reaction between glycerol (1,2,3-propanetriol) and three long-chain fatty acids. One of the methods used to characterize a fat or an oil is a determination of its saponification number. When treated with boiling aqueous KOH, an ester saponifies into the parent alcohol and fatty acids (as carboxylate ions). The saponification number is the number of milligrams of KOH required to saponify 1.000 gram of the fat or the oil. In a typical analysis a 2.085-g sample of butter is added to 25.00 mL of 0.5131 M KOH. After saponification is complete the excess KOH is back titrated with 10.26 mL of 0.5000 M HCl. What is the saponification number for this sample of butter?

23. A 250.0-mg sample of an organic weak acid is dissolved in an appropriate solvent and titrated with 0.0556 M NaOH, requiring 32.58 mL to reach the end point. Determine the compound's equivalent weight.

24. The figure below shows a potentiometric titration curve for a 0.4300-g sample of a purified amino acid that was dissolved in 50.00 mL of water and titrated with 0.1036 M NaOH. Identify the amino acid from the possibilities listed in the table.



amino acid	formula weight (g/mol)	K_a
alanine	89.1	1.35×10^{-10}
glycine	75.1	1.67×10^{-10}
methionine	149.2	8.9×10^{-10}
taurine	125.2	1.8×10^{-9}
asparagine	150	1.9×10^{-9}
leucine	131.2	1.79×10^{-10}
phenylalanine	166.2	4.9×10^{-10}
valine	117.2	1.91×10^{-10}

25. Using its titration curve, determine the acid dissociation constant for the weak acid in problem 9.6.

26. Where in the scale of operations do the microtitration techniques discussed in Chapter 9.7 belong?

27. An acid–base titration can be used to determine an analyte's equivalent weight, but it can not be used to determine its formula weight. Explain why.

28. Commercial washing soda is approximately 30–40% w/w Na_2CO_3. One procedure for the quantitative analysis of washing soda contains the following instructions:

Transfer an approximately 4-g sample of the washing soda to a 250-mL volumetric flask. Dissolve the sample in about 100 mL of H_2O and then dilute to the mark. Using a pipet, transfer a 25-mL aliquot of this solution to a 125-mL Erlenmeyer flask and add 25-mL of H_2O and 2 drops of bromocresol green indicator. Titrate the sample with 0.1 M HCl to the indicator's end point.

What modifications, if any, are necessary if you want to adapt this procedure to evaluate the purity of commercial Na_2CO_3 that is >98% pure?

29. A variety of systematic and random errors are possible when standardizing a solution of NaOH against the primary weak acid standard potassium hydrogen phthalate (KHP). Identify, with justification, whether the following are sources of systematic error or random error, or if they have no affect on the error. If the error is systematic, then indicate whether the experimentally determined molarity for NaOH is too high or too low. The standardization reaction is

$$C_8H_5O_4^-(aq) + OH^-(aq) \rightarrow C_8H_4O_4^-(aq) + H_2O(l)$$

(a) The balance used to weigh KHP is not properly calibrated and always reads 0.15 g too low.

(b) The indicator for the titration changes color between a pH of 3–4.

(c) An air bubble, which is lodged in the buret's tip at the beginning of the analysis, dislodges during the titration.

(d) Samples of KHP are weighed into separate Erlenmeyer flasks, but the balance is tarred only for the first flask.

(e) The KHP is not dried before it is used.

(f) The NaOH is not dried before it is used.

(g) The procedure states that the sample of KHP should be dissolved in 25 mL of water, but it is accidentally dissolved in 35 mL of water.

30. The concentration of *o*-phthalic acid in an organic solvent, such as *n*-butanol, is determined by an acid–base titration using aqueous NaOH as the titrant. As the titrant is added, the *o*-phthalic acid extracts into the aqueous solution where it reacts with the titrant. The titrant is added slowly to allow sufficient time for the extraction to take place.

(a) What type of error do you expect if the titration is carried out too quickly?

(b) Propose an alternative acid–base titrimetric method that allows for a more rapid determination of the concentration of *o*-phthalic acid in *n*-butanol.

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> Appendix 13: Standard State Reduction Potentials

31. Calculate or sketch titration curves for 50.0 mL of 0.100 Mg^{2+} with 0.100 M EDTA at a pH of 7 and 10. Locate the equivalence point for each titration curve.

32. Calculate or sketch titration curves for 25.0 mL of 0.0500 M Cu^{2+} with 0.025 M EDTA at a pH of 10 and in the presence of 10^{-3} M and 10^{-1} M NH_3. Locate the equivalence point for each titration curve.

33. Sketch the spectrophotometric titration curve for the titration of a mixture of 5.00×10^{-3} M Bi^{3+} and 5.00×10^{-3} M Cu^{2+} with 0.0100 M EDTA. Assume that only the Cu^{2+}–EDTA complex absorbs at the selected wavelength.

34. The EDTA titration of mixtures of Ca^{2+} and Mg^{2+} can be followed thermometrically because the formation of the Ca^{2+}–EDTA complex is exothermic and the formation of the Mg^{2+}–EDTA complex is endothermic. Sketch the thermometric titration curve for a mixture of 5.00×10^{-3} M Ca^{2+} and 5.00×10^{-3} M Mg^{2+} using 0.0100 M EDTA as the titrant. The heats of formation for CaY^{2-} and MgY^{2-} are, respectively, –23.9 kJ/mole and 23.0 kJ/mole.

35. EDTA is one member of a class of aminocarboxylate ligands that form very stable 1:1 complexes with metal ions. The following table provides logK_f values for the complexes of six such ligands with Ca^{2+} and Mg^{2+}. Which ligand is the best choice for a direct titration of Ca^{2+} in the presence of Mg^{2+}?

ligand	Mg2+	Ca2+
EDTA: ethylenediaminetetraacetica acid	8.7	10.7
HEDTA: N-hydroxyethylenediametriacetic acid	7.0	8.0
EEDTA: ethyletherdiaminetetraacetic acid	8.3	10.0
EGTA: ethyleneglycol-bis(β-aminoethylether)-N,N'-tetraacetic acid	5.4	10.9
DTPA: diethylenetriaminpentaacetic acid	9.0	107
CyDTA: cycloheanediaminetetraacetic acid	10.3	12.3

36. The amount of calcium in physiological fluids is determined by a complexometric titration with EDTA. In one such analysis a 0.100-mL sample of a blood serum is made basic by adding 2 drops of NaOH and titrated with 0.00119 M EDTA, requiring 0.268 mL to reach the end point. Report the concentration of calcium in the sample as milligrams Ca per 100 mL.

37. After removing the membranes from an eggshell, the shell is dried and its mass recorded as 5.613 g. The eggshell is transferred to a 250-mL beaker and dissolved in 25 mL of 6 M HCl. After filtering, the solution that contains the dissolved eggshell is diluted to 250 mL in a volumetric flask. A 10.00-mL aliquot is placed in a 125-mL Erlenmeyer flask and buffered to a pH of 10. Titrating with 0.04988 M EDTA requires 44.11 mL to reach the end point. Determine the amount of calcium in the eggshell as %w/w $CaCO_3$.

38. The concentration of cyanide, CN^-, in a copper electroplating bath is determined by a complexometric titration using Ag^+ as the titrant, forming the soluble $Ag(CN)_2^-$ complex. In a typical analysis a 5.00-mL sample from an electroplating bath is transferred to a 250-mL Erlenmeyer flask, and treated with 100 mL of H_2O, 5 mL of 20% w/v NaOH and 5 mL of 10% w/v KI. The sample is titrated with 0.1012 M $AgNO_3$, requiring 27.36 mL to reach the end point as signaled by the formation of a yellow precipitate of AgI. Report the concentration of cyanide as parts per million of NaCN.

39. Before the introduction of EDTA most complexation titrations used Ag^+ or CN^- as the titrant. The analysis for Cd^{2+}, for example, was accomplished indirectly by adding an excess of KCN to form $Cd(CN)_4^{2-}$, and back-titrating the excess CN^- with Ag^+, forming $Ag(CN)_2^-$. In one such analysis a 0.3000-g sample of an ore is dissolved and treated with 20.00 mL of 0.5000 M KCN. The excess CN^- requires 13.98 mL of 0.1518 M $AgNO_3$ to reach the end point. Determine the %w/w Cd in the ore.

40. Solutions that contain both Fe^{3+} and Al^{3+} are selectively analyzed for Fe^{3+} by buffering to a pH of 2 and titrating with EDTA. The pH of the solution is then raised to 5 and an excess of EDTA added, resulting in the formation of the Al^{3+}–EDTA complex. The excess EDTA is back-titrated using a standard solution of Fe^{3+}, providing an indirect analysis for Al^{3+}.

(a) At a pH of 2, verify that the formation of the Fe^{3+}–EDTA complex is favorable, and that the formation of the Al^{3+}–EDTA complex is not favorable.

(b) A 50.00-mL aliquot of a sample that contains Fe^{3+} and Al^{3+} is transferred to a 250-mL Erlenmeyer flask and buffered to a pH of 2. A small amount of salicylic acid is added, forming the soluble red-colored Fe^{3+}–salicylic acid complex. The solution is titrated with 0.05002 M EDTA, requiring 24.82 mL to reach the end point as signaled by the disappearance of the Fe^{3+}–salicylic acid complex's red color. The solution is buffered to a pH of 5 and 50.00 mL of 0.05002 M EDTA is added. After ensuring that the formation of the Al^{3+}–EDTA complex is complete, the excess EDTA is back titrated with 0.04109 M Fe^{3+}, requiring 17.84 mL to reach the end point as signaled by the reappearance of the red-colored Fe^{3+}–salicylic acid complex. Report the molar concentrations of Fe^{3+} and A^{l3+} in the sample.

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41. Prada and colleagues described an indirect method for determining sulfate in natural samples, such as seawater and industrial effluents [Prada, S.; Guekezian, M.; Suarez-Iha, M. E. V. *Anal. Chim. Acta* **1996**, *329*, 197–202]. The method consists of three steps: precipitating the sulfate as $PbSO_4$; dissolving the $PbSO_4$ in an ammonical solution of excess EDTA to form the soluble PbY^{2-} complex; and titrating the excess EDTA with a standard solution of Mg^{2+}. The following reactions and equilibrium constants are known

$$PbSO_4(s) \rightleftharpoons Pb^{2+}(aq) + SO_4^{2-}(aq) \quad K_{sp} = 1.6 \times 10^{-8}$$

$$Pb^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons PbY^{2-}(aq) \quad K_f = 1.1 \times 10^{18}$$

$$Mg^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons MgY^{2-}(aq) \quad K_f = 4.9 \times 10^{8}$$

$$Zn^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons ZnY^{2-}(aq) \quad K_f = 3.2 \times 10^{16}$$

(a) Verify that a precipitate of $PbSO_4$ will dissolve in a solution of Y^{4-}.

(b) Sporek proposed a similar method using Zn^{2+} as a titrant and found that the accuracy frequently was poor [Sporek, K. F. *Anal. Chem.* **1958**, *30*, 1030–1032]. One explanation is that Zn^{2+} might react with the PbY^{2-} complex, forming ZnY^{2-}. Show that this might be a problem when using Zn^{2+} as a titrant, but that it is not a problem when using Mg^{2+} as a titrant. Would such a displacement of Pb^{2+} by Zn^{2+} lead to the reporting of too much or too little sulfate?

(c) In a typical analysis, a 25.00-mL sample of an industrial effluent is carried through the procedure using 50.00 mL of 0.05000 M EDTA. Titrating the excess EDTA requires 12.42 mL of 0.1000 M Mg^{2+}. Report the molar concentration of SO_4^{2-} in the sample of effluent.

42. Table 9.3.1 provides values for the fraction of EDTA present as Y^{4-}, $\alpha_{Y^{4-}}$. Values of $\alpha_{Y^{4-}}$ are calculated using the equation

$$\alpha_{Y^{4-}} = \frac{[Y^{4-}]}{C_{EDTA}}$$

where [Y^{4-}] is the concentration of the fully deprotonated EDTA and C_{EDTA} is the total concentration of EDTA in all of its forms

$$C_{EDTA} = [H_6Y^{2+}] + [H_5Y^{+}] + [H_4Y] + [H_3Y^{-}] + [H_2Y^{2-}] + [H_Y^{3-}] + [Y^{4-}]$$

$$H_6Y^{2+}(aq) + H_2O(l) \rightleftharpoons H_3O^{+}(aq) + H_5Y^{+}(aq) \quad K_{a1}$$

$$H_5Y^{+}(aq) + H_2O(l) \rightleftharpoons H_3O^{+}(aq) + H_4Y(aq) \quad K_{a2}$$

$$H_4Y(aq) + H_2O(l) \rightleftharpoons H_3O^{+}(aq) + H_3Y^{-}(aq) \quad K_{a3}$$

$$H_3Y^{-}(aq) + H_2O(l) \rightleftharpoons H_3O^{+}(aq) + H_2Y^{2-}(aq) \quad K_{a4}$$

$$H_2Y^{2-}(aq) + H_2O(l) \rightleftharpoons H_3O^{+}(aq) + HY^{3-}(aq) \quad K_{a5}$$

$$HY^{2-}(aq) + H_2O(l) \rightleftharpoons H_3O^{+}(aq) + Y^{4-}(aq) \quad K_{a6}$$

to show that

$$\alpha_{Y^{4-}} = \frac{K_{a1}K_{a2}K_{a3}K_{a4}K_{a5}K_{a6}}{d}$$

where

$$d = [H_3O^+]^6 + [H_3O^+]^5 K_{a1} + [H_3O^+]^4 K_{a1} K_{a2} + [H_3O^+]^3 K_{a1} K_{a2} K_{a3} + [H_3O^+]^2 K_{a1} K_{a2} K_{a3} K_{a4} + [H_3O^+] K_{a1} K_{a2} K_{a3} K_{a4} K_{a5} + K_{a1} K_{a2} K_{a3} K_{a4} K_{a5} K_{a6}$$

43. Calculate or sketch titration curves for the following redox titration reactions at 25ºC. Assume the analyte initially is present at a concentration of 0.0100 M and that a 25.0-mL sample is taken for analysis. The titrant, which is the **bold** species in each reaction, has a concentration of 0.0100 M.

(a) $V^{2+}(aq)$ + $\mathbf{Ce^{4+}}(aq) \rightarrow V^{3+}(aq) + Ce^{3+}(aq)$

(b) $Sn^{2+}(aq) + 2\mathbf{Ce^{4+}}(aq) \rightarrow Sn^{4+}(aq) + 2Ce^{3+}(aq)$

(c) $5Fe^{2+}(aq) + \mathbf{MnO_4^-}(aq) + 8H^+(aq) \rightarrow 5Fe^{3+}(aq) + Mn^{2+}(aq) + 4H_2O(l)$ at a pH of 1

44. What is the equivalence point for each titration in problem 43?

45. Suggest an appropriate indicator for each titration in problem 43.

46. The iron content of an ore is determined by a redox titration that uses $K_2Cr_2O_7$ as the titrant. A sample of the ore is dissolved in concentrated HCl using Sn^{2+} to speed its dissolution by reducing Fe^{3+} to Fe^{2+}. After the sample is dissolved, Fe^{2+} and any excess Sn^{2+} are oxidized to Fe^{3+} and Sn^{4+} using MnO_4^-. The iron is then carefully reduced to Fe^{2+} by adding a 2–3 drop excess of Sn^{2+}. A solution of $HgCl_2$ is added and, if a white precipitate of Hg_2Cl_2 forms, the analysis is continued by titrating with $K_2Cr_2O_7$. The sample is discarded without completing the analysis if a precipitate of Hg_2Cl_2 does not form or if a gray precipitate (due to Hg) forms.

(a) Explain why the sample is discarded if a white precipitate of Hg_2Cl_2 does not form or if a gray precipitate forms.

(b) Is a determinate error introduced if the analyst forgets to add Sn^{2+} in the step where the iron ore is dissolved?

(c) Is a determinate error introduced if the iron is not quantitatively oxidized back to Fe^{3+} by the MnO_4^-?

47. The amount of Cr^{3+} in an inorganic salt is determined by a redox titration. A portion of sample that contains approximately 0.25 g of Cr^{3+} is accurately weighed and dissolved in *50 mL of H_2O*. The Cr^{3+} is oxidized to $Cr_2O_7^{2-}$ by adding *20 mL of 0.1 M $AgNO_3$*, which serves as a catalyst, and *50 mL of 10%w/v $(NH_4)_2S_2O_8$*, which serves as the oxidizing agent. After the reaction is complete, the resulting solution is boiled for 20 minutes to destroy the excess $S_2O_8^{2-}$, cooled to room temperature, and diluted to 250 mL in a volumetric flask. A *50-mL portion of the resulting solution* is transferred to an Erlenmeyer flask, treated with *50 mL of a standard solution of Fe^{2+}*, and acidified with *200 mL of 1 M H_2SO_4*, reducing the $Cr_2O_7^{2-}$ to Cr^{3+}. The excess Fe^{2+} is then determined by a back titration with a standard solution of $K_2Cr_2O_7$ using an appropriate indicator. The results are reported as %w/w Cr^{3+}.

(a) There are several places in the procedure where a reagent's volume is specified (see *italicized text*). Which of these measurements must be made using a volumetric pipet.

(b) Excess peroxydisulfate, $S_2O_8^{2-}$ is destroyed by boiling the solution. What is the effect on the reported %w/w Cr^{3+} if some of the $S_2O_8^{2-}$ is not destroyed during this step?

(c) Solutions of Fe^{2+} undergo slow air oxidation to Fe^{3+}. What is the effect on the reported %w/w Cr^{3+} if the standard solution of Fe^{2+} is inadvertently allowed to be partially oxidized?

48. The exact concentration of H_2O_2 in a solution that is nominally 6% w/v H_2O_2 is determined by a redox titration using MnO_4^- as the titrant. A 25-mL aliquot of the sample is transferred to a 250-mL volumetric flask and diluted to volume with distilled water. A 25-mL aliquot of the diluted sample is added to an Erlenmeyer flask, diluted with 200 mL of distilled water, and acidified with 20 mL of 25% v/v H_2SO_4. The resulting solution is titrated with a standard solution of $KMnO_4$ until a faint pink color persists for 30 s. The results are reported as %w/v H_2O_2.

(a) Many commercially available solutions of H_2O_2 contain an inorganic or an organic stabilizer to prevent the autodecomposition of the peroxide to H_2O and O_2. What effect does the presence of this stabilizer have on the reported %w/v H_2O_2 if it also reacts with MnO_4^-?

(b) Laboratory distilled water often contains traces of dissolved organic material that may react with MnO_4^-. Describe a simple method to correct for this potential interference.

(c) What modifications to the procedure, if any, are needed if the sample has a nominal concentration of 30% w/v H_2O_2.

49. The amount of iron in a meteorite is determined by a redox titration using $KMnO_4$ as the titrant. A 0.4185-g sample is dissolved in acid and the liberated Fe^{3+} quantitatively reduced to Fe^{2+} using a Walden reductor. Titrating with 0.02500 M $KMnO_4$ requires 41.27 mL to reach the end point. Determine the %w/w Fe_2O_3 in the sample of meteorite.

50. Under basic conditions, MnO_4^- is used as a titrant for the analysis of Mn^{2+}, with both the analyte and the titrant forming MnO_2. In the analysis of a mineral sample for manganese, a 0.5165-g sample is dissolved and the manganese reduced to Mn^{2+}. The solution is made basic and titrated with 0.03358 M $KMnO_4$, requiring 34.88 mL to reach the end point. Calculate the %w/w Mn in the mineral sample.

> Some of the problems that follow require one or more equilibrium constants or standard state potentials. For your convenience, here are hyperlinks to the appendices containing these constants:

Appendix 10: Solubility Products

Appendix 11: Acid Dissociation Constants

Appendix 12: Metal-Ligand Formation Constants

Appendix 13: Standard State Reduction Potentials

51. The amount of uranium in an ore is determined by an indirect redox titration. The analysis is accomplished by dissolving the ore in sulfuric acid and reducing UO_2^+ to U^{4+} with a Walden reductor. The solution is treated with an excess of Fe^{3+}, forming Fe^{2+} and U^{6+}. The Fe^{2+} is titrated with a standard solution of $K_2Cr_2O_7$. In a typical analysis a 0.315-g sample of ore is passed through the Walden reductor and treated with 50.00 mL of 0.0125 M Fe^{3+}. Back titrating with 0.00987 M $K_2Cr_2O_7$ requires 10.52 mL. What is the %w/w U in the sample?

52. The thickness of the chromium plate on an auto fender is determined by dissolving a 30.0-cm^2 section in acid and oxidizing Cr^{3+} to $Cr_2O_7^{2-}$ with peroxydisulfate. After removing excess peroxydisulfate by boiling, 500.0 mg of $Fe(NH_4)_2(SO_4)_2 \cdot 6H_2O$ is added, reducing the $Cr_2O_7^{2-}$ to Cr^{3+}. The excess Fe^{2+} is back titrated, requiring 18.29 mL of 0.00389 M $K_2Cr_2O_7$ to reach the end point. Determine the average thickness of the chromium plate given that the density of Cr is 7.20 g/cm^3.

53. The concentration of CO in air is determined by passing a known volume of air through a tube that contains I_2O_5, forming CO_2 and I_2. The I_2 is removed from the tube by distilling it into a solution that contains an excess of KI, producing I_3^-. The I_3^- is titrated with a standard solution of $Na_2S_2O_3$. In a typical analysis a 4.79-L sample of air is sampled as described here, requiring 7.17 mL of 0.00329 M $Na_2S_2O_3$ to reach the end point. If the air has a density of 1.23×10^{-3} g/mL, determine the parts per million CO in the air.

54. The level of dissolved oxygen in a water sample is determined by the Winkler method. In a typical analysis a 100.0-mL sample is made basic and treated with a solution of $MnSO_4$, resulting in the formation of MnO_2. An excess of KI is added and the solution is acidified, resulting in the formation of Mn^{2+} and I_2. The liberated I_2 is titrated with a solution of 0.00870 M $Na_2S_2O_3$, requiring 8.90 mL to reach the starch indicator end point. Calculate the concentration of dissolved oxygen as parts per million O_2.

55. Calculate or sketch the titration curve for the titration of 50.0 mL of 0.0250 M KI with 0.0500 M $AgNO_3$. Prepare separate titration curves using pAg and pI on the *y*-axis.

56. Calculate or sketch the titration curve for the titration of a 25.0 mL mixture of 0.0500 M KI and 0.0500 M KSCN using 0.0500 M $AgNO_3$ as the titrant.

57. The analysis for Cl^- using the Volhard method requires a back titration. A known amount of $AgNO_3$ is added, precipitating AgCl. The unreacted Ag^+ is determined by back titrating with KSCN. There is a complication, however, because AgCl is more soluble than AgSCN.

(a) Why do the relative solubilities of AgCl and AgSCN lead to a titration error?

(b) Is the resulting titration error a positive or a negative determinate error?

(c) How might you modify the procedure to eliminate this source of determinate error?

(d) Is this source of determinate error of concern when using the Volhard method to determine Br^-?

58. Voncina and co-workers suggest that a precipitation titration can be monitored by measuring pH as a function of the volume of titrant if the titrant is a weak base [VonČina, D. B.; DobČnik, D.; GomiŠČek, S. *Anal. Chim. Acta* **1992**, *263*, 147–153]. For example, when titrating Pb^{2+} with K_2CrO_4 the solution that contains the analyte initially is acidified to a pH of 3.50 using HNO_3. Before the equivalence point the concentration of CrO_4^{2-} is controlled by the solubility product of $PbCrO_4$. After the equivalence point the concentration of CrO_4^{2-} is determined by the amount of excess titrant. Considering the reactions that control the concentration of CrO_4^{2-}, sketch the expected titration curve of pH versus volume of titrant.

59. A 0.5131-g sample that contains KBr is dissolved in 50 mL of distilled water. Titrating with 0.04614 M $AgNO_3$ requires 25.13 mL to reach the Mohr end point. A blank titration requires 0.65 mL to reach the same end point. Report the %w/w KBr in the sample.

60. A 0.1093-g sample of impure Na_2CO_3 is analyzed by the Volhard method. After adding 50.00 mL of 0.06911 M $AgNO_3$, the sample is back titrated with 0.05781 M KSCN, requiring 27.36 mL to reach the end point. Report the purity of the Na_2CO_3 sample.

61. A 0.1036-g sample that contains only $BaCl_2$ and NaCl is dissolved in 50 mL of distilled water. Titrating with 0.07916 M $AgNO_3$ requires 19.46 mL to reach the Fajans end point. Report the %w/w $BaCl_2$ in the sample.

Some of the problems that follow require one or more equilibrium constants or standard state potentials. For your convenience, here are hyperlinks to the appendices containing these constants:

Appendix 10: Solubility Products

Appendix 11: Acid Dissociation Constants

Appendix 12: Metal-Ligand Formation Constants

Appendix 13: Standard State Reduction Potentials

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9.6: ADDITIONAL RESOURCES

The following set of experiments introduce students to the applications of titrimetry. Experiments are grouped into four categories based on the type of reaction (acid–base, complexation, redox, and precipitation). Additional experiments emphasizing potentiometric electrodes are found in Chapter 11.

Acid–base Titrimetry

- Boiani, J. A. "The Gran Plot Analysis of an Acid Mixture," *J. Chem. Educ.* **1986**, *63*, 724–726.
- Castillo, C. A.; Jaramillo, A. "An Alternative Procedure for Titration Curves of a Mixture of Acids of Different Strengths," *J. Chem. Educ.* **1989**, *66*, 341.
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- Clay, J. T.; Walters, E. A.; Brabson, G. D. "A Dibasic Acid Titration for the Physical Chemistry Laboratory" *J. Chem. Educ.* **1995**, *72*, 665–667.
- Crossno, S. K; Kalbus, L. H.; Kalbus, G. E. "Determinations of Carbon Dioxide by Titration," *J. Chem. Educ.* **1996**, *73*, 175–176.
- Flowers, P. A. "Potentiometric Measurement of Transition Ranges and Titration Errors for Acid/Base Indicators," *J. Chem. Educ.* **1997**, *74*, 846–847.
- Fuchsam, W. H.; Garg, Sandhya "Acid Content of Beverages," *J. Chem. Educ.* **1990**, *67*, 67–68
- Graham. R.C.; DePew, S. "Determination of Ammonia in Household Cleaners," *J. Chem. Educ.* **1983**, *60*, 765–766.
- Kalbus, L. H.; Petrucci, R. H.; Forman, J. E.; Kalbus, G. E. "Titration of Chromate-Dichromate Mixtures," *J. Chem. Educ.* **1991**, *68*, 677–678.
- Kooser, A. S.; Jenkins, J. L.; Welch, L. E. "Acid–Base Indicators: A New Look at an Old Topic," *J. Chem. Educ.* **2001**, *78*, 1504–1506.
- Kraft, A. "The Determination of the p*K*a of Multiprotic, Weak Acids by Analyzing Potentiometric Acid–Base Titration Data with Difference Plots," *J. Chem. Educ.* **2003**, *80*, 554–559.
- Murphy, J. "Determination of Phosphoric Acid in Cola Beverages," *J. Chem. Educ.* **1983**, *60*, 420–421.
- Nyasulu, F.; Barlag, R.; Macklin, J. *Chem. Educator* **2008**, *13*, 289–294.
- Ophardt, C. E. "Acid Rain Analysis by Standard Addition Titration," *J. Chem. Educ.* **1985**, *62*, 257– 258.
- Partanen, J. I.; Kärki, M. H. "Determination of the Thermodynamic Dissociation Constant of a Weak Acid by Potentiometric Acid-Base Titration," *J. Chem. Educ.* **1994**, *71*, A120–A122.
- Thompson, R. Q. "Identification of Weak Acids and Bases by Titration with Primary Standards," *J. Chem. Educ.* **1988**, *65*, 179–180.
- Tucker, S. A.; Amszi, V. L.; Acree, Jr. W. E. "Studying Acid-Base Equilibria in Two-Phase Solvent Media," *J. Chem. Educ.* **1993**, *70*, 80–82.
- Tucker, S. A.; Acree, Jr., W. E. "A Student-Designed Analytical Laboratory Method," *J. Chem. Educ.* **1994**, *71*, 71–74.
- Werner, J. A.; Werner, T. C. "Multifunctional Base Unknowns in the Introductory Analytical Chemistry Lab," *J. Chem. Educ.* **1991**, *68*, 600–601.

Complexation Titrimetry

- Ceretti, H.; Hughes, E. A.; Zalts, A. "The Softening of Hard Water and Complexometric Titrations," *J. Chem. Educ.* **1999**, *76*, 1420–1421.
- Fulton, R.; Ross, M.; Schroeder, K. "Spectrophotometric Titration of a Mixture of Calcium and Magnesium," *J. Chem. Educ.* **1986**, *63*, 721–723.
- Novick, S. G. "Complexometric Titration of Zinc," *J. Chem. Educ.* **1997**, *74*, 1463.
- Olsen, K. G.; Ulicny, L. J. "Reduction of Calcium Concentrations by the Brita Water Filtration System: A Practical Experiment in Titrimetry and Atomic Absorption Spectroscopy," *J. Chem. Educ.* **2001**, *78*, 941.
- Smith, R. L.; Popham, R. E. "The Quantitative Resolution of a Mixture of Group II Metal Ions by Thermometric Titration with EDTA," *J. Chem. Educ.* **1983**, *60*, 1076–1077.
- Yappert, M. C.; DuPré, D. B. "Complexometric Titrations: Competition of Complexing Agents in the Determination of Water Hardness with EDTA," *J. Chem. Educ.* **1997**, *74*, 1422–1423.

Redox Titrimetry

- Guenther, W. B. "Supertitrations: High-Precision Methods," *J. Chem. Educ.* **1988**, *65*, 1097–1098.
- Haddad, P. "Vitamin C Content of Commercial Orange Juices," *J. Chem. Educ.* **1977**, *54*, 192–193.
- Harris, D. C.; Hills, M. E.; Hewston, T. A. "Preparation, Iodometric Analysis and Classroom Demonstration of Superconductivity in $YBa_2Cu_3O_{8-x}$," *J. Chem. Educ.* **1987**, *64*, 847–850.
- Lau, O.-W.; Luk, S.-F.; Cheng, N. L. N.; Woo, H.-O. "Determination of Free Lime in Clinker and Cement by Iodometry," *J. Chem. Educ.* **2001**, *78*, 1671–1673.

- Michalowski, T.; Asuero, A. G.; Ponikvar-Svet, M.; Michalowska-Kaczmarczyk, A. M.; Wybraniec, S. “Some Examples of Redox Back Titrations,” *Chem. Educator* **2014**, *19*, 217–222.
- Phinyocheep, P.; Tang, I. M. “Determination of the Hole Concentration (Copper Valency) in the High Tc Superconductors,” *J. Chem. Educ.* **1994**, *71*, A115–A118.
- Powell, J. R.; Tucker, S. A.; Acree, Jr., W. E.; Sees, J. A.; Hall, L. M. “A Student-Designed Potentiometric Titration: Quantitative Determination of Iron(II) by Caro’s Acid Titration,” *J. Chem. Educ.* 1996, **73**, 984–986

Precipitation Titrimetry

- Ueno, K.; Kina, K. “Colloid Titration - A Rapid Method for the Determination of Charged Colloid,” *J. Chem . Educ.* **1985**, *62*, 627–629.

For a general history of titrimetry, see the following sources.

- *A History of Analytical Chemistry; Laitinen, H. A.; Ewing, G. W., Eds.; The Division of Analytical Chemistry of the American Chemical Society: Washington, D. C., 1977, pp. 52–93.*
- Kolthoff, I. M. “Analytical Chemistry in the USA in the First Quarter of This Century,” *Anal. Chem.* **1994**, *66*, 241A–249A.

The use of weight instead of volume as a signal for titrimetry is reviewed in the following paper.

- Kratochvil, B.; Maitra, C. “Weight Titrations: Past and Present,” *Am. Lab.* **1983**, January, 22–29.

A more thorough discussion of non-aqueous titrations, with numerous practical examples, is provided in the following text.

- Fritz, J. S. *Acid-Base Titrations in Nonaqueous Solvents*; Allyn and Bacon, Boston; 1973.

The sources listed below provides more details on the how potentiometric titration data may be used to calculate equilibrium constants.

- BabiĆ, S.; Horvat, A. J. M.; PavloviĆ, D. M.; KaŠtelan-Macan, M. “Determination of pK_a values of active pharmaceutical ingredients,” *Trends Anal. Chem.* **2007**, *26*, 1043–1061.
- Meloun, M.; Havel, J.; Högfeldt, E. *Computation of Solution Equilibria*, Ellis Horwood Limited:Chichester, England; 1988.

The following provides additional information about Gran plots.

- Michalowski, T.; Kupiec, K.; Rymanowski, M. *Anal. Chim. Acta* **2008**, *606*, 172–183.
- Schwartz, L. M. “Advances in Acid-Base Gran Plot Methodology,” *J. Chem. Educ.* **1987**, *64*, 947–950.
- Schwartz, L. M. “Uncertainty of a Titration Equivalence Point,” *J. Chem. Educ.* **1992**, *69*, 879–883.

The following provide additional information about calculating or sketching titration curves.

- Barnum, D. “Predicting Acid–Base Titration Curves without Calculations,” *J. Chem. Educ.* **1999**, *76*, 938–942.
- de Levie, R. “A simple expression for the redox titration curve,” *J. Electroanal. Chem.* **1992**, *323*, 347–355.
- González-Gómez, D.; Rogríguez, D. A.; Cañada-Cañada, F.; Jeong, J. S. “A Comprehensive Application to Assist in Acid–Base Titration Self-Learning: An Approach for High School and Undergraduate Students,” *J. Chem. Educ.* **2015**, *92*, 855–863.
- King, D. W. “A General Approach for Calculating Speciation and Posing Capacity of Redox Systems with Multiple Oxidation States: Application to Redox Titrations and the Generation of pe–pH,” *J. Chem. Educ.* **2002**, *79*, 1135–1140.
- Smith, G. C.; Hossain, M. M; MacCarthy, P. “3-D Surface Visualization of pH Titration Topos: Equivalence Cliffs, Dilution Ramps, and Buffer Plateaus,” *J. Chem. Educ.* **2014**, *91*, 225–231.

For a complete discussion of the application of complexation titrimetry see the texts and articles listed below.

- Pribil, R. *Applied Complexometry*, Pergamon Press: Oxford, 1982.
- Reilly, C. N.; Schmid, R. W. “Principles of End Point Detection in Chelometric Titrations Using Metal- lochromic Indicators: Characterization of End Point Sharpness,” *Anal. Chem.* **1959**, *31*, 887–897.
- Ringbom, A. *Complexation in Analytical Chemistry*, John Wiley and Sons, Inc.: New York, 1963.
- Schwarzenbach, G. *Complexometric Titrations*, Methuen & Co. Ltd: London, 1957.

A good source for additional examples of the application of all forms of titrimetry is

- *Vogel’s Textbook of Quantitative Inorganic Analysis*, Longman: London, 4th Ed., 1981

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9.7: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

In a titrimetric method of analysis, the volume of titrant that reacts stoichiometrically with a titrand provides quantitative information about the amount of analyte in a sample. The volume of titrant that corresponds to this stoichiometric reaction is called the equivalence point. Experimentally we determine the titration's end point using an indicator that changes color near the equivalence point. Alternatively, we can locate the end point by monitoring a property of the titrand's solution—absorbance, potential, and temperature are typical examples—that changes as the titration progresses. In either case, an accurate result requires that the end point closely match the equivalence point. Knowing the shape of a titration curve is critical to evaluating the feasibility of a titrimetric method.

Many titrations are direct, in which the analyte participates in the titration as the titrand or the titrant. Other titration strategies are possible when a direct reaction between the analyte and titrant is not feasible. In a back titration a reagent is added in excess to a solution that contains the analyte. When the reaction between the reagent and the analyte is complete, the amount of excess reagent is determined by a titration. In a displacement titration the analyte displaces a reagent, usually from a complex, and the amount of displaced reagent is determined by an appropriate titration.

Titrimetric methods have been developed using acid–base, complexation, oxidation–reduction, and precipitation reactions. Acid–base titrations use a strong acid or a strong base as a titrant. The most common titrant for a complexation titration is EDTA. Because of their stability against air oxidation, most redox titrations use an oxidizing agent as a titrant. Titrations with reducing agents also are possible. Precipitation titrations often involve Ag^+ as either the analyte or titrant.

KEY TERMS

acid–base titration	acidity	alkalinity
argentometric titration	asymmetric equivalence point	auxiliary complexing agent
auxiliary oxidizing agent	auxiliary reducing agent	back titration
buret	complexation titration	conditional formation constant
direct titration	displacement titration	end point
equivalence point	Fajans method	formal potential
Gran plot	indicator	Jones reductor
Kjeldahl analysis	leveling	metallochromic indicator
Mohr method	potentiometric titration	precipitation titration
redox indicator	redox titration	spectrophotometric titration
symmetric equivalence point	thermometric titration	titrand
titrant	titration curve	titration error
titrimetry	Volhard method	Walden reductor

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CHAPTER OVERVIEW

10: ELECTROCHEMICAL METHODS

In Chapter 10 we examined several spectroscopic techniques that take advantage of the interaction between electromagnetic radiation and matter. In this chapter we turn our attention to electrochemical techniques in which the potential, current, or charge in an electrochemical cell serves as the analytical signal.

Although there are only three fundamental electrochemical signals, there are many possible experimental designs—too many, in fact, to cover adequately in an introductory textbook. The simplest division of electrochemical techniques is between bulk techniques, in which we measure a property of the solution in the electrochemical cell, and interfacial techniques, in which the potential, current, or charge depends on the species present at the interface between an electrode and the solution in which it sits. The measurement of a solution's conductivity, which is proportional to the total concentration of dissolved ions, is one example of a bulk electrochemical technique. A determination of pH using a pH electrode is an example of an interfacial electrochemical technique. Only interfacial electrochemical methods receive further consideration in this chapter.

10.1: Overview of Electrochemistry
10.2: Potentiometric Methods
10.3: Redox Titrations
10.4: Problems
10.5: Additional Resources
10.6: Chapter Summary and Key Terms

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10.1: OVERVIEW OF ELECTROCHEMISTRY

The focus of this chapter is on analytical techniques that use a measurement of potential, current, or charge to determine an analyte's concentration or to characterize an analyte's chemical reactivity. Collectively we call this area of analytical chemistry ***electrochemistry*** because its originated from the study of the movement of electrons in an oxidation–reduction reaction.

Despite the difference in instrumentation, all electrochemical techniques share several common features. Before we consider individual examples in greater detail, let's take a moment to consider some of these similarities. As you work through the chapter, this overview will help you focus on similarities between different electrochemical methods of analysis. You will find it easier to understand a new analytical method when you can see its relationship to other similar methods.

FIVE IMPORTANT CONCEPTS

To understand electrochemistry we need to appreciate five important and interrelated concepts: (1) the electrode's potential determines the analyte's form at the electrode's surface; (2) the concentration of analyte at the electrode's surface may not be the same as its concentration in bulk solution; (3) in addition to an oxidation–reduction reaction, the analyte may participate in other chemical reactions; (4) current is a measure of the rate of the analyte's oxidation or reduction; and (5) we cannot control simultaneously current and potential.

> The material in this section—particularly the five important concepts—draws upon a vision for understanding electrochemistry outlined by Larry Faulkner in the article "Understanding Electrochemistry: Some Distinctive Concepts," *J. Chem. Educ.* **1983**, *60*, 262–264. See also, Kissinger, P. T.; Bott, A. W. "Electrochemistry for the Non-Electrochemist," *Current Separations*, **2002**, *20:2*, 51–53.

THE ELECTRODE'S POTENTIAL DETERMINES THE ANALYTE'S FORM

In Chapter 6 we introduced the ladder diagram as a tool for predicting how a change in solution conditions affects the position of an equilibrium reaction. Figure 11.1.1 , for example, shows a ladder diagram for the Fe^{3+}/Fe^{2+} and the Sn^{4+}/Sn^{2+} equilibria. If we place an electrode in a solution of Fe^{3+} and Sn^{4+} and adjust its potential to +0.500 V, Fe^{3+} is reduced to Fe^{2+} but Sn^{4+} is not reduced to Sn^{2+}.

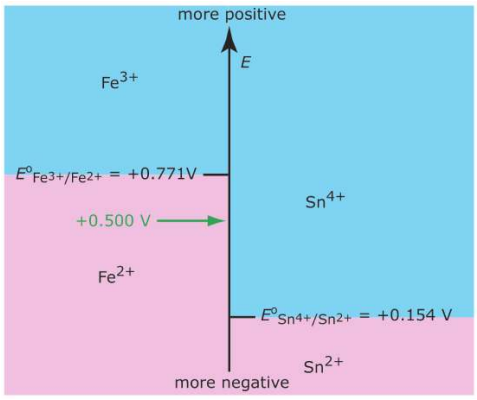


Figure 11.1.1 . Redox ladder diagram for Fe^{3+}/Fe^{2+} and for Sn^{4+}/Sn^{2+} redox couples. The areas in blue show the potential range where the oxidized forms are the predominate species; the reduced forms are the predominate species in the areas shown in pink. Note that a more positive potential favors the oxidized forms. At a potential of +0.500 V (green arrow) Fe^{3+} reduces to Fe^{2+}, but Sn^{4+} remains unchanged. You may wish to review the earlier treatment of oxidation–reduction reactions in Chapter 6.4 and the development of ladder diagrams for oxidation–reduction reactions in Chapter 6.6.

INTERFACIAL CONCENTRATIONS MAY NOT EQUAL BULK CONCENTRATIONS

In Chapter 6 we introduced the Nernst equation, which provides a mathematical relationship between the electrode's potential and the concentrations of an analyte's oxidized and reduced forms in solution. For example, the Nernst equation for Fe^{3+} and Fe^{2+} is

$$E = E_{Fe^{3+}/Fe^{2+}} - \frac{RT}{nF}\ln\frac{[Fe^{2+}]}{[Fe^{3+}]} = \frac{0.05916}{1}\log\frac{[Fe^{2+}]}{[Fe^{3+}]} \tag{10.1.1}$$

where E is the electrode's potential and $E^{\circ}_{Fe^{3+}/Fe^{2+}}$ is the standard-state reduction potential for the reaction $Fe^{3+}(aq) \rightleftharpoons Fe^{2+}(aq) + e^{-}$. Because it is the potential of the electrode that determines the analyte's form at the electrode's surface, the concentration terms in Equation 10.1.1 are those of Fe^{2+} and Fe^{3+} at the electrode's surface, not their concentrations in bulk solution.

This distinction between a species' surface concentration and its bulk concentration is important. Suppose we place an electrode in a solution of Fe^{3+} and fix its potential at 1.00 V. From the ladder diagram in Figure 11.1.1 , we know that Fe^{3+} is stable at this potential and, as shown in Figure 11.1.2 a, the concentration of Fe^{3+} is the same at all distances from the electrode's surface. If we change the electrode's

potential to +0.500 V, the concentration of Fe^{3+} at the electrode's surface decreases to approximately zero. As shown in Figure 11.1.2 b, the concentration of Fe^{3+} increases as we move away from the electrode's surface until it equals the concentration of Fe^{3+} in bulk solution. The resulting concentration gradient causes additional Fe^{3+} from the bulk solution to diffuse to the electrode's surface.

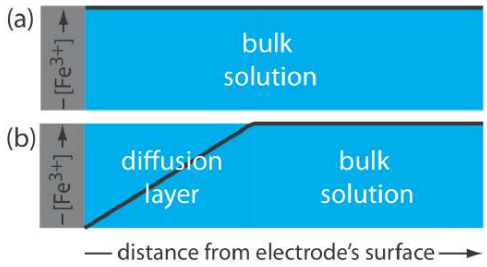


Figure 11.1.2 . Concentration of Fe^{3+} as a function of distance from the electrode's surface at (a) E = +1.00 V and (b) E = +0.500 V. The electrode is shown in gray and the solution in blue.

We call the region of solution that contains this concentration gradient in Fe^{3+} the diffusion layer. We will have more to say about this in Chapter 11.4.

THE ANALYTE MAY PARTICIPATE IN OTHER REACTIONS

Figure 11.1.1 and Figure 11.1.2 shows how the electrode's potential affects the concentration of Fe^{3+} and how the concentration of Fe^{3+} varies as a function of distance from the electrode's surface. The reduction of Fe^{3+} to Fe^{2+}, which is governed by Equation 10.1.1, may not be the only reaction that affects the concentration of Fe^{3+} in bulk solution or at the electrode's surface. The adsorption of Fe^{3+} at the electrode's surface or the formation of a metal–ligand complex in bulk solution, such as $Fe(OH)^{2+}$, also affects the concentration of Fe^{3+}.

CURRENT IS A MEASURE OF RATE

The reduction of Fe^{3+} to Fe^{2+} consumes an electron, which is drawn from the electrode. The oxidation of another species, perhaps the solvent, at a second electrode is the source of this electron. Because the reduction of Fe^{3+} to Fe^{2+} consumes one electron, the flow of electrons between the electrodes—in other words, the current—is a measure of the rate at which Fe^{3+} is reduced. One important consequence of this observation is that the current is zero when the reaction $\mathrm{Fe}^{3+}(aq) \rightleftharpoons \mathrm{Fe}^{2+}(aq) + e^-$ is at equilibrium.

The rate of the reaction $\mathrm{Fe}^{3+}(aq) \rightleftharpoons \mathrm{Fe}^{2+}(aq) + e^-$ is the change in the concentration of Fe^{3+} as a function of time.

WE CANNOT CONTROL SIMULTANEOUSLY BOTH THE CURRENT AND THE POTENTIAL

If a solution of Fe^{3+} and Fe^{2+} is at equilibrium, the current is zero and the potential is given by Equation 10.1.1. If we change the potential away from its equilibrium position, current flows as the system moves toward its new equilibrium position. Although the initial current is quite large, it decreases over time, reaching zero when the reaction reaches equilibrium. The current, therefore, changes in response to the applied potential. Alternatively, we can pass a fixed current through the electrochemical cell, forcing the reduction of Fe^{3+} to Fe^{2+}. Because the concentrations of Fe^{3+} decreases and the concentration of Fe^{2+} increases, the potential, as given by Equation 10.1.1, also changes over time. In short, if we choose to control the potential, then we must accept the resulting current, and we must accept the resulting potential if we choose to control the current.

CONTROLLING AND MEASURING CURRENT AND POTENTIAL

Electrochemical measurements are made in an electrochemical cell that consists of two or more electrodes and the electronic circuitry needed to control and measure the current and the potential. In this section we introduce the basic components of electrochemical instrumentation.

The simplest electrochemical cell uses two electrodes. The potential of one electrode is sensitive to the analyte's concentration, and is called the ***working electrode*** or the ***indicator electrode***. The second electrode, which we call the ***counter electrode***, completes the electrical circuit and provides a reference potential against which we measure the working electrode's potential. Ideally the counter electrode's potential remains constant so that we can assign to the working electrode any change in the overall cell potential. If the counter electrode's potential is not constant, then we replace it with two electrodes: a ***reference electrode*** whose potential remains constant and an ***auxiliary electrode*** that completes the electrical circuit.

Because we cannot control simultaneously the current and the potential, there are only three basic experimental designs: (1) we can measure the potential when the current is zero, (2) we can measure the potential while we control the current, and (3) we can measure the current while we control the potential. Each of these experimental designs relies on ***Ohm's law***, which states that the current, i, passing through an electrical circuit of resistance, R, generates a potential, E.

$$E = iR$$

Each of these experimental designs uses a different type of instrument. To help us understand how we can control and measure current and potential, *we will describe these instruments as if the analyst is operating them manually*. To do so the analyst observes a change in the current or the potential and manually adjusts the instrument's settings to maintain the desired experimental conditions. It is important to understand that modern electrochemical instruments provide an automated, electronic means for controlling and measuring current and potential, and that they do so by using very different electronic circuitry than that described here.

> This point bears repeating: It is important to understand that the experimental designs in Figure 11.1.3 , Figure 11.1.4 , and Figure 11.1.5 do not represent the electrochemical instruments you will find in today's analytical labs. For further information about modern electrochemical instrumentation, see this chapter's additional resources.

POTENTIOMETERS

To measure the potential of an electrochemical cell under a condition of zero current we use a ***potentiometer***. Figure 11.1.3 shows a schematic diagram for a manual potentiometer that consists of a power supply, an electrochemical cell with a working electrode and a counter electrode, an ammeter to measure the current that passes through the electrochemical cell, an adjustable, slide-wire resistor, and a tap key for closing the circuit through the electrochemical cell. Using Ohm's law, the current in the upper half of the circuit is

$$i_{\text{upper}} = \frac{E_{\text{PS}}}{R_{ab}}$$

where E_{PS} is the power supply's potential, and R_{ab} is the resistance between points *a* and *b* of the slide-wire resistor. In a similar manner, the current in the lower half of the circuit is

$$i_{\text{lower}} = \frac{E_{\text{cell}}}{R_{cb}}$$

where E_{cell} is the potential difference between the working electrode and the counter electrode, and R_{cb} is the resistance between the points *c* and *b* of the slide-wire resistor. When $i_{\text{upper}} = i_{\text{lower}} = 0$, no current flows through the ammeter and the potential of the electrochemical cell is

$$E_{\text{coll}} = \frac{R_{cb}}{R_{ab}} \times E_{\text{PS}} \tag{10.1.2}$$

To determine E_{cell} we briefly press the tap key and observe the current at the ammeter. If the current is not zero, then we adjust the slide wire resistor and remeasure the current, continuing this process until the current is zero. When the current is zero, we use Equation 10.1.2 to calculate E_{cell}.

Using the tap key to briefly close the circuit through the electrochemical cell minimizes the current that passes through the cell and limits the change in the electrochemical cell's composition. For example, passing a current of 10^{-9} A through the electrochemical cell for 1 s changes the concentrations of species in the cell by approximately 10^{-14} moles. Modern potentiometers use operational amplifiers to create a high-impedance voltmeter that measures the potential while drawing a current of less than 10^{-9} A.

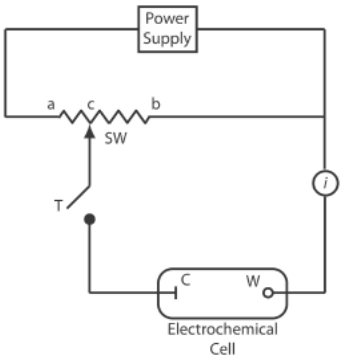


Figure 11.1.3 . Schematic diagram of a manual potentiometer: C is the counter electrode; W is the working electrode; SW is a slide-wire resistor; T is a tap key and *i* is an ammeter for measuring current.

GALVANOSTATS

A ***galvanostat***, a schematic diagram of which is shown in Figure 11.1.4 , allows us to control the current that flows through an electrochemical cell. The current from the power supply through the working electrode is

$$i = \frac{E_{\text{PS}}}{R + R_{\text{cell}}}$$

where E_{PS} is the potential of the power supply, R is the resistance of the resistor, and R_{cell} is the resistance of the electrochemical cell. If $R >> R_{cell}$, then the current between the auxiliary and working electrodes

$$i = \frac{E_{PS}}{R} \approx \text{constant}$$

maintains a constant value. To monitor the working electrode's potential, which changes as the composition of the electrochemical cell changes, we can include an optional reference electrode and a high-impedance potentiometer.

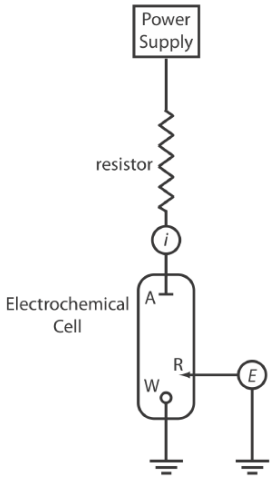


Figure 11.1.4 . Schematic diagram of a galvanostat: A is the auxiliary electrode; W is the working electrode; R is an optional reference electrode, E is a high-impedance potentiometer, and i is an ammeter. The working electrode and the optional reference electrode are connected to a ground.

POTENTIOSTATS

A ***potentiostat***, a schematic diagram of which is shown in Figure 11.1.5 , allows us to control the working electrode's potential. The potential of the working electrode is measured relative to a constant-potential reference electrode that is connected to the working electrode through a high-impedance potentiometer. To set the working electrode's potential we adjust the slide wire resistor that is connected to the auxiliary electrode. If the working electrode's potential begins to drift, we adjust the slide wire resistor to return the potential to its initial value. The current flowing between the auxiliary electrode and the working electrode is measured with an ammeter. Modern potentiostats include waveform generators that allow us to apply a time-dependent potential profile, such as a series of potential pulses, to the working electrode.

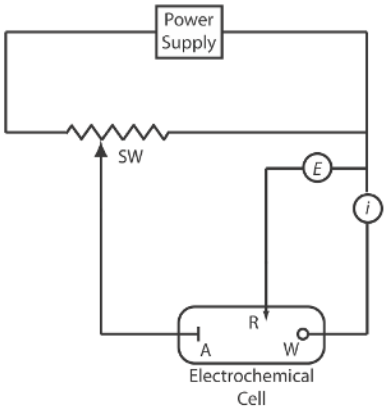


Figure 11.1.5 . Schematic diagram for a manual potentiostat: W is the working electrode; A is the auxiliary electrode; R is the reference electrode; SW is a slide-wire resistor, E is a high-impendance potentiometer; and i is an ammeter.

INTERFACIAL ELECTROCHEMICAL TECHNIQUES

Because interfacial electrochemistry is such a broad field, let's use Figure 11.1.6 to organize techniques by the experimental conditions we choose to use (Do we control the potential or the current? How do we change the applied potential or applied current? Do we stir the solution?) and the analytical signal we decide to measure (Current? Potential?).

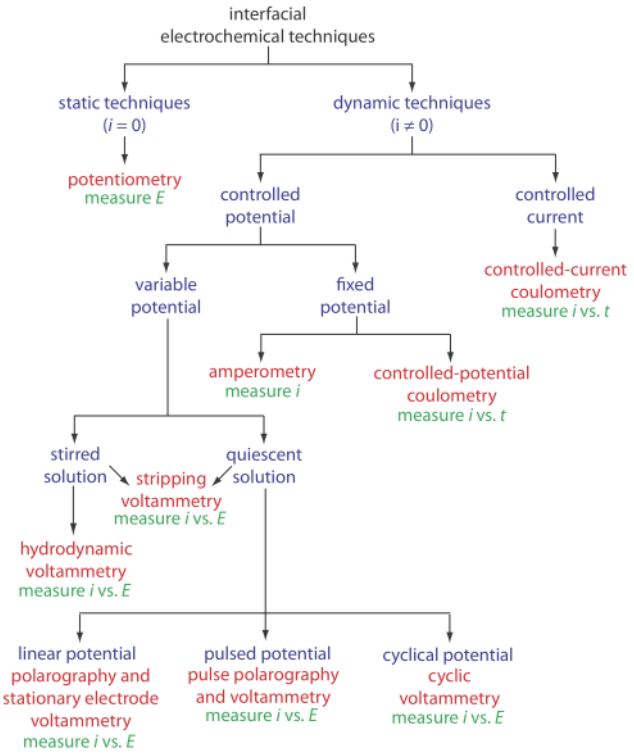


Figure 11.1.6 . Family tree that highlights the similarities and differences between a number of interfacial electrochemical techniques. The specific techniques are shown in red, the experimental conditions are shown in blue, and the analytical signals are shown in green.

At the first level, we divide interfacial electrochemical techniques into static techniques and dynamic techniques. In a static technique we do not allow current to pass through the electrochemical cell and, as a result, the concentrations of all species remain constant. Potentiometry, in which we measure the potential of an electrochemical cell under static conditions, is one of the most important quantitative electrochemical methods and is discussed in detail in Chapter 11.2.

Dynamic techniques, in which we allow current to flow and force a change in the concentration of species in the electrochemical cell, comprise the largest group of interfacial electrochemical techniques. Coulometry, in which we measure current as a function of time, is covered in Chapter 11.3. Amperometry and voltammetry, in which we measure current as a function of a fixed or variable potential, is the subject of Chapter 11.4.

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10.2: POTENTIOMETRIC METHODS

In potentiometry we measure the potential of an electrochemical cell under static conditions. Because no current—or only a negligible current—flows through the electrochemical cell, its composition remains unchanged. For this reason, potentiometry is a useful quantitative method of analysis. The first quantitative potentiometric applications appeared soon after the formulation, in 1889, of the Nernst equation, which relates an electrochemical cell's potential to the concentration of electroactive species in the cell [Stork, J. T. *Anal. Chem.* **1993**, *65*, 344A–351A].

> For an on-line introduction to much of the material in this section, see Analytical Electrochemistry: Potentiometry by Erin Gross, Richard S. Kelly, and Donald M. Cannon, Jr., a resource that is part of the Analytical Sciences Digital Library.

Potentiometry initially was restricted to redox equilibria at metallic electrodes, which limited its application to a few ions. In 1906, Cremer discovered that the potential difference across a thin glass membrane is a function of pH when opposite sides of the membrane are in contact with solutions that have different concentrations of H_3O^+. This discovery led to the development of the glass pH electrode in 1909. Other types of membranes also yield useful potentials. For example, in 1937 Kolthoff and Sanders showed that a pellet of AgCl can be used to determine the concentration of Ag^+. Electrodes based on membrane potentials are called ion-selective electrodes, and their continued development extends potentiometry to a diverse array of analytes.

POTENTIOMETRIC MEASUREMENTS

As shown in Figure 11.1.3, we use a potentiometer to determine the difference between the potential of two electrodes. The potential of one electrode—the working or indicator electrode—responds to the analyte's activity and the other electrode—the counter or reference electrode—has a known, fixed potential. In this section we introduce the conventions for describing potentiometric electrochemical cells, and the relationship between the measured potential and the analyte's activity.

> In Chapter 6 we noted that a chemical reaction's equilibrium position is a function of the activities of the reactants and products, not their concentrations. To be correct, we should write the Nernst equation in terms of activities. So why didn't we use activities in Chapter 9 when we calculated redox titration curves? There are two reasons for that choice. First, concentrations are always easier to calculate than activities. Second, in a redox titration we determine the analyte's concentration from the titration's end point, not from the potential at the end point. The only reasons for calculating a titration curve is to evaluate its feasibility and to help us select a useful indicator. In most cases, the error we introduce by assuming that concentration and activity are identical is too small to be a significant concern.
>
> In potentiometry we cannot ignore the difference between activity and concentration. Later in this section we will consider how we can design a potentiometric method so that we can ignore the difference between activity and concentration. See Chapter 6.9 to review our earlier discussion of activity and concentration.

POTENTIOMETRIC ELECTROCHEMICAL CELLS

A schematic diagram of a typical potentiometric electrochemical cell is shown in Figure 11.2.1 . The electrochemical cell consists of two half-cells, each of which contains an electrode immersed in a solution of ions whose activities determine the electrode's potential. A ***salt bridge*** that contains an inert electrolyte, such as KCl, connects the two half-cells. The ends of the salt bridge are fixed with porous frits, which allow the electrolyte's ions to move freely between the half-cells and the salt bridge. This movement of ions in the salt bridge completes the electrical circuit.

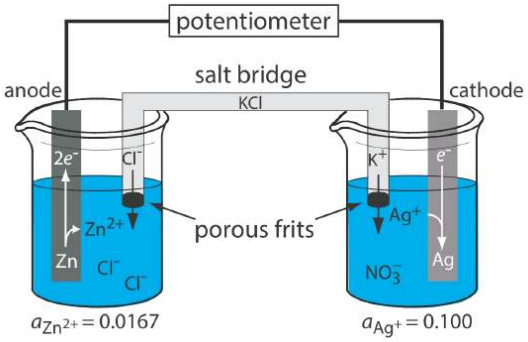


Figure 11.2.1 . Example of a potentiometric electrochemical cell. The activities of Zn^{2+} and Ag^+ are shown below the two half-cells.

By convention, we identify the electrode on the left as the ***anode*** and assign to it the oxidation reaction; thus

$$Zn(s) \rightleftharpoons Zn^{2+}(aq) + 2e^-$$

The electrode on the right is the ***cathode***, where the reduction reaction occurs.

$$Ag^+(aq) + e^- \rightleftharpoons Ag(s)$$

The potential of the electrochemical cell in Figure 11.2.1 is for the reaction

$$Zn(s) + 2Ag^+(aq) \rightleftharpoons 2Ag(s) + Zn^{2+}(aq)$$

We also define potentiometric electrochemical cells such that the cathode is the indicator electrode and the anode is the reference electrode.

> The reason for separating the electrodes is to prevent the oxidation reaction and the reduction reaction from occurring at one of the electrodes. For example, if we place a strip of Zn metal in a solution of $AgNO_3$, the reduction of Ag^+ to Ag occurs on the surface of the Zn at the same time as a potion of the Zn metal oxidizes to Zn^{2+}. Because the transfer of electrons from Zn to Ag^+ occurs at the electrode's surface, we can not pass them through the potentiometer.

SHORTHAND NOTATION FOR ELECTROCHEMICAL CELLS

Although Figure 11.2.1 provides a useful picture of an electrochemical cell, it is not a convenient way to represent it (Imagine having to draw a picture of each electrochemical cell you are using!). A more useful way to describe an electrochemical cell is a shorthand notation that uses symbols to identify different phases and that lists the composition of each phase. We use a vertical slash (|) to identify a boundary between two phases where a potential develops, and a comma (,) to separate species in the same phase or to identify a boundary between two phases where no potential develops. Shorthand cell notations begin with the anode and continue to the cathode. For example, we describe the electrochemical cell in Figure 11.2.1 using the following shorthand notation.

$$Zn(s)|ZnCl_2(aq, a_{Zn^{2+}} = 0.0167)||AgNO_3(aq, a_{Ag^+} = 0.100)|Ag(s)$$

The double vertical slash (||) represents the salt bridge, the contents of which we usually do not list. Note that a double vertical slash implies that there is a potential difference between the salt bridge and each half-cell.

✔ EXAMPLE 11.2.1

What are the anodic, the cathodic, and the overall reactions responsible for the potential of the electrochemical cell in Figure 11.2.2 ? Write the shorthand notation for the electrochemical cell.

Solution

The oxidation of Ag to Ag^+ occurs at the anode, which is the left half-cell. Because the solution contains a source of Cl^-, the anodic reaction is

$$Ag(s) + Cl^-(aq) \rightleftharpoons AgCl(s) + e^-$$

The cathodic reaction, which is the right half-cell, is the reduction of Fe^{3+} to Fe^{2+}.

$$Fe^{3+}(aq) + e^- \rightleftharpoons Fe^{2+}(aq)$$

The overall cell reaction, therefore, is

$$Ag(s) + Fe^{3+}(aq) + Cl^-(aq) \rightleftharpoons AgCl(s) + Fe^{2+}(aq)$$

The electrochemical cell's shorthand notation is

$$Ag(s)|HCl(aq, a_{Cl^-} = 0.100), AgCl(sat'd)||FeCl_2(aq, a_{Fe^{2+}} = 0.0100), Fe^{3+}(aq, a_{Fe^{3+}} = 0.0500)|Pt(s)$$

Note that the Pt cathode is an inert electrode that carries electrons to the reduction half-reaction. The electrode itself does not undergo reduction.

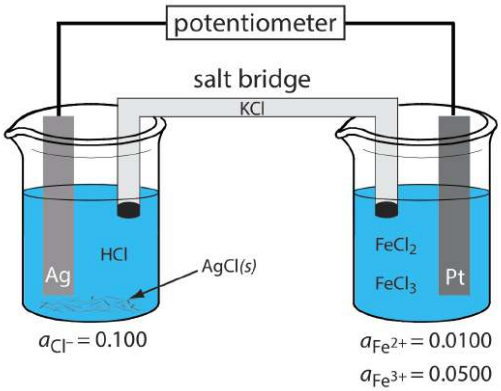


Figure 11.2.2 . Potentiometric electrochemical cell for Example 11.2.1 .

EXERCISE 11.2.1

Write the reactions occurring at the anode and the cathode for the potentiometric electrochemical cell with the following shorthand notation.

$$\mathrm{Pt}(s) \mid \mathrm{H_2}(g), \mathrm{H^+}(aq) \parallel \mathrm{Cu^{2+}}(aq) \mid \mathrm{Cu}(s)$$

Answer

The oxidation of H_2 to H^+ occurs at the anode

$$\mathrm{H_2}(g) \rightleftharpoons 2\mathrm{H^+}(aq) + 2e^-$$

and the reduction of Cu^{2+} to Cu occurs at the cathode.

$$\mathrm{Cu^{2+}}(aq) + 2e^- \rightleftharpoons \mathrm{Cu}(s)$$

The overall cell reaction, therefore, is

$$\mathrm{Cu^{2+}}(aq) + \mathrm{H_2}(g) \rightleftharpoons 2\mathrm{H^+}(aq) + \mathrm{Cu}(s)$$

POTENTIAL AND ACTIVITY—THE NERNST EQUATION

The potential of a potentiometric electrochemical cell is

$$E_{\text{cell}} = E_{\text{cathode}} - E_{\text{anode}} \tag{10.2.1}$$

where E_{cathode} and E_{anode} are reduction potentials for the redox reactions at the cathode and the anode, respectively. Each reduction potential is given by the Nernst equation

$$E = E^\circ - \frac{RT}{nF} \ln Q$$

where E^o is the standard-state reduction potential, R is the gas constant, T is the temperature in Kelvins, n is the number of electrons in the redox reaction, F is Faraday's constant, and Q is the reaction quotient. At a temperature of 298 K (25°C) the Nernst equation is

$$E = E^\circ - \frac{0.05916}{n} \log Q \tag{10.2.2}$$

where E is in volts.

Using Equation 10.2.2, the potential of the anode and cathode in Figure 11.2.1 are

$$E_{\text{anode}} = E^\circ_{\mathrm{Zn^{2+}/Zn}} - \frac{0.05916}{2} \log \frac{1}{a_{\mathrm{Zn^{2+}}}}$$

$$E_{\text{anode}} = E^\circ_{\mathrm{Ag^{+}/Ag}} - \frac{0.05916}{1} \log \frac{1}{a_{\mathrm{Ag^{+}}}}$$

Even though an oxidation reaction is taking place at the anode, we define the anode's potential in terms of the corresponding reduction reaction and the standard-state reduction potential. See Chapter 6.4 for a review of using the Nernst equation in calculations.

Substituting E_{cathode} and E_{anode} into Equation 10.2.1, along with the activities of Zn^{2+} and Ag^{+} and the standard-state reduction potentials, gives E_{cell} as

$$E_{\text{cell}} = \left(E^{\circ}_{Ag^{+}/Ag} - \frac{0.05916}{1}\log\frac{1}{a_{Ag^{+}}}\right) - \left(E^{\circ}_{Zn^{2+}/Zn} - \frac{0.05916}{2}\log\frac{1}{a_{Zn^{2+}}}\right)$$

$$E_{\text{cell}} = \left(0.7996 - \frac{0.05916}{1}\log\frac{1}{0.100}\right) - \left(-0.7618 - \frac{0.05916}{2}\log\frac{1}{0.0167}\right) = 1.555\ \text{V}$$

You will find values for the standard-state reduction potentials in Appendix 13.

EXAMPLE 11.2.2

What is the potential of the electrochemical cell shown in Example 11.2.1 ?

Solution

Substituting E_{cathode} and E_{anode} into Equation 10.2.1, along with the concentrations of Fe^{3+}, Fe^{2+}, and Cl^{-} and the standard-state reduction potentials gives

$$E_{\text{cell}} = \left(E^{\circ}_{Fe^{3+}/Fe^{2+}} - \frac{0.05916}{1}\log\frac{a_{Fe^{2+}}}{a_{Fe^{3+}}}\right) - \left(E^{\circ}_{AgCl/Ag} - \frac{0.05916}{1}\log a_{Cl^{-}}\right)$$

$$E_{\text{cell}} = \left(0.771 - \frac{0.05916}{1}\log\frac{0.0100}{0.0500}\right) - \left(0.2223 - \frac{0.05916}{1}\log(0.100)\right) = 0.531\ \text{V}$$

EXERCISE 11.2.2

What is the potential for the electrochemical cell in Exercise 11.2.1 if the activity of H^{+} in the anodic half-cell is 0.100, the fugacity of H_2 in the anodic half-cell is 0.500, and the activity of Cu^{2+} in the cathodic half-cell is 0.0500? Fugacity, f, is the equivalent term for the activity of a gas.

Answer

Making appropriate substitutions into Equation 10.2.1 and solving for E_{cell} gives its value as

$$E_{\text{cell}} = \left(E^{\circ}_{Cu^{2+}/Cu} - \frac{0.05916}{2}\log\frac{1}{a_{Cu^{2+}}}\right) - \left(E^{\circ}_{H^{+}/H_2} - \frac{0.05916}{2}\log\frac{f_{H_2}}{a^{2}_{H^{+}}}\right)$$

$$E_{\text{cell}} = \left(0.3419 - \frac{0.05916}{2}\log\frac{1}{0.0500}\right) - \left(0.0000 - \frac{0.05916}{2}\log\frac{0.500}{(0.100)^2}\right) = 0.3537\ \text{V}$$

In potentiometry, we assign the reference electrode to the anodic half-cell and assign the indicator electrode to the cathodic half-cell. Thus, if the potential of the cell in Figure 11.2.1 is +1.50 V and the activity of Zn^{2+} is 0.0167, then we can solve the following equation for $a_{Ag^{+}}$

$$1.50\ \text{V} = \left(0.7996 - \frac{0.05916}{1}\log\frac{1}{a_{Ag^{+}}}\right) - \left(-0.7618 - \frac{0.05916}{2}\log\frac{1}{0.0167}\right)$$

obtaining an activity of 0.0118.

EXAMPLE 11.2.3

What is the activity of Fe^{3+} in an electrochemical cell similar to that in Example 11.2.1 if the activity of Cl^{-} in the left-hand cell is 1.0, the activity of Fe^{2+} in the right-hand cell is 0.015, and E_{cell} is +0.546 V?

Solution

Making appropriate substitutions into Equation 10.2.1

$$0.546 = \left(0.771 - \frac{0.05916}{1}\log\frac{0.0100}{a_{Fe^{3+}}}\right) - \left(0.2223 - \frac{0.05916}{1}\log(1.0)\right)$$

and solving for $a_{Fe^{3+}}$ gives its activity as 0.0135.

EXERCISE 11.2.3

What is the activity of Cu^{2+} in the electrochemical cell in Exercise 11.2.1 if the activity of H^+ in the anodic half-cell is 1.00 with a fugacity of 1.00 for H_2, and an E_{cell} of +0.257 V?

Answer

Making appropriate substitutions into Equation 10.2.1

$$0.257\text{ V} = \left(0.3419 - \frac{0.05916}{2}\log\frac{1}{a_{Cu^{2+}}}\right) - \left(0.0000 - \frac{0.05916}{2}\log\frac{1.00}{(1.00)^2}\right)$$

and solving for $a_{Cu^{2+}}$ gives its activity as 1.35×10^{-3}.

Despite the apparent ease of determining an analyte's activity using the Nernst equation, there are several problems with this approach. One problem is that standard-state potentials are temperature-dependent and the values in reference tables usually are for a temperature of 25ºC. We can overcome this problem by maintaining the electrochemical cell at 25ºC or by measuring the standard-state potential at the desired temperature.

Another problem is that a standard-sate reduction potential may have a significant matrix effect. For example, the standard-state reduction potential for the Fe^{3+}/Fe^{2+} redox couple is +0.735 V in 1 M $HClO_4$, +0.70 V in 1 M HCl, and +0.53 V in 10 M HCl. The difference in potential for equimolar solutions of HCl and $HClO_4$ is the result of a difference in the activity coefficients for Fe^{3+} and Fe^{2+} in these two media. The shift toward a more negative potential with an increase in the concentration of HCl is the result of chloride's ability to form a stronger complex with Fe^{3+} than with Fe^{2+}. We can minimize this problem by replacing the standard-state potential with a matrix-dependent formal potential. Most tables of standard-state potentials, including those in Appendix 13, include selected formal potentials.

Finally, a more serious problem is the presence of additional potentials in the electrochemical cell not included in Equation 10.2.1. In writing the shorthand notation for an electrochemical cell we use a double slash (||) to indicate the salt bridge, suggesting a potential exists at the interface between each end of the salt bridge and the solution in which it is immersed. The origin of this potential is discussed in the following section.

JUNCTION POTENTIALS

A ***junction potential*** develops at the interface between two ionic solution if there is a difference in the concentration and mobility of the ions. Consider, for example, a porous membrane that separations a solution of 0.1 M HCl from a solution of 0.01 M HCl (Figure 11.2.3 a). Because the concentration of HCl on the membrane's left side is greater than that on the right side of the membrane, H^+ and Cl^- will diffuse in the direction of the arrows. The mobility of H^+, however, is greater than that for Cl^-, as shown by the difference in the lengths of their respective arrows. Because of this difference in mobility, the solution on the right side of the membrane develops an excess concentration of H^+ and a positive charge (Figure 11.2.3 b). Simultaneously, the solution on the membrane's left side develops a negative charge because there is an excess concentration of Cl^-. We call this difference in potential across the membrane a junction potential and represent it as E_j.

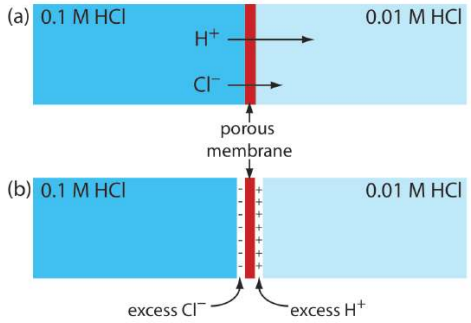


Figure 11.2.3 . Origin of the junction potential between a solution of 0.1 M HCl and a solution of 0.01 M HCl.

The magnitude of the junction potential depends upon the difference in the concentration of ions on the two sides of the interface, and may be as large as 30–40 mV. For example, a junction potential of 33.09 mV has been measured at the interface between solutions of 0.1 M HCl and 0.1 M NaCl [Sawyer, D. T.; Roberts, J. L., Jr. *Experimental Electrochemistry for Chemists*, Wiley-Interscience: New York, 1974, p. 22]. A salt bridge's junction potential is minimized by using a salt, such as KCl, for which the mobilities of the cation and anion are approximately equal. We also can minimize the junction potential by incorporating a high concentration of the salt in the salt bridge. For this reason salt bridges frequently are constructed using solutions that are saturated with KCl. Nevertheless, a small junction potential, generally of unknown magnitude, is always present.

When we measure the potential of an electrochemical cell, the junction potential also contributes to E_{cell}; thus, we rewrite Equation 10.2.1 as

$$E_{\text{cell}} = E_{\text{cathode}} - E_{\text{anode}} + E_j$$

to include its contribution. If we do not know the junction potential's actual value—which is the usual situation—then we cannot directly calculate the analyte's concentration using the Nernst equation. Quantitative analytical work is possible, however, if we use one of the standardization methods—external standards, the method of standard additions, or internal standards—discussed in Chapter 5.3.

REFERENCE ELECTRODES

In a potentiometric electrochemical cell one of the two half-cells provides a fixed reference potential and the potential of the other half-cell responds the analyte's concentration. By convention, the reference electrode is the anode; thus, the short hand notation for a potentiometric electrochemical cell is

reference electrode || indicator electrode

and the cell potential is

$$E_{\text{cell}} = E_{\text{ind}} - E_{\text{ref}} + E_j$$

The ideal reference electrode provides a stable, known potential so that we can attribute any change in E_{cell} to the analyte's effect on the indicator electrode's potential. In addition, it should be easy to make and to use the reference electrode. Three common reference electrodes are discussed in this section.

STANDARD HYDROGEN ELECTRODE

Although we rarely use the ***standard hydrogen electrode*** (SHE) for routine analytical work, it is the reference electrode used to establish standard-state potentials for other half-reactions. The SHE consists of a Pt electrode immersed in a solution in which the activity of hydrogen ion is 1.00 and in which the fugacity of $H_2(g)$ is 1.00 (Figure 11.2.4). A conventional salt bridge connects the SHE to the indicator half-cell. The short hand notation for the standard hydrogen electrode is

$$\text{Pt}(s),\ \text{H}_2\ (g, f_{\text{H}_2} = 1.00)\ |\ \text{H}^+\ (aq, a_{\text{H}^+} = 1.00)\ ||$$

and the standard-state potential for the reaction

$$\text{H}^+(aq) + e^- = \frac{1}{2}\text{H}_2(g)$$

is, by definition, 0.00 V at all temperatures. Despite its importance as the fundamental reference electrode against which we measure all other potentials, the SHE is rarely used because it is difficult to prepare and inconvenient to use.

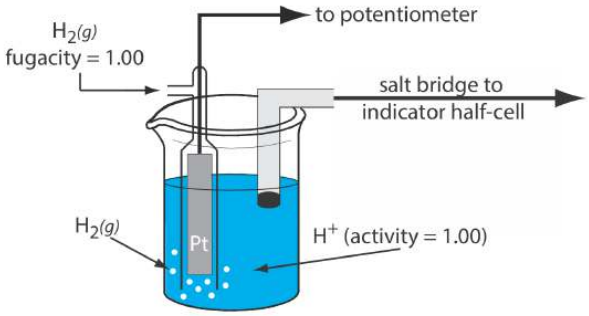


Figure 11.2.4 . Schematic diagram showing the standard hydrogen electrode.

CALOMEL ELECTRODES

A calomel reference electrode is based on the following redox couple between Hg_2Cl_2 and Hg (calomel is the common name for Hg_2Cl_2)

$$\text{Hg}_2\text{Cl}_2(s) + 2e^- \rightleftharpoons 2\text{Hg}(l) + 2\text{Cl}^-(aq)$$

for which the potential is

$$E = E^{\circ}_{\text{Hg}_2\text{Cl}_2/\text{Hg}} - \frac{0.05916}{2}\log\left(a_{\text{Cl}^-}\right)^2 = +0.2682\text{V} - \frac{0.05916}{2}\log\left(a_{\text{Cl}^-}\right)^2$$

The potential of a calomel electrode, therefore, depends on the activity of Cl^- in equilibrium with Hg and Hg_2Cl_2.

As shown in Figure 11.2.5 , in a ***saturated calomel electrode*** (SCE) the concentration of Cl^- is determined by the solubility of KCl. The electrode consists of an inner tube packed with a paste of Hg, Hg_2Cl_2, and KCl, situated within a second tube that contains a saturated solution of KCl. A small hole connects the two tubes and a porous wick serves as a salt bridge to the solution in which the SCE is immersed. A stopper in the outer tube provides an opening for adding addition saturated KCl. The short hand notation for this cell is

$$\mathrm{Hg}(l)|\mathrm{Hg_2Cl_2}(s),\mathrm{KCl}(aq,\ \mathrm{sat'd}\ )||$$

Because the concentration of Cl^- is fixed by the solubility of KCl, the potential of an SCE remains constant even if we lose some of the inner solution to evaporation. A significant disadvantage of the SCE is that the solubility of KCl is sensitive to a change in temperature. At higher temperatures the solubility of KCl increases and the electrode's potential decreases. For example, the potential of the SCE is +0.2444 V at 25°C and +0.2376 V at 35°C. The potential of a calomel electrode that contains an unsaturated solution of KCl is less dependent on the temperature, but its potential changes if the concentration, and thus the activity of Cl^-, increases due to evaporation.

> For example, the potential of a calomel electrode is +0.280 V when the concentration of KCl is 1.00 M and +0.336 V when the concentration of KCl is 0.100 M. If the activity of Cl^- is 1.00, the potential is +0.2682 V.

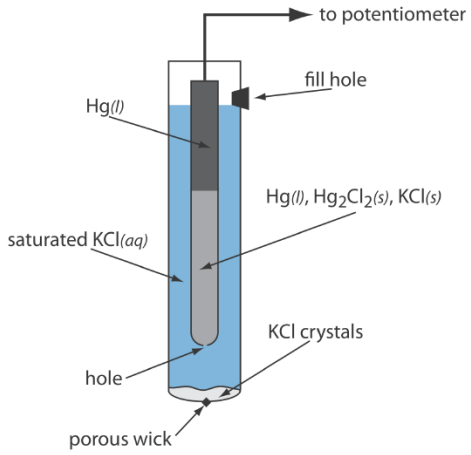


Figure 11.2.5 . Schematic diagram showing the saturated calomel electrode.

SILVER/SILVER CHLORIDE ELECTRODES

Another common reference electrode is the ***silver/silver chloride electrode***, which is based on the reduction of AgCl to Ag.

$$\mathrm{AgCl}(s) + e^- \rightleftharpoons \mathrm{Ag}(s) + \mathrm{Cl}^-(aq)$$

As is the case for the calomel electrode, the activity of Cl^- determines the potential of the Ag/AgCl electrode; thus

$$E = E^\circ_{\mathrm{AgCl/Ag}} - 0.05916 \log a_{\mathrm{Cl}^-} = 0.2223\ \mathrm{V} - 0.05916 \log a_{\mathrm{Cl}^-}$$

When prepared using a saturated solution of KCl, the electrode's potential is +0.197 V at 25°C. Another common Ag/AgCl electrode uses a solution of 3.5 M KCl and has a potential of +0.205 V at 25°C. As you might expect, the potential of a Ag/AgCl electrode using a saturated solution of KCl is more sensitive to a change in temperature than an electrode that uses an unsaturated solution of KCl.

A typical Ag/AgCl electrode is shown in Figure 11.2.6 and consists of a silver wire, the end of which is coated with a thin film of AgCl, immersed in a solution that contains the desired concentration of KCl. A porous plug serves as the salt bridge. The electrode's short hand notation is

$$\mathrm{Ag}(s)|\,\mathrm{AgCl}(s),\mathrm{KCl}\,(aq, a_{\mathrm{Cl}^-} = x)\,||$$

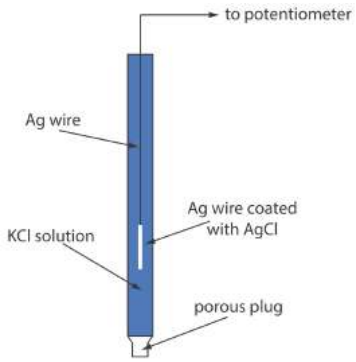


Figure 11.2.6 . Schematic diagram showing a Ag/AgCl electrode. Because the electrode does not contain solid KCl, this is an example of an unsaturated Ag/AgCl electrode.

CONVERTING POTENTIALS BETWEEN REFERENCE ELECTRODES

The standard state reduction potentials in most tables are reported relative to the standard hydrogen electrode's potential of +0.00 V. Because we rarely use the SHE as a reference electrode, we need to convert an indicator electrode's potential to its equivalent value when using a different reference electrode. As shown in the following example, this is easy to do.

EXAMPLE 11.2.4

The potential for an Fe^{3+}/Fe^{2+} half-cell is +0.750 V relative to the standard hydrogen electrode. What is its potential if we use a saturated calomel electrode or a saturated silver/silver chloride electrode?

Solution

When we use a standard hydrogen electrode the potential of the electrochemical cell is

$$E_{\text{cell}} = E_{\text{Fe}^{3+}/\text{Fe}^{2+}} - E_{\text{SHE}} = 0.750\ \text{V} - 0.000\ \text{V} = 0.750\ \text{V}$$

We can use the same equation to calculate the potential if we use a saturated calomel electrode

$$E_{\text{cell}} = E_{\text{Fe}^{3+}/\text{Fe}^{2+}} - E_{\text{SHE}} = 0.750\ \text{V} - 0.2444\ \text{V} = 0.506\ \text{V}$$

or a saturated silver/silver chloride electrode

$$E_{\text{cell}} = E_{\text{Fe}^{3+}/\text{Fe}^{2+}} - E_{\text{SHE}} = 0.750\ \text{V} - 0.197\ \text{V} = 0.553\ \text{V}$$

Figure 11.2.7 provides a pictorial representation of the relationship between these different potentials.

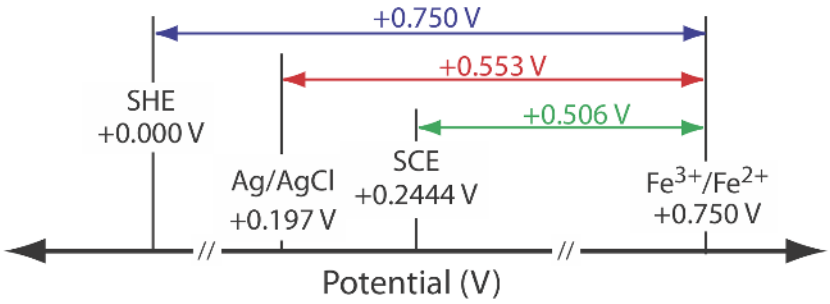


Figure 11.2.7 . Relationship between the potential of an Fe^{3+}/Fe^{2+} half-cell relative to the reference electrodes in Example 11.2.4 . The potential relative to a standard hydrogen electrode is shown in blue, the potential relative to a saturated silver/silver chloride electrode is shown in red, and the potential relative to a saturated calomel electrode is shown in green.

EXERCISE 11.2.4

The potential of a UO_2^+/U^{4+} half-cell is –0.0190 V relative to a saturated calomel electrode. What is its potential when using a saturated silver/silver chloride electrode or a standard hydrogen electrode?

Answer

When using a saturated calomel electrode, the potential of the electro- chemical cell is

$$E_{\text{cell}} = E_{\text{UO}_2^+/\text{U}^{4+}} - E_{\text{SCE}}$$

Substituting in known values

$$-0.0190\ \text{V} = E_{\text{UO}_2^+/\text{U}^{4+}} - 0.2444\ \text{V}$$

and solving for $E_{\text{UO}_2^+/\text{U}^{4+}}$ gives its value as +0.2254 V. The potential relative to the Ag/AgCl electrode is

$$E_{\text{cell}} = E_{\text{UO}_2^+/\text{U}^{4+}} - E_{\text{Ag/AgCl}} = 0.2254\ \text{V} - 0.197\ \text{V} = 0.028\ \text{V}$$

and the potential relative to the standard hydrogen electrode is

$$E_{\text{cell}} = E_{\text{UO}_2^+/\text{U}^{4+}} - E_{\text{SHE}} = 0.2254\ \text{V} - 0.000\ \text{V} = 0.2254\ \text{V}$$

METALLIC INDICATOR ELECTRODES

In potentiometry, the potential of the indicator electrode is proportional to the analyte's activity. Two classes of indicator electrodes are used to make potentiometric measurements: metallic electrodes, which are the subject of this section, and ion-selective electrodes, which are covered in the next section.

ELECTRODES OF THE FIRST KIND

If we place a copper electrode in a solution that contains Cu^{2+}, the electrode's potential due to the reaction

$$\text{Cu}^{2+}(aq) + 2e^- \rightleftharpoons \text{Cu}(s)$$

is determined by the activity of Cu^{2+}.

$$E = E^{\text{o}}_{\text{Cu}^{2+}/\text{Cu}} - \frac{0.05916}{2}\log\frac{1}{a_{\text{Cu}^{2+}}} = +0.3419\text{V} - \frac{0.05916}{2}\log\frac{1}{a_{\text{Cu}^{2+}}}$$

If copper is the indicator electrode in a potentiometric electrochemical cell that also includes a saturated calomel reference electrode

$$\text{SCE}\|\text{Cu}^{2+}\,(aq, a_{\text{Cu}^{2+}} = x)\,|\text{Cu}(s)$$

then we can use the cell potential to determine an unknown activity of Cu^{2+} in the indicator electrode's half-cell

$$E_{\text{cell}} = E_{\text{ind}} - E_{\text{SCE}} + E_j = +0.3419\text{V} - \frac{0.05916}{2}\log\frac{1}{a_{\text{Cu}^{2+}}} - 0.2224\text{V} + E_j$$

An indicator electrode in which the metal is in contact with a solution containing its ion is called an ***electrode of the first kind***. In general, if a metal, M, is in a solution of M^{n+}, the cell potential is

$$E_{\text{call}} = K - \frac{0.05916}{n}\log\frac{1}{a_{M^{n+}}} = K + \frac{0.05916}{n}\log a_{M^{n+}}$$

where K is a constant that includes the standard-state potential for the M^{n+}/M redox couple, the potential of the reference electrode, and the junction potential.

Note that including E_j in the constant K means we do not need to know the junction potential's actual value; however, the junction potential must remain constant if K is to maintain a constant value.

For a variety of reasons—including the slow kinetics of electron transfer at the metal–solution interface, the formation of metal oxides on the electrode's surface, and interfering reactions—electrodes of the first kind are limited to the following metals: Ag, Bi, Cd, Cu, Hg, Pb, Sn, Tl, and Zn.

Many of these electrodes, such as Zn, cannot be used in acidic solutions because they are easily oxidized by H^+.

$$\text{Zn}(s) + 2\text{H}^+(aq) \rightleftharpoons \text{H}_2(g) + \text{Zn}^{2+}(aq)$$

ELECTRODES OF THE SECOND KIND

The potential of an electrode of the first kind responds to the activity of M^{n+}. We also can use this electrode to determine the activity of another species if it is in equilibrium with M^{n+}. For example, the potential of a Ag electrode in a solution of Ag^+ is

$$E = 0.7996\text{V} + 0.05916 \log a_{\text{Ag}^+} \tag{10.2.3}$$

If we saturate the indicator electrode's half-cell with AgI, the solubility reaction

$$\text{AgI}(s) \rightleftharpoons \text{Ag}^+(aq) + \text{I}^-(aq)$$

determines the concentration of Ag^+; thus

$$a_{\text{Ag}^+} = \frac{K_{\text{sp,AgI}}}{a_{\text{I}^-}} \tag{10.2.4}$$

where $K_{sp,AgI}$ is the solubility product for AgI. Substituting Equation 10.2.4 into Equation 10.2.3

$$E = 0.7996 \text{ V} + 0.05916 \log \frac{K_{\text{sp, AgI}}}{a_{\text{I}^-}}$$

shows that the potential of the silver electrode is a function of the activity of I^-. If we incorporate this electrode into a potentiometric electrochemical cell with a saturated calomel electrode

$$\text{SCE} \| \text{AgI}(s),\ \text{I}^-\ (aq, a_{\text{I}^-} = x)\ | \text{Ag(s)}$$

then the cell potential is

$$E_{\text{cell}} = K - 0.05916 \log a_{\text{I}^-}$$

where K is a constant that includes the standard-state potential for the Ag^+/Ag redox couple, the solubility product for AgI, the reference electrode's potential, and the junction potential.

If an electrode of the first kind responds to the activity of an ion in equilibrium with M^{n+}, we call it an ***electrode of the second kind***. Two common electrodes of the second kind are the calomel and the silver/silver chloride reference electrodes.

> In an electrode of the second kind we link together a redox reaction and another reaction, such as a solubility reaction. You might wonder if we can link together more than two reactions. The short answer is yes. An electrode of the third kind, for example, links together a redox reaction and two other reactions. Such electrodes are less common and we will not consider them in this text.

REDOX ELECTRODES

An electrode of the first kind or second kind develops a potential as the result of a redox reaction that involves the metallic electrode. An electrode also can serve as a source of electrons or as a sink for electrons in an unrelated redox reaction, in which case we call it a ***redox electrode.*** The Pt cathode in Figure 11.2.2 and Example 11.2.1 is a redox electrode because its potential is determined by the activity of Fe^{2+} and Fe^{3+} in the indicator half-cell. Note that a redox electrode's potential often responds to the activity of more than one ion, which limits its usefulness for direct potentiometry.

MEMBRANE ELECTRODES

If metals were the only useful materials for constructing indicator electrodes, then there would be few useful applications of potentiometry. In 1906, Cremer discovered that the potential difference across a thin glass membrane is a function of pH when opposite sides of the membrane are in contact with solutions that have different concentrations of H_3O^+. The existence of this ***membrane potential*** led to the development of a whole new class of indicator electrodes, which we call ***ion-selective electrodes*** (ISEs). In addition to the glass pH electrode, ion-selective electrodes are available for a wide range of ions. It also is possible to construct a membrane electrode for a neutral analyte by using a chemical reaction to generate an ion that is monitored with an ion-selective electrode. The development of new membrane electrodes continues to be an active area of research.

MEMBRANE POTENTIALS

Figure 11.2.8 shows a typical potentiometric electrochemical cell equipped with an ion-selective electrode. The short hand notation for this cell is

$$\text{ref (sample)}\ \|[\text{A}]_{\text{samp}}\ (aq, a_{\text{A}} = x)\,|[\text{A}]_{\text{int}}\ (aq, a_{\text{A}} = y)\|\ \text{ref (internal)}$$

where the ion-selective membrane is represented by the vertical slash that separates the two solutions that contain analyte: the sample solution and the ion-selective electrode's internal solution. The potential of this electrochemical cell includes the potential of each reference electrode, a junction potential, and the membrane's potential

$$E_{\text{cell}} = E_{\text{ref(int)}} - E_{\text{ref(samp)}} + E_{\text{mem}} + E_j \tag{10.2.5}$$

where E_{mem} is the potential across the membrane and The notations ref(sample) and ref(internal) represent a reference electrode immersed in the sample and a reference electrode immersed in the ISE's internal solution. Because the junction potential and the potential of the two reference electrodes are constant, any change in E_{cell} reflects a change in the membrane's potential.

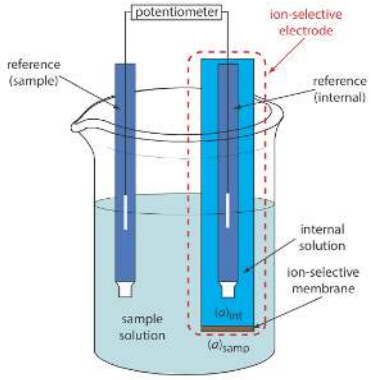


Figure 11.2.8 . Schematic diagram that shows a typical potentiometric cell with an ion-selective electrode. The ion-selective electrode's membrane separates the sample, which contains the analyte at an activity of $(a_A)_{samp}$, from an internal solution that contains the analyte with an activity of $(a_A)_{int}$.

The analyte's interaction with the membrane generates a membrane potential if there is a difference in its activity on the membrane's two sides. Current is carried through the membrane by the movement of either the analyte or an ion already present in the membrane's matrix. The membrane potential is given by the following Nernst-like equation

$$E_{mem} = E_{asym} - \frac{RT}{zF} \ln \frac{(a_A)_{int}}{(a_A)_{samp}} \tag{10.2.6}$$

where $(a_A)_{samp}$ is the analyte's activity in the sample, $(a_A)_{int}$ is the analyte's activity in the ion-selective electrode's internal solution, and z is the analyte's charge. Ideally, E_{mem} is zero when $(a_A)_{int} = (a_A)_{samp}$. The term E_{asym}, which is an ***asymmetry potential***, accounts for the fact that E_{mem} usually is not zero under these conditions.

> For now we simply note that a difference in the analyte's activity results in a membrane potential. As we consider different types of ion-selective electrodes, we will explore more specifically the source of the membrane potential.

Substituting Equation 10.2.6 into Equation 10.2.5, assuming a temperature of 25ºC, and rearranging gives

$$E_{cell} = K + \frac{0.05916}{z} \log (a_A)_{samp} \tag{10.2.7}$$

where K is a constant that includes the potentials of the two reference electrodes, the junction potentials, the asymmetry potential, and the analyte's activity in the internal solution. Equation 10.2.7 is a general equation and applies to all types of ion-selective electrodes.

SELECTIVITY OF MEMBRANES

A membrane potential results from a chemical interaction between the analyte and active sites on the membrane's surface. Because the signal depends on a chemical process, most membranes are not selective toward a single analyte. Instead, the membrane potential is proportional to the concentration of each ion that interacts with the membrane's active sites. We can rewrite Equation 10.2.7 to include the contribution to the potential of an interferent, I

$$E_{cell} = K + \frac{0.05916}{z_A} \log \left\{ a_A + K_{A,I} (a_I)^{z_A/z_I} \right\}$$

where z_A and z_I are the charges of the analyte and the interferent, and $K_{A,I}$ is a selectivity coefficient that accounts for the relative response of the interferent. The selectivity coefficient is defined as

$$K_{A,I} = \frac{(a_A)_e}{(a_I)_e^{z_A/z_I}} \tag{10.2.8}$$

where $(a_A)_e$ and $(a_I)_e$ are the activities of analyte and the interferent that yield identical cell potentials. When the selectivity coefficient is 1.00, the membrane responds equally to the analyte and the interferent. A membrane shows good selectivity for the analyte when $K_{A,I}$ is significantly less than 1.00.

Selectivity coefficients for most commercially available ion-selective electrodes are provided by the manufacturer. If the selectivity coefficient is not known, it is easy to determine its value experimentally by preparing a series of solutions, each of which contains the same activity of interferent, $(a_I)_{add}$, but a different activity of analyte. As shown in Figure 11.2.9 , a plot of cell potential versus the log of the analyte's activity has two distinct linear regions. When the analyte's activity is significantly larger than $K_{A,I} \times (a_I)_{add}$, the potential is a linear function of $\log(a_A)$, as given by Equation 10.2.7. If $K_{A,I} \times (a_I)_{add}$ is significantly larger than the analyte's activity, however, the cell's potential remains constant. The activity of analyte and interferent at the intersection of these two linear regions is used to calculate $K_{A,I}$.

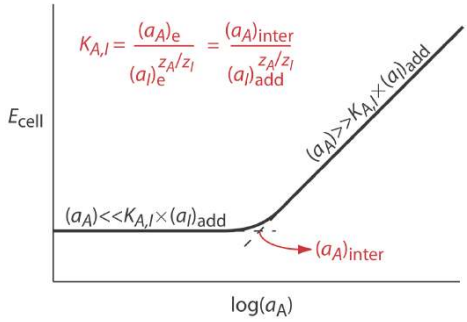


Figure 11.2.9 . Diagram showing the experimental determination of an ion-selective electrode's selectivity for an analyte. The activity of analyte that corresponds to the intersection of the two linear portions of the curve, $(a_A)_{inter}$, produces a cell potential identical to that of the interferent. The equation for the selectivity coefficient, $K_{A,I}$, is shown in red.

EXAMPLE 11.2.5

Sokalski and co-workers described a method for preparing ion-selective electrodes with significantly improved selectivities [Sokalski, T.; Ceresa, A.; Zwicki, T.; Pretsch, E. *J. Am. Chem. Soc.* **1997**, *119*, 11347–11348]. For example, a conventional Pb^{2+} ISE has a $\log K_{Pb^{2+}/Mg^{2+}}$ of –3.6. If the potential for a solution in which the activity of Pb^{2+} is 4.1×10^{-12} is identical to that for a solution in which the activity of Mg^{2+} is 0.01025, what is the value of $\log K_{Pb^{2+}/Mg^{2+}}$ for their ISE?

Solution

Making appropriate substitutions into Equation 10.2.8, we find that

$$K_{Pb^{2+}/Mg^{2+}} = \frac{(a_{Pb^{2+}})_e}{(a_{Mg^{2+}})_e^{z_{Pb^{2+}}/z_{Mg^{2+}}}} = \frac{4.1 \times 10^{-12}}{(0.01025)^{+2/+2}} = 4.0 \times 10^{-10}$$

The value of $\log K_{Pb^{2+}/Mg^{2+}}$, therefore, is –9.40.

EXERCISE 11.2.5

A ion-selective electrode for NO_2^- has $\log K_{A,I}$ values of –3.1 for F^-, –4.1 for SO_4^{2-}, –1.2 for I^-, and –3.3 for NO_3^-. Which ion is the most serious interferent and for what activity of this interferent is the potential equivalent to a solution in which the activity of NO_2^- is 2.75×10^{-4} ?

Answer

The larger the value of $K_{A,I}$ the more serious the interference. Larger values for $K_{A,I}$ correspond to more positive (less negative) values for $\log K_{A,I}$; thus, I^-, with a $K_{A,I}$ of 6.3×10^{-2}, is the most serious of these interferents. To find the activity of I^- that gives a potential equivalent to a NO_2^- activity of 2.75×10^{-4}, we note that

$$a_{NO_2^-} = K_{A,I} \times a_{I^-}$$

Making appropriate substitutions

$$2.75 \times 10^{-4} = \left(6.3 \times 10^{-2}\right) \times a_{I^-}$$

and solving for a_{I^-} gives its activity as 4.4×10^{-3}.

GLASS ION-SELECTIVE ELECTRODES

The first commercial ***glass electrodes*** were manufactured using Corning 015, a glass with a composition that is approximately 22% Na_2O, 6% CaO, and 72% SiO_2. When immersed in an aqueous solution for several hours, the outer approximately 10 nm of the membrane's

surface becomes hydrated, resulting in the formation of negatively charged sites, —SiO^-. Sodium ions, Na^+, serve as counter ions. Because H^+ binds more strongly to —SiO^- than does Na^+, they displace the sodium ions

$$H^+ + -SiO^-Na^+ \rightleftharpoons -SiO^-H^+ + Na^+$$

explaining the membrane's selectivity for H^+. The transport of charge across the membrane is carried by the Na^+ ions. The potential of a glass electrode using Corning 015 obeys the equation

$$E_{cell} = K + 0.05916 \log a_{H^+} \tag{10.2.9}$$

over a pH range of approximately 0.5 to 9. At more basic pH values the glass membrane is more responsive to other cations, such as Na^+ and K^+.

EXAMPLE 11.2.6

For a Corning 015 glass membrane, the selectivity coefficient K_{H^+/Na^+} is $\approx 10^{-11}$. What is the expected error if we measure the pH of a solution in which the activity of H^+ is 2×10^{-13} and the activity of Na^+ is 0.05?

Solution

A solution in which the actual activity of H^+, $(a_{H^+})_{act}$, is 2×10^{-13} has a pH of 12.7. Because the electrode responds to both H^+ and Na^+, the apparent activity of H^+, $(a_{H^+})_{app}$, is

$$(a_{H^+})_{app} = (a_{H^+})_{act} + (K_{H^+/Na^+} \times a_{Na^+}) = 2 \times 10^{-13} + (10^{-11} \times 0.05) = 7 \times 10^{-13}$$

The apparent activity of H^+ is equivalent to a pH of 12.2, an error of –0.5 pH units.

Replacing Na_2O and CaO with Li_2O and BaO extends the useful pH range of glass membrane electrodes to pH levels greater than 12.

Glass membrane pH electrodes often are available in a combination form that includes both the indicator electrode and the reference electrode. The use of a single electrode greatly simplifies the measurement of pH. An example of a typical combination electrode is shown in Figure 11.2.10 .

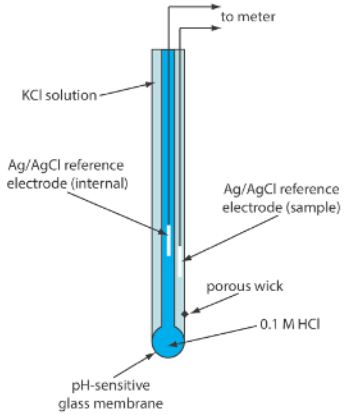


Figure 11.2.10 . Schematic diagram showing a combination glass electrode for measuring pH. The indicator electrode consists of a pH-sensitive glass membrane and an internal Ag/AgCl reference electrode in a solution of 0.1 M HCl. The sample's reference electrode is a Ag/AgCl electrode in a solution of KCl (which may be saturated with KCl or contain a fixed concentration of KCl). A porous wick serves as a salt bridge between the sample and its reference electrode.

The observation that the Corning 015 glass membrane responds to ions other than H^+ (see Example 11.2.6) led to the development of glass membranes with a greater selectivity for other cations. For example, a glass membrane with a composition of 11% Na_2O, 18% Al_2O_3, and 71% SiO_2 is used as an ion-selective electrode for Na^+. Other glass ion-selective electrodes have been developed for the analysis of Li^+, K^+, Rb^+, Cs^+, NH_4^+, Ag^+, and Tl^+. Table 11.2.1 provides several examples.

Table 11.2.1 . Representative Examples of Glass Membrane Ion-Selective Electrodes for Analytes Other Than H^+

analyte	membrane composition	selectivity coefficients
Na^+	11% Na_2O, 18% Al_2O_3, 71% SiO_2	$K_{Na^+/H^+} = 1000$ $K_{Na^+/K^+} = 0.001$ $K_{Na^+/Li^+} = 0.001$
Li^+	15% Li_2O, 25% Al_2O_3, 60% SiO_2	$K_{Li^+/Na^+} = 0.3$ $K_{Li^+/K^+} = 0.001$
K^+	27% Na_2O, 5% Al_2O_3, 68% SiO_2	$K_{K^+/Na^+} = 0.05$

Selectivity coefficients are approximate; values found experimentally may vary substantially from the listed values. See Cammann, K. *Working With Ion-Selective Electrodes*, Springer-Verlag: Berlin, 1977.

Because an ion-selective electrode's glass membrane is very thin—it is only about 50 μm thick—they must be handled with care to avoid cracks or breakage. Glass electrodes usually are stored in a storage buffer recommended by the manufacturer, which ensures that the membrane's outer surface remains hydrated. If a glass electrode dries out, it is reconditioned by soaking for several hours in a solution that contains the analyte. The composition of a glass membrane will change over time, which affects the electrode's performance. The average lifetime for a typical glass electrode is several years.

SOLID-STATE ION-SELECTIVE ELECTRODES

A ***solid-state ion-selective electrode*** has a membrane that consists of either a polycrystalline inorganic salt or a single crystal of an inorganic salt. We can fashion a polycrystalline solid-state ion-selective electrode by sealing a 1–2 mm thick pellet of AgS—or a mixture of AgS and a second silver salt or another metal sulfide—into the end of a nonconducting plastic cylinder, filling the cylinder with an internal solution that contains the analyte, and placing a reference electrode into the internal solution. Figure 11.2.11 shows a typical design.

> The NaCl in a salt shaker is an example of polycrystalline material because it consists of many small crystals of sodium chloride. The NaCl salt plates used in IR spectroscopy (see Chapter 10), on the other hand, are an example of a single crystal of sodium chloride.

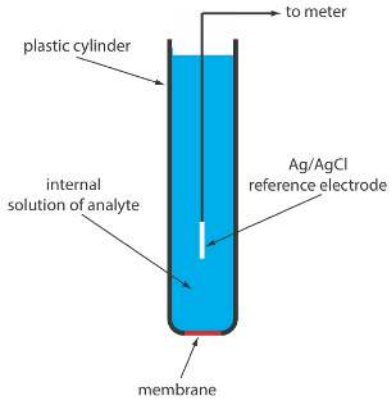


Figure 11.2.11 . Schematic diagram of a solid-state electrode. The internal solution contains a solution of analyte of fixed activity.

The membrane potential for a Ag_2S pellet develops as the result of a difference in the extent of the solubility reaction

$$Ag_2S(s) \rightleftharpoons 2Ag^+(aq) + S^{2-}(aq)$$

on the membrane's two sides, with charge carried across the membrane by Ag^+ ions. When we use the electrode to monitor the activity of Ag^+, the cell potential is

$$E_{cell} = K + 0.05916 \log a_{Ag^+}$$

The membrane also responds to the activity of S^{2-}, with a cell potential of

$$E_{cell} = K - \frac{0.05916}{2} \log a_{S^{2-}}$$

If we combine an insoluble silver salt, such as AgCl, with the Ag_2S, then the membrane potential also responds to the concentration of Cl^-, with a cell potential of

$$E_{cell} = K - 0.05916 \log a_{Cl^-}$$

By mixing Ag_2S with CdS, CuS, or PbS, we can make an ion-selective electrode that responds to the activity of Cd^{2+}, Cu^{2+}, or Pb^{2+}. In this case the cell potential is

$$E_{\text{cell}} = K + \frac{0.05916}{2} \ln a_{M^{2+}}$$

where $a_{M^{2+}}$ is the activity of the metal ion.

Table 11.2.2 provides examples of polycrystalline, Ag_2S-based solid-state ion-selective electrodes. The selectivity of these ion-selective electrodes depends on the relative solubility of the compounds. A Cl^- ISE using a Ag_2S/AgCl membrane is more selective for Br^- ($K_{Cl^-/Br^-} = 10^2$) and for I^- ($K_{Cl^-/I^-} = 10^6$) because AgBr and AgI are less soluble than AgCl. If the activity of Br^- is sufficiently high, AgCl at the membrane/solution interface is replaced by AgBr and the electrode's response to Cl^- decreases substantially. Most of the polycrystalline ion-selective electrodes listed in Table 11.2.2 operate over an extended range of pH levels. The equilibrium between S^{2-} and HS^- limits the analysis for S^{2-} to a pH range of 13–14.

11.2.2 . Representative Examples of Polycrystalline Solid-State Ion-Selective Electrodes

analyte	membrane composition	selectivity coefficients
Ag^+	Ag_2S	$K_{Ag^+/Cu^{2+}} = 10^{-6}$ $K_{Ag^+/Pb^{2+}} = 10^{-10}$ Hg^{2+} interferes
Cd^{2+}	CdS/Ag_2S	$K_{Cd^{2+}/Fe^{2+}} = 200$ $K_{Cd^{2+}/Pb^{2+}} = 6$ Ag^+, Hg^{2+}, and Cu^{2+} must be absent
Cu^{2+}	CuS/Ag_2S	$K_{Cu^{2+}/Fe^{3+}} = 10$ $K_{Cu^{2+}/Cu^+} = 10^{-6}$ Ag^+ and Hg^{2+} must be absent
Pb^{2+}	PbS/Ag_2S	$K_{Pb^{2+}/Fe^{3+}} = 1$ $K_{Pb^{2+}/Cd^{2+}} = 1$ Ag^+, Hg^{2+}, and Cu^{2+} must be absent
Br^-	$AgBr/Ag_2S$	$K_{Br^-/I^-} = 5000$ $K_{Br^-/Cl^-} = 0.005$ $K_{Br^-/OH^-} = 10^{-5}$ S^{2-} must be absent
Cl^-	$AgCl/Ag_2S$	$K_{Cl^-/I^-} = 10^6$ $K_{Cl^-/Br^-} = 100$ $K_{Cl^-/OH^-} = 0.01$ S^{2-} must be absent
I^-	AgI/Ag_2S	$K_{I^-/S^{2-}} = 30$ $K_{I^-/Br^-} = 10^{-4}$ $K_{I^-/Cl^-} = 10^{-6}$ $K_{I^-/OH^-} = 10^{-7}$
SCN^-	$AgSCN/Ag_2S$	$K_{SCN^-/I^-} = 10^3$ $K_{SCN^-/Br^-} = 100$ $K_{SCN^-/Cl^-} = 0.1$ $K_{SCN^-/OH^-} = 0.01$ S^{2-} must be absent
S^{2-}	Ag_2S	Hg^{2+} must be absent

Selectivity coefficients are approximate; values found experimentally may vary substantially from the listed values. See Cammann, K. *Working With Ion-Selective Electrodes*, Springer-Verlag: Berlin, 1977.

The membrane of a F^- ion-selective electrode is fashioned from a single crystal of LaF_3, which usually is doped with a small amount of EuF_2 to enhance the membrane's conductivity. Because EuF_2 provides only two F^- ions—compared to the three F^- ions in LaF_3—each EuF_2 produces a vacancy in the crystal's lattice. Fluoride ions pass through the membrane by moving into adjacent vacancies. As shown in Figure 11.2.11 , the LaF_3 membrane is sealed into the end of a non-conducting plastic cylinder, which contains a standard solution of F^-, typically 0.1 M NaF, and a Ag/AgCl reference electrode.

The membrane potential for a F^- ISE results from a difference in the solubility of LaF_3 on opposite sides of the membrane, with the potential given by

$$E_{\text{cell}} = K - 0.05916 \log a_{F^-}$$

One advantage of the F^- ion-selective electrode is its freedom from interference. The only significant exception is OH^- ($K_{F^-/OH^-} = 0.1$), which imposes a maximum pH limit for a successful analysis. Below a pH of 4 the predominate form of fluoride in solution is HF, which

does not contribute to the membrane potential. For this reason, an analysis for fluoride is carried out at a pH greater than 4.

EXAMPLE 11.2.7

What is the maximum pH that we can tolerate if we need to analyze a solution in which the activity of F^- is 1×10^{-5} with an error of less than 1%?

Solution

In the presence of OH^- the cell potential is

$$E_{\text{cell}} = K - 0.05916 \left\{ a_{F^-} + K_{F^-/OH^-} \times a_{OH^-} \right\}$$

To achieve an error of less than 1%, the term $K_{F^-/OH^-} \times a_{OH^-}$ must be less than 1% of a_{F^-}; thus

$$K_{F^-/OH^-} \times a_{OH^-} \leq 0.01 \times a_{F^-}$$

$$0.10 \times a_{OH^-} \leq 0.01 \times \left(1.0 \times 10^{-5}\right)$$

Solving for a_{OH^-} gives the maximum allowable activity for OH^- as 1×10^{-6}, which corresponds to a pH of less than 8.

EXERCISE 11.2.6

Suppose you wish to use the nitrite-selective electrode in Exercise 11.2.5 to measure the activity of NO_2^-. If the activity of NO_2^- is 2.2×10^{-4}, what is the maximum pH you can tolerate if the error due to OH^- must be less than 10%? The selectivity coefficient for OH^-, $K_{NO_2^-/OH^-}$, is 630. Do you expect the electrode to have a lower pH limit? Clearly explain your answer.

Answer

In the presence of OH^- the cell potential is

$$E_{\text{cell}} = K - 0.05916 \log \left\{ a_{NO_2^-} + K_{NO_2^-/OH^-} \times a_{OH^-} \right\}$$

To achieve an error of less than 10%, the term $K_{NO_2^-/OH^-} \times a_{OH^-}$ must be less than 1% of $a_{NO_2^-}$; thus

$$K_{NO_2^-/OH^-} \times a_{OH^-} \leq 0.10 \times a_{NO_2^-}$$

$$630 \times a_{OH^-} \leq 0.10 \times \left(2.2 \times 10^{-4}\right)$$

Solving for a_{OH^-} gives its maximum allowable activity as 3.5×10^{-8}, which corresponds to a pH of less than 6.54.

The electrode does have a lower pH limit. Nitrite is the conjugate weak base of HNO_2, a species to which the ISE does not respond. As shown by the ladder diagram below, at a pH of 4.15 approximately 10% of nitrite is present as HNO_2. A minimum pH of 4.5 is the usual recommendation when using a nitrite ISE. This corresponds to a NO_2^-/HNO_2 ratio of

$$\text{pH} = \text{p}K_a + \log \frac{[NO_2^-]}{[HNO_2]}$$

$$4.5 = 3.15 + \log \frac{[NO_2^-]}{[HNO_2]}$$

$$\frac{[NO_2^-]}{[HNO_2]} \approx 22$$

Thus, at a pH of 4.5 approximately 96% of nitrite is present as NO_2^-.

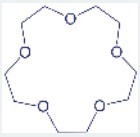
Unlike a glass membrane ion-selective electrode, a solid-state ISE does not need to be conditioned before it is used, and it may be stored dry. The surface of the electrode is subject to poisoning, as described above for a Cl^- ISE in contact with an excessive concentration of Br^-. If an electrode is poisoned, it can be returned to its original condition by sanding and polishing the crystalline membrane.

> Poisoning simply means that the surface has been chemically modified, such as AgBr forming on the surface of a AgCl membrane.

LIQUID-BASED ION-SELECTIVE ELECTRODES

Another class of ion-selective electrodes uses a hydrophobic membrane that contains a liquid organic complexing agent that reacts selectively with the analyte. Three types of organic complexing agents have been used: cation exchangers, anion exchangers, and neutral ionophores. A membrane potential exists if the analyte's activity is different on the two sides of the membrane. Current is carried through the membrane by the analyte.

An ***ionophore*** is a ligand whose exterior is hydrophobic and whose interior is hydrophilic. The crown ether shown here is one example of a neutral ionophore.



One example of a ***liquid-based ion-selective electrode*** is that for Ca^{2+}, which uses a porous plastic membrane saturated with the cation exchanger di-(*n*-decyl) phosphate. As shown in Figure 11.2.12 , the membrane is placed at the end of a non-conducting cylindrical tube and is in contact with two reservoirs. The outer reservoir contains di-(*n*-decyl) phosphate in di-*n*-octylphenylphosphonate, which soaks into the porous membrane. The inner reservoir contains a standard aqueous solution of Ca^{2+} and a Ag/AgCl reference electrode. Calcium ion-selective electrodes also are available in which the di-(*n*-decyl) phosphate is immobilized in a polyvinyl chloride (PVC) membrane that eliminates the need for the outer reservoir.

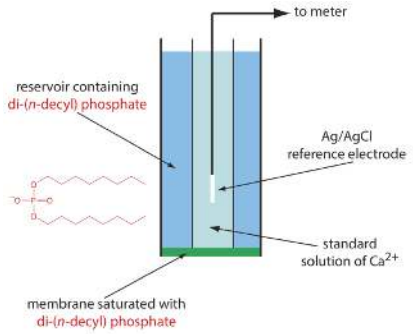


Figure 11.2.12 . Schematic diagram showing a liquid-based ion-selective electrode for Ca^{2+}. The structure of the cation exchanger, di-(*n*-decyl) phosphate, is shown in red.

The membrane potential for the Ca^{2+} ISE develops as the result of a difference in the extent of the complexation reaction

$$Ca^{2+}(aq) + 2(C_{10}H_{21}O)_2PO_2^-(mem) \rightleftharpoons Ca[(C_{10}H_{21}O)_2PO_2]_2(mem)$$

on the two sides of the membrane, where (*mem*) indicates a species that is present in the membrane. The cell potential for the Ca^{2+} ion-selective electrode is

$$E_{cell} = K + \frac{0.05916}{2}\log a_{ca^{2+}}$$

The selectivity of this electrode for Ca^{2+} is very good, with only Zn^{2+} showing greater selectivity.

Table 11.2.3 lists the properties of several liquid-based ion-selective electrodes. An electrode using a liquid reservoir can be stored in a dilute solution of analyte and needs no additional conditioning before use. The lifetime of an electrode with a PVC membrane, however, is proportional to its exposure to aqueous solutions. For this reason these electrodes are best stored by covering the membrane with a cap along with a small amount of wetted gauze to maintain a humid environment. Before using the electrode it is conditioned in a solution of analyte for 30–60 minutes.

Table 11.2.3 . Representative Examples of Liquid-Based Ion-Selective Electrodes

analyte	membrane composition	selectivity coefficients
Ca^{2+}	di-(*n*-decyl) phosphate in PVC	$K_{Ca^{2+}/Zn^{2+}} = 1 - 5$ $K_{Ca^{2+}/Al^{3+}} = 0.90$ $K_{Ca^{2+}/Mn^{2+}} = 0.38$ $K_{Ca^{2+}/Cu^{2+}} = 0.070$ $K_{Ca^{2+}/Mg^{2+}} = 0.032$
K^+	valinomycin in PVC	$K_{K^+/Rb^+} = 1.9$ $K_{K^+/Cs^+} = 0.38$ $K_{K^+/Li^+} = 10^{-4}$
Li^+	ETH 149 in PVC	$K_{Li^+/H^+} = 1$ $K_{Li^+/Na^+} = 0.03$ $K_{Li^+/K^+} = 0.007$
NH_4^+	nonactin and monactin in PVC	$K_{NH_4^+/K^+} = 0.12$ $K_{NH_4^+/H^+} = 0.016$ $K_{NH_4^+/Li^+} = 0.0042$ $K_{NH_4^+/Na^+} = 0.002$
ClO_3^-	$Fe(o\text{-phen})_3^{3+}$ in *p*-nitrocymene with porous membrane	$K_{ClO_4^-/OH^-} = 1$ $K_{ClO_4^-/I^-} = 0.012$ $K_{ClO_4^-/NO_3^-} = 0.0015$ $K_{ClO_4^-/Br^-} = 5.6 \times 10^{-4}$ $K_{ClO_4^-/Cl^-} = 2.2 \times 10^{-4}$
NO_3^-	tetradodecyl ammonium nitrate in pVC	$K_{NO_3^-/Cl^-} = 0.006$ $K_{NO_3^-/F^-} = 9 \times 10^{-4}$

Selectivity coefficients are approximate; values found experimentally may vary substantially from the listed values. See Cammann, K. *Working With Ion-Selective Electrodes*, Springer-Verlag: Berlin, 1977.

GAS-SENSING ELECTRODES

A number of membrane electrodes respond to the concentration of a dissolved gas. The basic design of a ***gas-sensing electrode***, as shown in Figure 11.2.13 , consists of a thin membrane that separates the sample from an inner solution that contains an ion-selective electrode. The membrane is permeable to the gaseous analyte, but impermeable to nonvolatile components in the sample's matrix. The gaseous analyte passes through the membrane where it reacts with the inner solution, producing a species whose concentration is monitored by the ion-selective electrode. For example, in a CO_2 electrode, CO_2 diffuses across the membrane where it reacts in the inner solution to produce H_3O^+.

$$CO_2(aq) + 2H_2O(l) \rightleftharpoons HCO_3^-(aq) + H_3O^+(aq) \tag{10.2.10}$$

The change in the activity of H_3O^+ in the inner solution is monitored with a pH electrode, for which the cell potential is given by Equation 10.2.9. To find the relationship between the activity of H_3O^+ in the inner solution and the activity of CO_2 in the inner solution we rearrange the equilibrium constant expression for reaction 10.2.10; thus

$$a_{H_3O^+} = K_a \times \frac{a_{CO_2}}{a_{HCO_3^-}} \tag{10.2.11}$$

where K_a is the equilibrium constant. If the activity of HCO_3^- in the internal solution is sufficiently large, then its activity is not affected by the small amount of CO_2 that passes through the membrane. Substituting Equation 10.2.11 into Equation 10.2.9 gives

$$E_{cell} = K' + 0.05916 \log a_{co_2}$$

where K′ is a constant that includes the constant for the pH electrode, the equilibrium constant for reaction 10.2.10 and the activity of HCO_3^- in the inner solution.

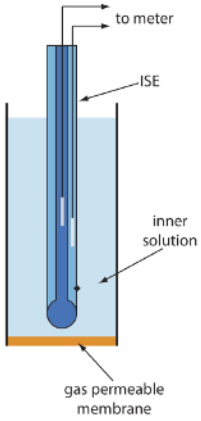


Figure 11.2.13 . Schematic diagram of a gas-sensing membrane electrode.

Table 11.2.4 lists the properties of several gas-sensing electrodes. The composition of the inner solution changes with use, and both the inner solution and the membrane must be replaced periodically. Gas-sensing electrodes are stored in a solution similar to the internal solution to minimize their exposure to atmospheric gases.

Table 11.2.4 . Representative Examples of Gas-Sensing Electrodes

analyte	inner solution	reaction in inner solution	ion-selective electrode
CO_2	10 mM $NaHCO_3$ 10 mM NaCl	$CO_2(aq) + 2H_2O(l) \rightleftharpoons HCO_3^-(aq) + H_3O^+(aq)$	glass pH ISE
HCN	10 mM $KAg(CN)_2$	$HCN(aq) + H_2O(l) \rightleftharpoons CN^-(aq) + H_3O^+(aq)$	Ag_2S solid-state ISE
HF	1 M H_3O^+	$HF(aq) + H_2O(l) \rightleftharpoons F^-(aq) + H_3O^+(aq)$	F^- solid-state ISE
H_2S	pH 5 citrate buffer	$H_2S(aq) + H_2O(l) \rightleftharpoons HS^-(aq) + H_3O^+(aq)$	Ag_2S solid state ISE
NH_3	10 mM NH_4Cl 0.1 M KNO_3	$NH_3(aq) + H_2O(l) \rightleftharpoons NH_4^+(aq) + OH^-(aq)$	glass pH ISE
NO_2	20 mM $NaNO_2$ 0.1 M KNO_3	$2NO_2(aq) + 3H_2O(l) \rightleftharpoons NO_3^-(aq) + NO_2^-(aq) + 2H_3O^+(aq)$	glass pH ISE
SO_2	1 mM $NaHSO_3$ pH 5	$SO_2(aq) + 2H_2O(l) \rightleftharpoons HSO_3^-(aq) + H_3O^+(aq)$	glass pH ISE

Source: Cammann, K. *Working With Ion-Selective Electrodes*, Springer-Verlag: Berlin, 1977.

POTENTIOMETRIC BIOSENSORS

The approach for developing gas-sensing electrodes can be modified to create potentiometric electrodes that respond to a biochemically important species. The most common class of potentiometric biosensors are ***enzyme electrodes***, in which we trap or immobilize an enzyme at the surface of a potentiometric electrode. The analyte's reaction with the enzyme produces a product whose concentration is monitored by the potentiometric electrode. Potentiometric biosensors also have been designed around other biologically active species, including antibodies, bacterial particles, tissues, and hormone receptors.

One example of an enzyme electrode is the urea electrode, which is based on the catalytic hydrolysis of urea by urease

$$CO(NH_2)_2(aq) + 2H_2O(l) \rightleftharpoons 2NH_4^+(aq) + CO_3^-(aq)$$

Figure 11.2.14 shows one version of the urea electrode, which modifies a gas-sensing NH_3 electrode by adding a dialysis membrane that traps a pH 7.0 buffered solution of urease between the dialysis membrane and the gas permeable membrane [(a) Papastathopoulos, D. S.; Rechnitz, G. A. *Anal. Chim. Acta* **1975**, *79*, 17–26; (b) Riechel, T. L. *J. Chem. Educ*. **1984**, *61*, 640–642]. An NH_3 electrode, as shown in Table 11.2.4 , uses a gas-permeable membrane and a glass pH electrode. The NH_3 diffuses across the membrane where it changes the pH of the internal solution.

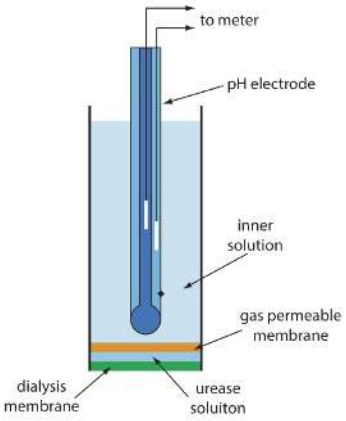


Figure 11.2.14 . Schematic diagram showing an enzyme-based potentiometric biosensor for urea. A solution of the enzyme urease is trapped between a dialysis membrane and a gas permeable membrane. Urea diffuses across the dialysis membrane and reacts with urease, producing NH_3 that diffuses across the gas permeable membrane. The resulting change in the internal solution's pH is measured with the pH electrode.

When immersed in the sample, urea diffuses through the dialysis membrane where it reacts with the enzyme urease to form the ammonium ion, NH_4^+, which is in equilibrium with NH_3.

$$NH_4^+(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + NH_3(aq)$$

The NH_3, in turn, diffuses through the gas permeable membrane where a pH electrode measures the resulting change in pH. The electrode's response to the concentration of urea is

$$E_{cell} = K - 0.05916 \log a_{urea} \tag{10.2.12}$$

Another version of the urea electrode (Figure 11.2.15) immobilizes the enzyme urease in a polymer membrane formed directly on the tip of a glass pH electrode [Tor, R.; Freeman, A. *Anal. Chem.* **1986**, *58*, 1042–1046]. In this case the response of the electrode is

$$pH = K a_{urea} \tag{10.2.13}$$

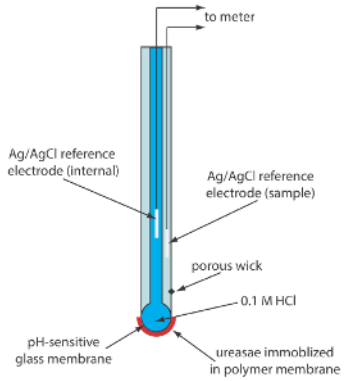


Figure 11.2.15 . Schematic diagram of an enzyme-based potentiometric biosensor for urea in which urease is immobilized in a polymer membrane coated onto the pH-sensitive glass membrane of a pH electrode.

Few potentiometric biosensors are available commercially. As shown in Figure 11.2.14 and Figure 11.2.15 , however, it is possible to convert an ion-selective electrode or a gas-sensing electrode into a biosensor. Several representative examples are described in Table 11.2.5 , and additional examples can be found in this chapter's additional resources.

Table 11.2.5 . Representative Examples of Potentiometric Biosensors

analyte	biologically active phase	substance determined
5′-AMP	AMP-deaminase (E)	NH_3
L-arginine	arginine and urease (E)	NH_3
asparagine	asparaginase (E)	NH_4^+
L-cysteine	*Proteus morganii* (B)	H_2S
L-glutamate	yellow squash (T)	CO_2
L-glutamine	*Sarcina flava* (B)	NH_3
oxalate	oxalate decarboxylase (E)	CO_2
penicillin	penicllinase (E)	H_3O^+
L-phenylalanine	L-amino acid oxidase/horseradish peroxidase (E)	I^-
sugars	bacteria from dental plaque (B)	H_3O^+
urea	urease (E)	NH_3 or H_3O^+

Source: Complied from Cammann, K. *Working With Ion-Selective Electrodes*, Springer-Verlag: Berlin, 1977 and Lunte, C. E.; Heineman, W. R. "Electrochemical techniques in Bioanalysis," in Steckham, E. ed. *Topics in Current Chemistry*, Vol. 143, Springer-Verlag: Berlin, 1988, p.8.
Abbreviations for biologically active phase: E = enzyme; B = bacterial particle; T = tissue.

QUANTITATIVE APPLICATIONS

The potentiometric determination of an analyte's concentration is one of the most common quantitative analytical techniques. Perhaps the most frequent analytical measurement is the determination of a solution's pH, a measurement we will consider in more detail later in this section. Other areas where potentiometry is important are clinical chemistry, environmental chemistry, and potentiometric titrations. Before we consider representative applications, however, we need to examine more closely the relationship between cell potential and the analyte's concentration and methods for standardizing potentiometric measurements.

ACTIVITY AND CONCENTRATION

The Nernst equation relates the cell potential to the analyte's activity. For example, the Nernst equation for a metallic electrode of the first kind is

$$E_{\text{cll}} = K + \frac{0.05916}{n} \log a_{M^{n+}} \tag{10.2.14}$$

where $a_{M^{n+}}$ is the metal ion's activity. When we use a potentiometric electrode, however, our goal is to determine the analyte's concentration. As we learned in Chapter 6, an ion's activity is the product of its concentration, $[M^{n+}]$, and a matrix-dependent activity coefficient, $\gamma_{Mn^{n+}}$.

$$a_{M^{n+}} = \left[M^{n+}\right] \gamma_{M^{n+}} \tag{10.2.15}$$

Substituting Equation 10.2.15 into Equation 10.2.14 and rearranging, gives

$$E_{\text{cell}} = K + \frac{0.05916}{n} \log \gamma_{M^{n+}} + \frac{0.05916}{n} \log\left[M^{n+}\right] \tag{10.2.16}$$

We can solve Equation 10.2.16 for the metal ion's concentration if we know the value for its activity coefficient. Unfortunately, if we do not know the exact ionic composition of the sample's matrix—which is the usual situation—then we cannot calculate the value of $\gamma_{Mn^{n+}}$. There is a solution to this dilemma. If we design our system so that the standards and the samples have an identical matrix, then the value of $\gamma_{Mn^{n+}}$ remains constant and Equation 10.2.16 simplifies to

$$E_{\text{cell}} = K' + \frac{0.05916}{n} \log\left[M^{n+}\right]$$

where K' includes the activity coefficient.

QUANTITATIVE ANALYSIS USING EXTERNAL STANDARDS

Before we can determine the concentration of analyte in a sample, we must standardize the electrode. If the electrode's response obeys the Nernst equation, then we can determine the constant K using a single external standard. Because a small deviation from the ideal slope of $\pm RT/nF$ or $\pm RT/zF$ is not unexpected, we usually use two or more external standards.

> To review the use of external standards, see Chapter 5.3.

In the absence of interferents, a calibration curve of E_{cell} versus $\log a_A$, where A is the analyte, is a straight-line. A plot of E_{cell} versus $\log[A]$, however, may show curvature at higher concentrations of analyte as a result of a matrix-dependent change in the analyte's activity

coefficient. To maintain a consistent matrix we add a high concentration of an inert electrolyte to all samples and standards. If the concentration of added electrolyte is sufficient, then the difference between the sample's matrix and the matrix of the standards will not affect the ionic strength and the activity coefficient essentially remains constant. The inert electrolyte added to the sample and the standards is called a ***total ionic strength adjustment buffer*** (TISAB).

EXAMPLE 11.2.8

The concentration of Ca^{2+} in a water sample is determined using the method of external standards. The ionic strength of the samples and the standards is maintained at a nearly constant level by making each solution 0.5 M in KNO_3. The measured cell potentials for the external standards are shown in the following table.

$[Ca^{2+}]$ (M)	E_{cell} (V)
1.00×10^{-5}	–0.125
5.00×10^{-5}	–0.103
1.00×10^{-4}	–0.093
5.00×10^{-4}	–0.072
1.00×10^{-3}	–0.063
5.00×10^{-3}	–0.043
1.00×10^{-2}	–0.033

What is the concentration of Ca^{2+} in a water sample if its cell potential is found to be –0.084 V?

Solution

Linear regression gives the calibration curve in Figure 11.2.16 , with an equation of

$$E_{cell} = 0.027 + 0.0303 \log\left[Ca^{2+}\right]$$

Substituting the sample's cell potential gives the concentration of Ca^{2+} as 2.17×10^{-4} M. Note that the slope of the calibration curve, which is 0.0303, is slightly larger than its ideal value of 0.05916/2 = 0.02958; this is not unusual and is one reason for using multiple standards.

One reason that it is not unusual to find that the experimental slope deviates from its ideal value of 0.05916/*n* is that this ideal value assumes that the temperature is 25°C.

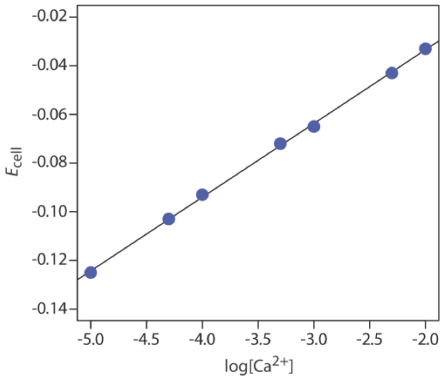


Figure 11.2.16 . Calibration curve for the data in Example 11.2.8 .

QUANTITATIVE ANALYSIS USING THE METHOD OF STANDARD ADDITIONS

Another approach to calibrating a potentiometric electrode is the method of standard additions. First, we transfer a sample with a volume of V_{samp} and an analyte concentration of C_{samp} into a beaker and measure the potential, $(E_{cell})_{samp}$. Next, we make a standard addition by adding to the sample a small volume, V_{std}, of a standard that contains a known concentration of analyte, C_{std}, and measure the potential, (E_{cell})std. If V_{std} is significantly smaller than V_{samp}, then we can safely ignore the change in the sample's matrix and assume that the analyte's activity coefficient is constant. Example 11.2.9 demonstrates how we can use a one-point standard addition to determine the concentration of analyte in a sample.

To review the method of standard additions, see Chapter 5.3.

EXAMPLE 11.2.9

The concentration of Ca^{2+} in a sample of sea water is determined using a Ca ion-selective electrode and a one-point standard addition. A 10.00-mL sample is transferred to a 100-mL volumetric flask and diluted to volume. A 50.00-mL aliquot of the sample is placed in a beaker with the Ca ISE and a reference electrode, and the potential is measured as –0.05290 V. After adding a 1.00-mL aliquot of a 5.00×10^{-2} M standard solution of Ca^{2+} the potential is –0.04417 V. What is the concentration of Ca^{2+} in the sample of sea water?

Solution

To begin, we write the Nernst equation before and after adding the standard addition. The cell potential for the sample is

$$(E_{\text{cell}})_{\text{samp}} = K + \frac{0.05916}{2}\log C_{\text{samp}}$$

and that following the standard addition is

$$(E_{\text{cell}})_{\text{std}} = K + \frac{0.05916}{2}\log\left\{\frac{V_{\text{samp}}}{V_{\text{tot}}}C_{\text{samp}} + \frac{V_{\text{std}}}{V_{\text{tot}}}C_{\text{std}}\right\}$$

where V_{tot} is the total volume (V_{samp} + V_{std}) after the standard addition. Subtracting the first equation from the second equation gives

$$\Delta E = (E_{\text{cell}})_{\text{std}} - (E_{\text{cell}})_{\text{samp}} = \frac{0.05916}{2}\log\left\{\frac{V_{\text{samp}}}{V_{\text{tot}}}C_{\text{samp}} + \frac{V_{\text{std}}}{V_{\text{tot}}}C_{\text{std}}\right\} - \frac{0.05916}{2}\log C_{\text{samp}}$$

Rearranging this equation leaves us with

$$\frac{2\Delta E_{cell}}{0.05916} = \log\left\{\frac{V_{\text{samp}}}{V_{\text{tot}}} + \frac{V_{\text{std}}\,C_{\text{std}}}{V_{\text{tot}}\,C_{\text{samp}}}\right\}$$

Substituting known values for ΔE, V_{samp}, V_{std}, V_{tot} and C_{std},

$$\frac{2\times\{-0.04417-(-0.05290)\}}{0.05916} = \log\left\{\frac{50.00\text{ mL}}{51.00\text{ mL}} + \frac{(1.00\text{ mL})(5.00\times10^{-2}\text{M})}{(51.00\text{ mL})C_{\text{samp}}}\right\}$$

$$0.2951 = \log\left\{0.9804 + \frac{9.804\times10^{-4}}{C_{\text{samp}}}\right\}$$

and taking the inverse log of both sides gives

$$1.973 = 0.9804 + \frac{9.804 \times 10^{-4}}{C_{\text{samp}}}$$

Finally, solving for C_{samp} gives the concentration of Ca^{2+} as 9.88×10^{-4} M. Because we diluted the original sample of seawater by a factor of 10, the concentration of Ca^{2+} in the seawater sample is 9.88×10^{-3} M.

FREE IONS VERSUS COMPLEXED IONS

Most potentiometric electrodes are selective toward the free, uncomplexed form of the analyte, and do not respond to any of the analyte's complexed forms. This selectivity provides potentiometric electrodes with a significant advantage over other quantitative methods of analysis if we need to determine the concentration of free ions. For example, calcium is present in urine both as free Ca^{2+} ions and as protein-bound Ca^{2+} ions. If we analyze a urine sample using atomic absorption spectroscopy, the signal is propor- tional to the total concentration of Ca^{2+} because both free and bound calcium are atomized. Analyzing urine with a Ca^{2+} ISE, however, gives a signal that is a function of only free Ca^{2+} ions because the protein-bound Ca^{2+} can not interact with the electrode's membrane.

> The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of F^- in toothpaste provides an instructive example of a typical procedure. The description here is based on Kennedy, J. H. *Analytical Chemistry— Practice*, Harcourt Brace Jaovanovich: San Diego, 1984, p. 117–118.

REPRESENTATIVE METHOD 11.2.1: DETERMINATION OF FLUORIDE IN TOOTHPASTE

Description of the Method

The concentration of fluoride in toothpastes that contains soluble F^- is determined with a F^- ion-selective electrode using a calibration curve prepared with external standards. Although the F^- ISE is very selective (only OH^- with a K_{F^-/OH^-} of 0.1 is a significant interferent), Fe^{3+} and

Al^{3+} interfere with the analysis because they form soluble fluoride complexes that do not interact with the ion-selective electrode's membrane. This interference is minimized by reacting any Fe^{3+} and Al^{3+} with a suitable complexing agent.

Procedure

Prepare 1 L of a standard solution of 1.00% w/v SnF_2 and transfer it to a plastic bottle for storage. Using this solution, prepare 100 mL each of standards that contain 0.32%, 0.36%, 0.40%, 0.44% and 0.48% w/v SnF_2, adding 400 mg of malic acid to each solution as a stabilizer. Transfer the standards to plastic bottles for storage. Prepare a total ionic strength adjustment buffer (TISAB) by mixing 500 mL of water, 57 mL of glacial acetic acid, 58 g of NaCl, and 4 g of disodium DCTA (*trans*-1,2-cyclohexanetetraacetic acid) in a 1-L beaker, stirring until dissolved. Cool the beaker in a water bath and add 5 M NaOH until the pH is between 5–5.5. Transfer the contents of the beaker to a 1-L volumetric flask and dilute to volume. Prepare each external standard by placing approximately 1 g of a fluoride-free toothpaste, 30 mL of distilled water, and 1.00 mL of standard into a 50-mL plastic beaker and mix vigorously for two min with a stir bar. Quantitatively transfer the resulting suspension to a 100-mL volumetric flask along with 50 mL of TISAB and dilute to volume with distilled water. Store the entire external standard in a 250-mL plastic beaker until you are ready to measure the potential. Prepare toothpaste samples by obtaining an approximately 1-g portion and treating in the same manner as the standards. Measure the cell potential for the external standards and the samples using a F^- ion-selective electrode and an appropriate reference electrode. When measuring the potential, stir the solution and allow two to three minutes to reach a stable potential. Report the concentration of F^- in the toothpaste %w/w SnF_2.

Questions

1. The total ionic strength adjustment buffer serves several purposes in this procedure. Identify these purposes.

The composition of the TISAB has three purposes:

(a) The high concentration of NaCl (the final solutions are approximately 1 M NaCl) ensures that the ionic strength of each external standard and each sample is essentially identical. Because the activity coefficient for fluoride is the same in all solutions, we can write the Nernst equation in terms of fluoride's concentration instead of its activity.

(b) The combination of glacial acetic acid and NaOH creates an acetic acid/acetate buffer of pH 5–5.5. As shown in Figure 11.2.17 , the pH of this buffer is high enough to ensure that the predominate form of fluoride is F^- instead of HF. This pH also is sufficiently acidic that it avoids an interference from OH^- (see Example 10.2.8)).

(c) DCTA is added as a complexing agent for Fe^{3+} or Al^{3+}, preventing the formation of FeF_6^{3-} or AlF_6^{3-} .

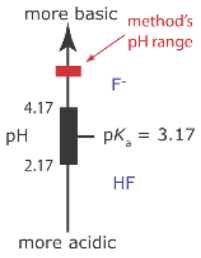


Figure 11.2.17 . Ladder diagram for HF/F^-. Maintaining a pH greater than 4.2 ensures that the only significant form of fluoride is F^-.

2. Why is a fluoride-free toothpaste added to the standard solutions?

Adding a fluoride-free toothpaste protects against any unaccounted for matrix effects that might influence the ion-selective electrode's response. This assumes, of course, that the matrices of the two toothpastes are otherwise similar.

3. The procedure specifies that the standards and the sample should be stored in plastic containers. Why is it a bad idea to store the solutions in glass containers?

The fluoride ion is capable of reacting with glass to form SiF_4.

4. Suppose your calibration curve has a slope of –57.98 mV for each 10-fold change in the concentration of F^-. The ideal slope from the Nernst equation is –59.16 mV per 10-fold change in concentration. What effect does this have on the quantitative analysis for fluoride in toothpaste?

No effect at all! This is why we prepare a calibration curve using multiple standards.

MEASUREMENT OF PH

With the availability of inexpensive glass pH electrodes and pH meters, the determination of pH is one of the most common quantitative analytical measurements. The potentiometric determination of pH, however, is not without complications, several of which we discuss in this section.

One complication is confusion over the meaning of pH [Kristensen, H. B.; Saloman, A.; Kokholm, G. *Anal. Chem.* **1991**, *63*, 885A–891A]. The conventional definition of pH in most general chemistry textbooks is

$$\text{pH} = -\log\left[\text{H}^+\right] \tag{10.2.17}$$

As we now know, pH actually is a measure of the activity of H^+.

$$\text{pH} = -\log a_{\text{H}^+} \tag{10.2.18}$$

> Try this experiment—find several general chemistry textbooks and look up *pH* in each textbook's index. Turn to the appropriate pages and see how it is defined. Next, look up *activity* or *activity coefficient* in each textbook's index and see if these terms are indexed.

Equation 10.2.17 only approximates the true pH. If we calculate the pH of 0.1 M HCl using Equation 10.2.17, we obtain a value of 1.00; the solution's actual pH, as defined by Equation 10.2.18, is 1.1 [Hawkes, S. J. *J. Chem. Educ.* **1994**, *71*, 747–749]. The activity and the concentration of H^+ are not the same in 0.1 M HCl because the activity coefficient for H^+ is not 1.00 in this matrix. Figure 11.2.18 shows a more colorful demonstration of the difference between activity and concentration.

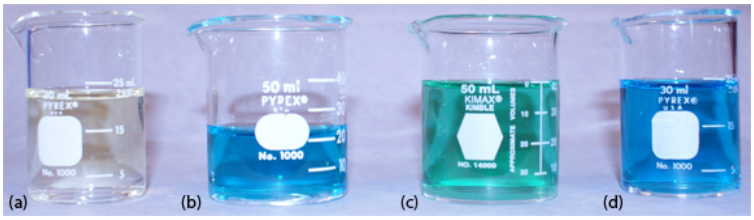


Figure 11.2.18 . A demonstration of the difference between activity and concentration using the indicator methyl green. The indicator is pale yellow in its acid form (beaker a: 1.0 M HCl) and is blue in its base form (beaker d: H_2O). In 10 mM HCl the indicator is in its base form (beaker b: 20 mL of 10 mM HCl with 3 drops of methyl green). Adding 20 mL of 5 M LiCl to this solution shifts the indicator's color to green (beaker c); although the concentration of HCl is cut in half to 5 mM, the activity of H^+ has increased as evidenced by the green color that is intermediate between the indicator's pale yellow, acid form and its blue, base form. The demonstration shown here is adapted from McCarty, C. G.; Vitz, E. "pH Paradoxes: Demonstrating That It Is Not True That pH ≡ –log[H^+]," *J. Chem. Educ.* **2006**, *83*, 752–757. This paper provides several additional demonstrations that illustrate the difference between concentration and activity.

A second complication in measuring pH is the uncertainty in the relationship between potential and activity. For a glass membrane electrode, the cell potential, (E_{cell})samp, for a sample of unknown pH is

$$(E_{\text{cell}})_{\text{samp}} = K - \frac{RT}{F}\ln\frac{1}{a_{\text{H}^+}} = K - \frac{2.303RT}{F}\text{pH}_{\text{samp}} \tag{10.2.19}$$

where K includes the potential of the reference electrode, the asymmetry potential of the glass membrane, and any junction potentials in the electrochemical cell. All the contributions to K are subject to uncertainty, and may change from day-to-day, as well as from electrode-to-electrode. For this reason, before using a pH electrode we calibrate it using a standard buffer of known pH. The cell potential for the standard, $(E_{\text{cell}})_{\text{std}}$, is

$$(E_{\text{ccll}})_{\text{std}} = K - \frac{2.303RT}{F}\text{pH}_{\text{std}} \tag{10.2.20}$$

where pH_{std} is the standard's pH. Subtracting Equation 10.2.20 from Equation 10.2.19 and solving for pH_{samp} gives

$$\text{pH}_{\text{samp}} = \text{pH}_{\text{std}} - \frac{\left\{(E_{\text{cell}})_{\text{samp}} - (E_{\text{cell}})_{\text{std}}\right\}F}{2.303RT} \tag{10.2.21}$$

which is the operational definition of pH adopted by the International Union of Pure and Applied Chemistry [Covington, A. K.; Bates, R. B.; Durst, R. A. *Pure & Appl. Chem.* **1985**, *57*, 531–542].

Calibrating a pH electrode presents a third complication because we need a standard with an accurately known activity for H^+. Table 11.2.6 provides pH values for several primary standard buffer solutions accepted by the National Institute of Standards and Technology.

Table 11.2.6 . pH Values for Selected NIST Primary Standard Buffers

temp (ºC)	saturated (at 25ºC) KHC_4H4O_7 (tartrate)	0.05 m $KH_2C_6H_5O_7$ (citrate)	0.05 m $KHC_8H_4O_4$ (phthlate)	0.025 m KH_2PO_4, 0.025 m $NaHPO_4$	0.008695 m KH_2PO_4, 0.03043 m Na_2HPO_4	0.01 m $Na_4B_4O_7$	0.025 m $NaHCO_3$, 0.025 m Na_2CO_3
0	—	3.863	4.003	6.984	7.534	9.464	10.317
5	—	3.840	3.999	6.951	7.500	9.395	10.245
10	—	3.820	3.998	6.923	7.472	9.332	10.179
15	—	3.802	3.999	6.900	7.448	9.276	10.118
20	—	3.788	4.002	6.881	7.429	9.225	10.062
25	3.557	3.776	4.008	6.865	7.413	9.180	10.012
30	3.552	3.766	4.015	6.854	7.400	9.139	9.966
35	3.549	3.759	4.024	6.844	7.389	9.012	9.925
40	3.547	3.753	4.035	6.838	7.380	9.068	9.889
45	3.547	3.750	4.047	6.834	7.373	9.038	9.856
50	3.549	3.749	4.060	6.833	7.367	9.011	9.828

Source: Values taken from Bates, R. G. *Determination of pH: Theory and Practice*, 2nd ed. Wiley: New York, 1973. See also Buck, R. P., et. al."Measurement of pH. Definition, Standards, and Procedures," *Pure. Appl. Chem.* **2002**, *74*, 2169–2200. All concentrations are molal (m).

To standardize a pH electrode using two buffers, choose one near a pH of 7 and one that is more acidic or basic depending on your sample's expected pH. Rinse your pH electrode in deionized water, blot it dry with a laboratory wipe, and place it in the buffer with the pH closest to 7. Swirl the pH electrode and allow it to equilibrate until you obtain a stable reading. Adjust the "Standardize" or "Calibrate" knob until the meter displays the correct pH. Rinse and dry the electrode, and place it in the second buffer. After the electrode equilibrates, adjust the "Slope" or "Temperature" knob until the meter displays the correct pH.

Some pH meters can compensate for a change in temperature. To use this feature, place a temperature probe in the sample and connect it to the pH meter. Adjust the "Temperature" knob to the solution's temperature and calibrate the pH meter using the "Calibrate" and "Slope" controls. As you are using the pH electrode, the pH meter compensates for any change in the sample's temperature by adjusting the slope of the calibration curve using a Nernstian response of $2.303RT/F$.

CLINICAL APPLICATIONS

Because of their selectivity for analytes in complex matricies, ion-selective electrodes are important sensors for clinical samples. The most common analytes are electrolytes, such as Na^+, K^+, Ca^{2+}, H^+, and Cl^-, and dissolved gases such as CO_2. For extracellular fluids, such as blood and urine, the analysis can be made *in vitro*. An *in situ* analysis, however, requires a much smaller electrode that we can insert directly into a cell. Liquid-based membrane microelectrodes with tip diameters smaller than 1 μm are constructed by heating and drawing out a hard-glass capillary tube with an initial diameter of approximately 1–2 mm (Figure 11.2.19). The microelectrode's tip is made hydrophobic by dipping into a solution of dichlorodimethyl silane, and an inner solution appropriate for the analyte and a Ag/AgCl wire reference electrode are placed within the microelectrode. The microelectrode is dipped into a solution of the liquid complexing agent, which through capillary action draws a small volume of the liquid complexing agent into the tip. Potentiometric microelectrodes have been developed for a number of clinically important analytes, including H^+, K^+, Na^+, Ca^{2+}, Cl^-, and I^- [Bakker, E.; Pretsch, E. *Trends Anal. Chem.* **2008**, *27*, 612–618].

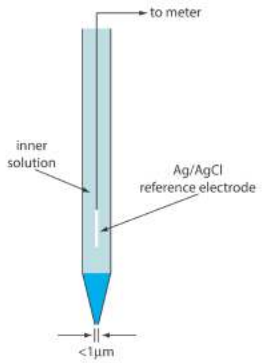


Figure 11.2.19 . Schematic diagram of a liquid-based ion-selective microelectrode.

ENVIRONMENTAL APPLICATIONS

Although ion-selective electrodes are used in environmental analysis, their application is not as widespread as in clinical analysis. Although standard potentiometric methods are available for the analysis of CN^-, F^-, NH_3, and NO_3^- in water and wastewater, other analytical methods generally provide better detection limits. One potential advantage of an ion-selective electrode is the ability to incorporate it into a flow cell for the continuous monitoring of wastewater streams.

POTENTIOMETRIC TITRATIONS

One method for determining the equivalence point of an acid–base titration is to use a pH electrode to monitor the change in pH during the titration. A potentiometric determination of the equivalence point is possible for acid–base, complexation, redox, and precipitation titrations, as well as for titrations in aqueous and nonaqueous solvents. Acid–base, complexation, and precipitation potentiometric titrations usually are monitored with an ion-selective electrode that responds the analyte, although an electrode that responds to the titrant or a reaction product also can be used. A redox electrode, such as a Pt wire, and a reference electrode are used for potentiometric redox titrations. More details about potentiometric titrations are found in Chapter 9.

EVALUATION

SCALE OF OPERATION

The working range for most ion-selective electrodes is from a maximum concentration of 0.1–1 M to a minimum concentration of $10^{-5} - 10^{-11}$ M [(a) Bakker, E.; Pretsch, E. *Anal. Chem.* **2002**, *74*, 420A–426A; (b) Bakker, E.; Pretsch, E. *Trends Anal. Chem.* **2005**, *24*, 199–207]. This broad working range extends from major analytes to ultratrace analytes, and is significantly greater than many other analytical techniques. To use a conventional ion-selective electrode we need a minimum sample volume of several mL (a macro sample). Microelectrodes, such as the one shown in Figure 11.2.19 , are used with an ultramicro sample, although care is needed to ensure that the sample is representative of the original sample.

ACCURACY

The accuracy of a potentiometric analysis is limited by the error in measuring E_{cell}. Several factors contribute to this measurement error, including the contribution to the potential from interfering ions, the finite current that passes through the cell while we measure the potential, differences between the analyte's activity coefficient in the samples and the standard solutions, and junction potentials. We can limit the effect of an interfering ion by including a separation step before the potentiometric analysis. Modern high impedance potentiometers minimize the amount of current that passes through the electrochemical cell. Finally, we can minimize the errors due to activity coefficients and junction potentials by matching the matrix of the standards to that of the sample. Even in the best circumstances, however, a difference of approximately ±1 mV for samples with equal concentrations of analyte is not unusual.

We can evaluate the effect of uncertainty on the accuracy of a potentiometric measurement by using a propagation of uncertainty. For a membrane ion-selective electrode the general expression for potential is

$$E_{\text{cell}} = K + \frac{RT}{zF}\ln[A]$$

where *z* is the analyte's, *A*, charge. From Table 4.3.1 in Chapter 4, the uncertainty in the cell potential, ΔE_{cell} is

$$\triangle E_{\text{cell}} = \frac{RT}{zF} \times \frac{\Delta[A]}{[A]}$$

Rearranging and multiplying through by 100 gives the percent relative error in concentration as

$$\%\text{ relative error } = \frac{\Delta[A]}{[A]} \times 100 = \frac{\triangle E_{\text{cell}}}{RT/zF} \times 100 \tag{10.2.22}$$

The relative error in concentration, therefore, is a function of the measurement error for the electrode's potential, ΔE_{cell}, and the analyte's charge. Table 11.2.7 provides representative values for ions with charges of ±1 and ±2 at a temperature of 25ºC. Accuracies of 1–5% for monovalent ions and 2–10% for divalent ions are typical. Although Equation 10.2.22 applies to membrane electrodes, we can use if for a metallic electrode by replacing *z* with *n*.

Table 11.2.7 . Relationship Between the Uncertainty in Measuring E_{cell} and the Relative Error in the Analyte's Concentration

ΔE_{cell} (± mV)	% relative error when $z = \pm 1$	% relative error when $z = \pm 2$
0.1	±0.4	±0.8
0.5	±1.9	±3.9
1.0	±3.0	±7.8
1.5	±5.8	±11.1
2.0	±7.8	±15.6

PRECISION

Precision in potentiometry is limited by variations in temperature and the sensitivity of the potentiometer. Under most conditions—and when using a simple, general-purpose potentiometer—we can measure the potential with a repeatability of ±0.1 mV. Using Table 11.2.7 , this corresponds to an uncertainty of ±0.4% for monovalent analytes and ±0.8% for divalent analytes. The reproducibility of potentiometric measurements is about a factor of ten poorer.

SENSITIVITY

The sensitivity of a potentiometric analysis is determined by the term RT/nF or RT/zF in the Nernst equation. Sensitivity is best for smaller values of n or z.

SELECTIVITY

As described earlier, most ion-selective electrodes respond to more than one analyte; the selectivity for the analyte, however, often is significantly greater than the sensitivity for the interfering ions. The manufacturer of an ion-selective usually provides an ISE's selectivity coefficients, which allows us to determine whether a potentiometric analysis is feasible for a given sample.

TIME, COST, AND EQUIPMENT

In comparison to other techniques, potentiometry provides a rapid, relatively low-cost means for analyzing samples. The limiting factor when analyzing a large number of samples is the need to rinse the electrode between samples. The use of inexpensive, disposable ion-selective electrodes can increase a lab's sample throughput. Figure 11.2.20 shows one example of a disposable ISE for Ag^+ [Tymecki, L.; Zwierkowska, E.; Głąb, S.; Koncki, R. *Sens. Actuators B* **2003**, *96*, 482–488]. Commercial instruments for measuring pH or potential are available in a variety of price ranges, and includes portable models for use in the field.

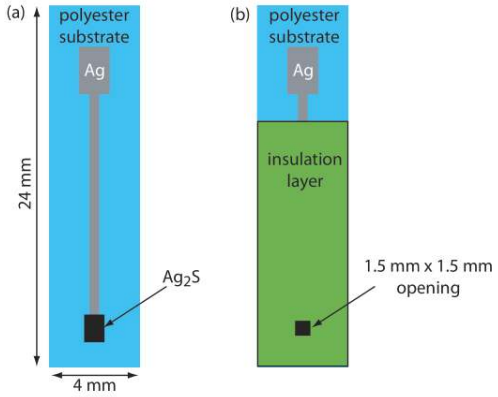


Figure 11.2.20 . Schematic diagram of a disposable ion-selective electrode created by screen-printing. In (a) a thin film of conducting silver is printed on a polyester substrate and a film of Ag_2S overlaid near the bottom. In (b) an insulation layer with a small opening is layered on top exposes a portion of the Ag_2S membrane that is immersed in the sample. The top of the polyester substrate remains uncoated, which allows us to connect the electrode to a potentiometer through the Ag film. The small inset shows the electrode's actual size.

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10.3: REDOX TITRATIONS

Analytical titrations using oxidation–reduction reactions were introduced shortly after the development of acid–base titrimetry. The earliest ***redox titration*** took advantage of chlorine's oxidizing power. In 1787, Claude Berthollet introduced a method for the quantitative analysis of chlorine water (a mixture of Cl_2, HCl, and HOCl) based on its ability to oxidize indigo, a dye that is colorless in its oxidized state. In 1814, Joseph Gay-Lussac developed a similar method to determine chlorine in bleaching powder. In both methods the end point is a change in color. Before the equivalence point the solution is colorless due to the oxidation of indigo. After the equivalence point, however, unreacted indigo imparts a permanent color to the solution.

The number of redox titrimetric methods increased in the mid-1800s with the introduction of MnO_4^-, $Cr_2O_7^{2-}$, and I_2 as oxidizing titrants, and of Fe^{2+} and $S_2O_3^{2-}$ as reducing titrants. Even with the availability of these new titrants, redox titrimetry was slow to develop due to the lack of suitable indicators. A titrant can serve as its own indicator if its oxidized and its reduced forms differ significantly in color. For example, the intensely purple MnO_4^- ion serves as its own indicator since its reduced form, Mn^{2+}, is almost colorless. Other titrants require a separate indicator. The first such indicator, diphenylamine, was introduced in the 1920s. Other redox indicators soon followed, increasing the applicability of redox titrimetry.

REDOX TITRATION CURVES

To evaluate a redox titration we need to know the shape of its titration curve. In an acid–base titration or a complexation titration, the titration curve shows how the concentration of H_3O^+ (as pH) or M^{n+} (as pM) changes as we add titrant. For a redox titration it is convenient to monitor the titration reaction's potential instead of the concentration of one species.

You may recall from Chapter 6 that the Nernst equation relates a solution's potential to the concentrations of reactants and products that participate in the redox reaction. Consider, for example, a titration in which a titrand in a reduced state, A_{red}, reacts with a titrant in an oxidized state, B_{ox}.

$$A_{red} + B_{ox} \rightleftharpoons B_{red} + A_{ox}$$

where A_{ox} is the titrand's oxidized form, B_{red} is the titrant's reduced form, and the stoichiometry between the two is 1:1. The reaction's potential, E_{rxn}, is the difference between the reduction potentials for each half-reaction.

$$E_{rxn} = E_{B_{ox}/B_{red}} - E_{A_{ox}/A_{red}}$$

After each addition of titrant the reaction between the titrand and the titrant reaches a state of equilibrium. Because the potential at equilibrium is zero, the titrand's and the titrant's reduction potentials are identical.

$$E_{B_{ox}/B_{red}} = E_{A_{ox}/A_{red}}$$

This is an important observation as it allows us to use either half-reaction to monitor the titration's progress.

Before the equivalence point the titration mixture consists of appreciable quantities of the titrand's oxidized and reduced forms. The concentration of unreacted titrant, however, is very small. The potential, therefore, is easier to calculate if we use the Nernst equation for the titrand's half-reaction

$$E = E_{A_{ox}/A_{red}} = E^\circ_{A_{ox}/A_{red}} - \frac{RT}{nF}\ln\frac{[A_{red}]}{[A_{ox}]}$$

After the equivalence point it is easier to calculate the potential using the Nernst equation for the titrant's half-reaction.

$$E = E_{B_{ox}/B_{red}} = E^\circ_{B_{ox}/B_{red}} - \frac{RT}{nF}\ln\frac{[B_{red}]}{[B_{ox}]}$$

> Although the Nernst equation is written in terms of the half-reaction's standard state potential, a matrix-dependent ***formal potential*** often is used in its place. See Appendix 13 for the standard state potentials and formal potentials for selected half-reactions.

CALCULATING THE TITRATION CURVE

Let's calculate the titration curve for the titration of 50.0 mL of 0.100 M Fe^{2+} with 0.100 M Ce^{4+} in a matrix of 1 M $HClO_4$. The reaction in this case is

$$Fe^{2+}(aq) + Ce^{4+}(aq) \rightleftharpoons Ce^{3+}(aq) + Fe^{3+}(aq) \tag{10.3.1}$$

Because the equilibrium constant for reaction 10.3.1 is very large—it is approximately 6×10^{15}—we may assume that the analyte and titrant react completely.

> In 1 M $HClO_4$, the formal potential for the reduction of Fe^{3+} to Fe^{2+} is +0.767 V, and the formal potential for the reduction of Ce^{4+} to Ce^{3+} is +1.70 V.

The first task is to calculate the volume of Ce needed to reach the titration's equivalence point. From the reaction's stoichiometry we know that

$$\text{mol Fe}^{2+} = M_{\text{Fe}} V_{\text{Fe}} = M_{\text{Ce}} V_{\text{Ce}} = \text{mol Ce}^{4+}$$

Solving for the volume of Ce^{4+} gives the equivalence point volume as

$$V_{eq} = V_{\text{Ce}} = \frac{M_{\text{Fe}} V_{\text{Fe}}}{M_{\text{Ce}}} = \frac{(0.100\text{ M})(50.0\text{ mL})}{(0.100\text{ M})} = 50.0\text{ mL}$$

Before the equivalence point, the concentration of unreacted Fe^{2+} and the concentration of Fe^{3+} are easy to calculate. For this reason we find the potential using the Nernst equation for the Fe^{3+}/Fe^{2+} half-reaction.

$$E = +0.767\text{ V} - 0.05916 \log \frac{[\text{Fe}^{2+}]}{[\text{Fe}^{3+}]} \tag{10.3.2}$$

For example, the concentrations of Fe^{2+} and Fe^{3+} after adding 10.0 mL of titrant are

$$[\text{Fe}^{2+}] = \frac{(\text{mol Fe}^{2+})_{\text{initial}} - (\text{mol Ce}^{4+})_{\text{added}}}{\text{total volume}} = \frac{M_{\text{Fe}} V_{\text{Fe}} - M_{\text{Ce}} V_{\text{Ce}}}{V_{\text{Fe}} + V_{\text{Ce}}}$$

$$[\text{Fe}^{2+}] = \frac{(0.100\text{ M})(50.0\text{ mL}) - (0.100\text{ M})(10.0\text{ mL})}{50.0\text{ mL} + 10.0\text{ mL}} = 6.67 \times 10^{-2}\text{ M}$$

$$[\text{Fe}^{3+}] = \frac{(\text{mol Ce}^{4+})_{\text{added}}}{\text{total volume}} = \frac{M_{\text{Ce}} V_{\text{Ce}}}{V_{\text{Fe}} + V_{\text{Ce}}}$$

$$[\text{Fe}^{3+}] = \frac{(0.100\text{ M})(10.0\text{ mL})}{50.0\text{ mL} + 10.0\text{ mL}} = 1.67 \times 10^{-2}\text{ M}$$

Substituting these concentrations into Equation 10.3.2 gives the potential as

$$E = +0.767\text{ V} - 0.05916 \log \frac{6.67 \times 10^{-2}}{1.67 \times 10^{-2}} = +0.731\text{ V}$$

After the equivalence point, the concentration of Ce^{3+} and the concentration of excess Ce^{4+} are easy to calculate. For this reason we find the potential using the Nernst equation for the Ce^{4+}/Ce^{3+} half-reaction in a manner similar to that used above to calculate potentials before the equivalence point.

$$E = +1.70\text{ V} - 0.05916 \log \frac{[\text{Ce}^{3+}]}{[\text{Ce}^{4+}]} \tag{10.3.3}$$

For example, after adding 60.0 mL of titrant, the concentrations of Ce^{3+} and Ce^{4+} are

$$[\text{Ce}^{3+}] = \frac{(\text{mol Fe}^{2+})_{\text{initial}}}{\text{total volume}} = \frac{M_{\text{Fe}} V_{\text{Fe}}}{V_{\text{Fe}} + V_{\text{Ce}}}$$

$$[\text{Ce}^{3+}] = \frac{(0.100\text{ M})(50.0\text{ mL})}{50.0\text{ mL} + 60.0\text{ mL}} = 4.55 \times 10^{-2}\text{ M}$$

$$[\text{Ce}^{4+}] = \frac{(\text{mol Ce}^{4+})_{\text{added}} - (\text{mol Fe}^{2+})_{\text{initial}}}{\text{total volume}} = \frac{M_{\text{Ce}} V_{\text{Ce}} - M_{\text{Fe}} V_{\text{Fe}}}{V_{\text{Fe}} + V_{\text{Ce}}}$$

$$[\text{Ce}^{4+}] = \frac{(0.100\text{ M})(60.0\text{ mL}) - (0.100\text{ M})(50.0\text{ mL})}{50.0\text{ mL} + 60.0\text{ mL}} = 9.09 \times 10^{-3}\text{ M}$$

Substituting these concentrations into Equation 10.3.3 gives a potential of

$$E = +1.70\text{ V} - 0.05916 \log \frac{4.55 \times 10^{-2}\text{ M}}{9.09 \times 10^{-3}\text{ M}} = +1.66\text{ V}$$

At the titration's equivalence point, the potential, E_{eq}, in Equation 10.3.2 and Equation 10.3.3 are identical. Adding the equations together to gives

$$2E_{eq} = E^{\circ}_{Fe^{3+}/Fe^{2+}} + E^{\circ}_{Ce^{4+}/Ce^{3+}} - 0.05916 \log \frac{[Fe^{2+}][Ce^{3+}]}{[Fe^{3+}][Ce^{4+}]}$$

Because $[Fe^{2+}] = [Ce^{4+}]$ and $[Ce^{3+}] = [Fe^{3+}]$ at the equivalence point, the log term has a value of zero and the equivalence point's potential is

$$E_{eq} = \frac{E^{\circ}_{Fe^{3+}/Fe^{2+}} + E^{\circ}_{Ce^{4+}/Ce^{3+}}}{2} = \frac{0.767\ V + 1.70\ V}{2} = +1.23\ V$$

Additional results for this titration curve are shown in Table 9.4.1 and Figure 9.4.1 .

Table 9.4.1 . Data for the Titration of 50.0 mL of 0.100 M Fe^{2+} with 0.100 M Ce^{4+}

volume of Ce^{4+} (mL)	E (V)	volume of Ce^{4+} (mL)	E (V)
10.0	0.731	60.0	1.66
20.0	0.757	70.0	1.68
30.0	0.777	80.0	1.69
40.0	0.803	90.0	1.69
50.0	1.23	100.0	1.70

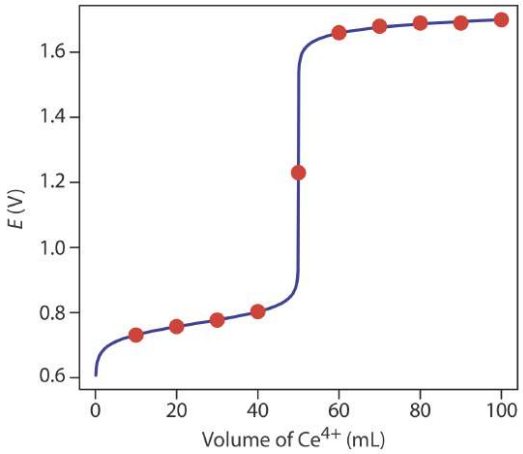


Figure 9.4.1 . Titration curve for the titration of 50.0 mL of 0.100 M Fe^{2+} with 0.100 M Ce^{4+}. The red points correspond to the data in Table 9.4.1 . The blue line shows the complete titration curve.

EXERCISE 9.4.1

Calculate the titration curve for the titration of 50.0 mL of 0.0500 M Sn^{2+} with 0.100 M Tl^{3+}. Both the titrand and the titrant are 1.0 M in HCl. The titration reaction is

$$Sn^{2+}(aq) + Tl^{3+} \rightleftharpoons Tl^{+}(aq) + Sn^{4+}(aq)$$

Answer

The volume of Tl^{3+} needed to reach the equivalence point is

$$V_{eq} = V_{Tl} = \frac{M_{Sn} V_{Sn}}{M_{Tl}} = \frac{(0.050\ M)(50.0\ mL)}{(0.100\ M)} = 25.0\ mL$$

Before the equivalence point, the concentration of unreacted Sn^{2+} and the concentration of Sn^{4+} are easy to calculate. For this reason we find the potential using the Nernst equation for the Sn^{4+}/Sn^{2+} half-reaction. For example, the concentrations of Sn^{2+} and Sn^{4+} after adding 10.0 mL of titrant are

$$[Sn^{2+}] = \frac{(0.050\ M)(50.0\ mL) - (0.100\ M)(10.0\ mL)}{50.0\ mL + 10.0\ mL} = 0.0250\ M$$

$$[Sn^{4+}] = \frac{(0.100\ M)(10.0\ mL)}{50.0\ mL + 10.0\ mL} = 0.0167\ M$$

and the potential is

$$E = +0.139\ \text{V} - \frac{0.05916}{2}\log\frac{0.0250\ \text{M}}{0.0167\ \text{M}} = +0.134\ \text{V}$$

After the equivalence point, the concentration of Tl^+ and the concentration of excess Tl^{3+} are easy to calculate. For this reason we find the potential using the Nernst equation for the Tl^{3+}/Tl^+ half-reaction. For example, after adding 40.0 mL of titrant, the concentrations of Tl^+ and Tl^{3+} are

$$[Tl^+] = \frac{(0.050\ \text{M})(50.0\ \text{mL})}{50.0\ \text{mL} + 40.0\ \text{mL}} = 0.0278\ \text{M}$$

$$[Tl^{3+}] = \frac{(0.100\ \text{M})(40.0\ \text{mL}) - (0.050\ \text{M})(50.0\ \text{mL})}{50.0\ \text{mL} + 40.0\ \text{mL}} = 0.0167\ \text{M}$$

and the potential is

$$E = +0.77\ \text{V} - \frac{0.05916}{2}\log\frac{0.0278\ \text{M}}{0.0167\ \text{M}} = +0.76\ \text{V}$$

At the titration's equivalence point, the potential, E_{eq}, potential is

$$E_{eq} = \frac{0.139\ \text{V} + 0.77\ \text{V}}{2} = +0.45\ \text{V}$$

Some additional results are shown here.

volume of Tl^{3+} (mL)	E (V)	volume of Tl^{3+} (mL)	E (V)
5.00	0.121	30.0	0.75
10.0	0.134	35.0	0.75
15.0	0.144	40.0	0.76
20.0	0.157	45.0	0.76
25.0	0.45		

SKETCHING A REDOX TITRATION CURVE

To evaluate the relationship between a titration's equivalence point and its end point we need to construct only a reasonable approximation of the exact titration curve. In this section we demonstrate a simple method for sketching a redox titration curve. Our goal is to sketch the titration curve quickly, using as few calculations as possible. Let's use the titration of 50.0 mL of 0.100 M Fe^{2+} with 0.100 M Ce^{4+} in a matrix of 1 M $HClO_4$.

> This is the same example that we used in developing the calculations for a redox titration curve. You can review the results of that calculation in Table 9.4.1 and Figure 9.4.1 .

We begin by calculating the titration's equivalence point volume, which, as we determined earlier, is 50.0 mL. Next, we draw our axes, placing the potential, E, on the y-axis and the titrant's volume on the x-axis. To indicate the equivalence point's volume, we draw a vertical line that intersects the x-axis at 50.0 mL of Ce^{4+}. Figure 9.4.2 a shows the result of the first step in our sketch.

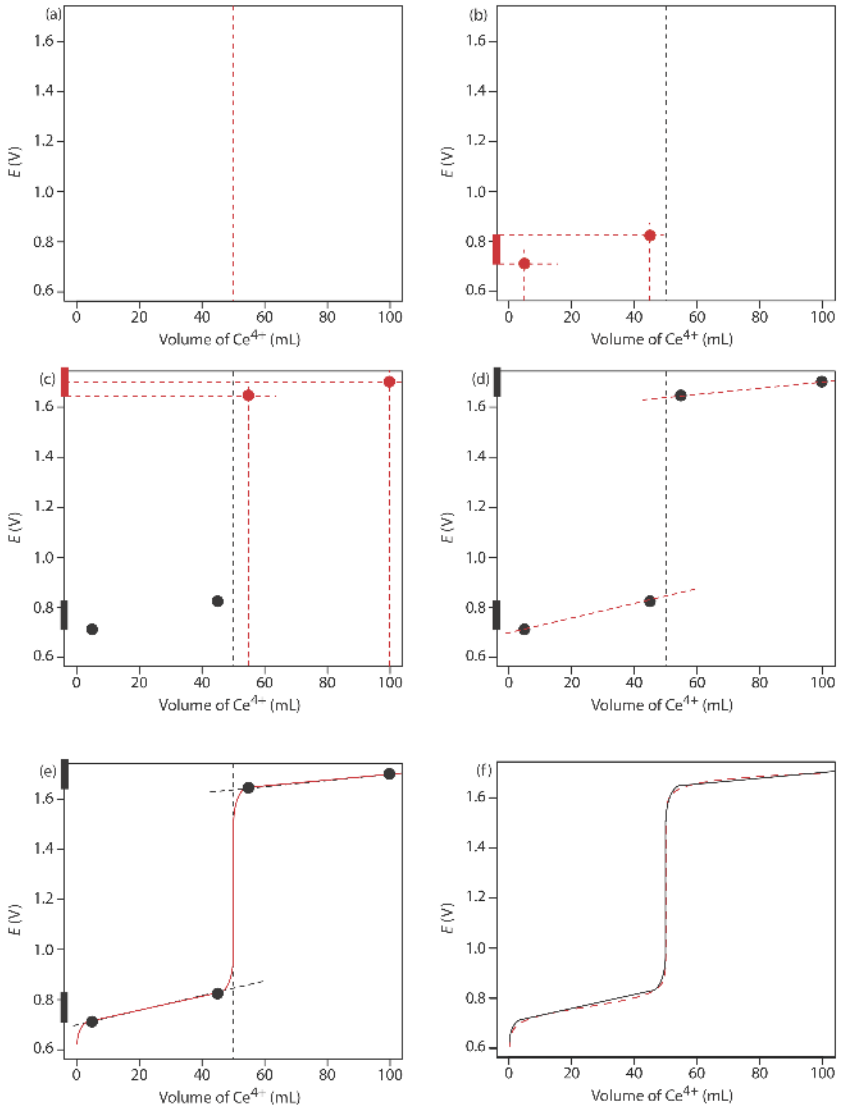


Figure 9.4.2 . Illustrations showing the steps in sketching an approximate titration curve for the titration of 50.0 mL of 0.100 M Fe^{2+} with 0.100 M Ce^{4+} in 1 M $HClO_4$: (a) locating the equivalence point volume; (b) plotting two points before the equivalence point; (c) plotting two points after the equivalence point; (d) preliminary approximation of titration curve using straight-lines; (e) final approximation of titration curve using a smooth curve; (f) comparison of approximate titration curve (solid black line) and exact titration curve (dashed red line). See the text for additional details.

Before the equivalence point, the potential is determined by a redox buffer of Fe^{2+} and Fe^{3+}. Although we can calculate the potential using the Nernst equation, we can avoid this calculation if we make a simple assumption. You may recall from Chapter 6 that a redox buffer operates over a range of potentials that extends approximately ±(0.05916/*n*) unit on either side of $E^{\circ}_{Fe^{3+}/Fe^{2+}}$. The potential at the buffer's lower limit is

$$E = E^{\circ}_{Fe^{3+}/Fe^{2+}} - 0.05916$$

when the concentration of Fe^{2+} is 10× greater than that of Fe^{3+}. The buffer reaches its upper potential of

$$E = E^{\circ}_{Fe^{3+}/Fe^{2+}} + 0.05916$$

when the concentration of Fe^{2+} is 10× smaller than that of Fe^{3+}. The redox buffer spans a range of volumes from approximately 10% of the equivalence point volume to approximately 90% of the equivalence point volume. Figure 9.4.2 b shows the second step in our sketch. First, we superimpose a ladder diagram for Fe on the *y*-axis, using its $E^{\circ}_{Fe^{3+}/Fe^{2+}}$ value of 0.767 V and including the buffer's range of potentials. Next, we add points for the potential at 10% of V_{eq} (a potential of 0.708 V at 5.0 mL) and for the potential at 90% of V_{eq} (a potential of 0.826 V at 45.0 mL).

We used a similar approach when sketching the acid–base titration curve for the titration of acetic acid with NaOH; see Chapter 9.2 for details.

The third step in sketching our titration curve is to add two points after the equivalence point. Here the potential is controlled by a redox buffer of Ce^{3+} and Ce^{4+}. The redox buffer is at its lower limit of

$$E = E^{\circ}_{Ce^{4+}/Ce^{3+}} - 0.05916$$

when the titrant reaches 110% of the equivalence point volume and the potential is $E^{\circ}_{Ce^{4+}/Ce^{3+}}$ when the volume of Ce is $2 \times V_{eq}$.

We used a similar approach when sketching the complexation titration curve for the titration of Mg^{2+} with EDTA; see Chapter 9.3 for details.

Figure 9.4.2 c shows the third step in our sketch. First, we superimpose a ladder diagram for Ce on the *y*-axis, using its $E^{\circ}_{Ce^{4+}/Ce^{3+}}$ value of 1.70 V and including the buffer's range. Next, we add points representing the potential at 110% of V_{eq} (a value of 1.66 V at 55.0 mL) and at 200% of V_{eq} (a value of 1.70 V at 100.0 mL).

Next, we draw a straight line through each pair of points, extending the line through the vertical line that indicates the equivalence point's volume (Figure 9.4.2 d). Finally, we complete our sketch by drawing a smooth curve that connects the three straight-line segments (Figure 9.4.2 e). A comparison of our sketch to the exact titration curve (Figure 9.4.2 f) shows that they are in close agreement.

? EXERCISE 9.4.2

Sketch the titration curve for the titration of 50.0 mL of 0.0500 M Sn^{4+} with 0.100 M Tl^{+}. Both the titrand and the titrant are 1.0 M in HCl. The titration reaction is

$$Sn^{2+}(aq) + Tl^{3+}(aq) \rightleftharpoons Tl^{+}(aq) + Sn^{4+}(aq)$$

Compare your sketch to your calculated titration curve from Exercise 9.4.1 .

Answer

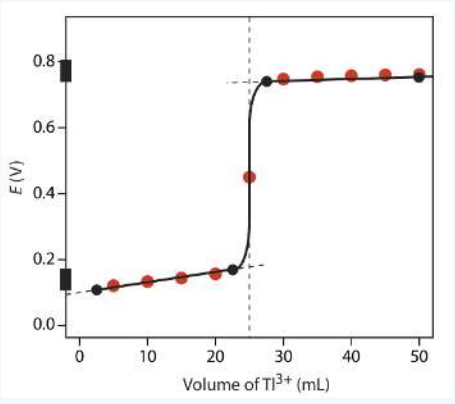
The figure below shows a sketch of the titration curve. The two points before the equivalence point

V_{Tl} = 2.5 mL, E = +0.109 V and V_{Tl} = 22.5 mL, E = +0.169 V

are plotted using the redox buffer for Sn^{4+}/Sn^{2+}, which spans a potential range of +0.139 ± 0.5916/2. The two points after the equivalence point

V_{Tl} = 27.5 mL, E = +0.74 V and V_{Tl} = 50 mL, E = +0.77 V

are plotted using the redox buffer for Tl^{3+}/Tl^{+}, which spans the potential range of +0.139 ± 0.5916/2. The black dots and curve are the approximate sketch of the titration curve. The points in red are the calculations from Exercise 9.4.1 .



SELECTING AND EVALUATING THE END POINT

A redox titration's equivalence point occurs when we react stoichiometrically equivalent amounts of titrand and titrant. As is the case for acid–base titrations and complexation titrations, we estimate the equivalence point of a redox titration using an experimental end point. A

variety of methods are available for locating a redox titration's end point, including indicators and sensors that respond to a change in the solution conditions.

WHERE IS THE EQUIVALENCE POINT

For an acid–base titration or a complexometric titration the equivalence point is almost identical to the inflection point on the steeply rising part of the titration curve. If you look back at Figure 9.2.2 and Figure 9.3.3, you will see that the inflection point is in the middle of this steep rise in the titration curve, which makes it relatively easy to find the equivalence point when you sketch these titration curves. We call this a ***symmetric equivalence point***. If the stoichiometry of a redox titration is 1:1—that is, one mole of titrant reacts with each mole of titrand—then the equivalence point is symmetric. If the titration reaction's stoichiometry is not 1:1, then the equivalence point is closer to the top or to the bottom of the titration curve's sharp rise. In this case we have an ***asymmetric equivalence point***.

EXAMPLE 9.4.1

Derive a general equation for the equivalence point's potential when titrating Fe^{2+} with MnO_4^-.

$$5Fe^{2+}(aq) + MnO_4^-(aq) + 8H^+(aq) \rightarrow 5Fe^{3+}(aq) + Mn^{2+}(aq) + 4H_2O(l)$$

Solution

The half-reactions for the oxidation of Fe^{2+} and the reduction of MnO_4^- are

$$Fe^{2+}(aq) \rightarrow Fe^{3+}(aq) + e^-$$

$$MnO_4^-(aq) + 8H^+(aq) + 5e^- \rightarrow Mn^{2+}(aq) + 4H_2O(l)$$

for which the Nernst equations are

$$E = E^\circ_{Fe^{3+}/Fe^{2+}} - 0.5916 \log \frac{[Fe^{2+}]}{[Fe^{3+}]}$$

$$E = E^\circ_{MnO_4^-/Mn^{2+}} - \frac{0.5916}{5} \log \frac{[Mn^{2+}]}{[MnO_4^-][H^+]^8}$$

Before we add together these two equations we must multiply the second equation by 5 so that we can combine the log terms; thus

$$6E_{eq} = E^\circ_{Fe^{3+}/Fe^{2+}} + 5E^\circ_{MnO_4^-/Mn^{2+}} - 0.05916 \log \frac{[Fe^{2+}][Mn^{2+}]}{[Fe^{3+}][MnO_4^-][H^+]^8}$$

At the equivalance point we know that

$$[Fe^{2+}] = 5 \times [MnO_4^-] \text{ and } [Fe^{3+}] = 5 \times [Mn^{2+}]$$

Substituting these equalities into the previous equation and rearranging gives us a general equation for the potential at the equivalence point.

$$6E_{eq} = E^\circ_{Fe^{3+}/Fe^{2+}} + 5E^\circ_{MnO_4^-/Mn^{2+}} - 0.05916 \log \frac{5[MnO_4^-][Mn^{2+}]}{5[Mn^{2+}][MnO_4^-][H^+]^8}$$

$$E_{eq} = \frac{E^\circ_{Fe^{3+}/Fe^{2+}} + 5E^\circ_{MnO_4^-/Mn^{2+}}}{6} - \frac{0.05916}{6} \log \frac{1}{[H^+]^8}$$

$$E_{eq} = \frac{E^\circ_{Fe^{3+}/Fe^{2+}} + 5E^\circ_{MnO_4^-/Mn^{2+}}}{6} + \frac{0.05916 \times 8}{6} \log [H^+]$$

$$E_{eq} = \frac{E^\circ_{Fe^{3+}/Fe^{2+}} + 5E^\circ_{MnO_4^-/Mn^{2+}}}{6} - 0.07888\text{pH}$$

Our equation for the equivalence point has two terms. The first term is a weighted average of the titrand's and the titrant's standard state potentials, in which the weighting factors are the number of electrons in their respective half-reactions. The second term shows that E_{eq} for this titration is pH-dependent. At a pH of 1 (in H_2SO_4), for example, the equivalence point has a potential of

$$E_{eq} = \frac{0.768 + 5 \times 1.51}{6} - 0.07888 \times 1 = 1.31 \text{ V}$$

Figure 9.4.3 shows a typical titration curve for titration of Fe^{2+} with MnO_4^-. Note that the titration's equivalence point is asymmetrical.

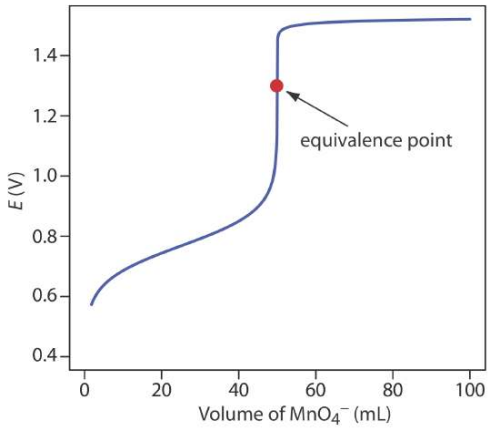


Figure 9.4.3 . Titration curve for the titration of 50.0 mL of 0.100 M Fe^{2+} with 0.0200 M MnO_4^- at a fixed pH of 1 (using H_2SO_4). The equivalence point is shown by the red dot.

EXERCISE 9.4.3

Derive a general equation for the equivalence point's potential for the titration of U^{4+} with Ce^{4+}. The unbalanced reaction is

$$Ce^{4+}(aq) + U^{4+}(aq) \rightarrow UO_2^{2+}(aq) + Ce^{3+}(aq)$$

What is the equivalence point's potential if the pH is 1?

Answer

The two half reactions are

$$Ce^{4+}(aq) + e^- \rightarrow Ce^{3+}(aq)$$

$$U^{4+}(aq) + 2H_2O(l) \rightarrow UO_2^{2+}(aq)) + 4H^+(aq) + 2e^-$$

for which the Nernst equations are

$$E = E^\circ_{Ce^{4+}/Ce^{3+}} - 0.05916 \log \frac{[Ce^{3+}]}{[Ce^{4+}]}$$

$$E = E^\circ_{UO_2^{2+}/U^{4+}} - \frac{0.05916}{2} \log \frac{[U^{4+}]}{[UO_2^{2+}][H^+]^4}$$

Before adding these two equations together we must multiply the second equation by 2 so that we can combine the log terms; thus

$$3E = E^\circ_{Ce^{4+}/Ce^{3+}} + 2E^\circ_{UO_2^{2+}/U^{4+}} - 0.05916 \log \frac{[Ce^{3+}][U^{4+}]}{[Ce^{4+}][UO_2^{2+}][H^+]^4}$$

At the equivalence point we know that

$$[Ce^{3+}] = 2 \times [UO_2^{2+}] \text{ and } [Ce^{4+}] = 2 \times [U^{4+}]$$

Substituting these equalities into the previous equation and rearranging gives us a general equation for the potential at the equivalence point.

$$3E = E^\circ_{Ce^{4+}/Ce^{3+}} + 2E^\circ_{UO_2^{2+}/U^{4+}} - 0.05916 \log \frac{2[UO_2^{2+}][U^{4+}]}{2[U^{4+}][UO_2^{2+}][H^+]^4}$$

$$E = \frac{E^\circ_{Ce^{4+}/Ce^{3+}} + 2E^\circ_{UO_2^{2+}/U^{4+}}}{3} - \frac{0.05916}{3} \log \frac{1}{[H^+]^4}$$

$$E = \frac{E^\circ_{Ce^{4+}/Ce^{3+}} + 2E^\circ_{UO_2^{2+}/U^{4+}}}{3} + \frac{0.05916 \times 4}{3} \log [H^+]^4$$

$$E = \frac{E^\circ_{Ce^{4+}/Ce^{3+}} + 2E^\circ_{UO_2^{2+}/U^{4+}}}{3} - 0.07888\text{pH}$$

At a pH of 1 the equivalence point has a potential of

$$E = \frac{1.72 + 2 \times 0.327}{3} - 0.07888 \times 1 = +0.712\text{ V}$$

FINDING THE END POINT WITH AN INDICATOR

Three types of indicators are used to signal a redox titration's end point. The oxidized and reduced forms of some titrants, such as MnO_4^-, have different colors. A solution of MnO_4^- is intensely purple. In an acidic solution, however, permanganate's reduced form, Mn^{2+}, is nearly colorless. When using MnO_4^- as a titrant, the titrand's solution remains colorless until the equivalence point. The first drop of excess MnO_4^- produces a permanent tinge of purple, signaling the end point.

Some indicators form a colored compound with a specific oxidized or reduced form of the titrant or the titrand. Starch, for example, forms a dark purple complex with I_3^-. We can use this distinct color to signal the presence of excess I_3^- as a titrant—a change in color from colorless to purple—or the completion of a reaction that consumes I_3^- as the titrand— a change in color from purple to colorless. Another example of a specific indicator is thiocyanate, SCN^-, which forms the soluble red-colored complex of $Fe(SCN)^{2+}$ in the presence of Fe^{3+}.

The most important class of indicators are substances that do not participate in the redox titration, but whose oxidized and reduced forms differ in color. When we add a ***redox indicator*** to the titrand, the indicator imparts a color that depends on the solution's potential. As the solution's potential changes with the addition of titrant, the indicator eventually changes oxidation state and changes color, signaling the end point.

To understand the relationship between potential and an indicator's color, consider its reduction half-reaction

$$In_{ox} + ne^- \rightleftharpoons In_{red}$$

where In_{ox} and In_{red} are, respectively, the indicator's oxidized and reduced forms.

> For simplicity, In_{ox} and In_{red} are shown without specific charges. Because there is a change in oxidation state, In_{ox} and In_{red} cannot both be neutral.

The Nernst equation for this half-reaction is

$$E = E^\circ_{In_{ox}/In_{red}} - \frac{0.05916}{n}\log\frac{[In_{red}]}{[In_{ox}]}$$

As shown in Figure 9.4.4 , if we assume the indicator's color changes from that of In_{ox} to that of In_{red} when the ratio $[In_{red}]/[In_{ox}]$ changes from 0.1 to 10, then the end point occurs when the solution's potential is within the range

$$E = E^\circ_{In_{ox}/In_{red}} \pm \frac{0.05916}{n}$$

> This is the same approach we took in considering acid–base indicators and complexation indicators.

A partial list of redox indicators is shown in Table 9.4.2 . Examples of an appropriate and an inappropriate indicator for the titration of Fe^{2+} with Ce^{4+} are shown in Figure 9.4.5 .

Table 9.4.2 . Selected Examples of Redox Indicators

indicator	color In_{ox}	color of In_{red}	E^o (V)
indigo tetrasulfate	blue	colorless	0.36
methylene blue	blue	colorless	0.53
diphenylamine	violet	colorless	0.75
diphenylamine sulfonic acid	red-violet	colorless	0.85
tris(2,2'-bipyradine)iron	pale blue	red	1.120
ferroin	pale blue	red	1.147
tris(5-nitro-1,10-phenanthroline)iron	pale blue	red-violet	1.25

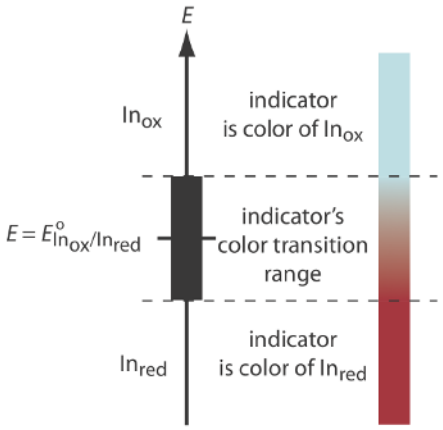


Figure 9.4.4 . Diagram showing the relationship between E and an indicator's color. The ladder diagram defines potentials where In_{red} and In_{ox} are the predominate species.

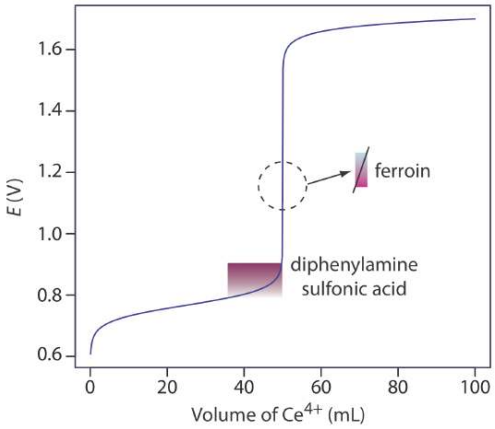


Figure 9.4.5 . Titration curve for titration of 50.0 mL of 0.100 M Fe^{2+} with 0.100 M Ce^{4+}. The end point transitions for the indicators diphenylamine sulfonic acid and ferroin are superimposed on the titration curve. Because the transition for ferroin is too small to see on the scale of the x-axis—it requires only 1–2 drops of titrant—the color change is expanded to the right.

OTHER METHODS FOR FINDING THE END POINT

Another method for locating a redox titration's end point is a potentiometric titration in which we monitor the change in potential while we add the titrant to the titrand. The end point is found by examining visually the titration curve. The simplest experimental design for a potentiometric titration consists of a Pt indicator electrode whose potential is governed by the titrand's or the titrant's redox half-reaction, and a reference electrode that has a fixed potential. Other methods for locating the titration's end point include thermometric titrations and spectrophotometric titrations.

> You will a further discussion of potentiometry in Chapter 11.

REPRESENTATIVE METHOD 9.4.1: DETERMINATION OF TOTAL CHLORINE RESIDUAL

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical redox titrimetric method. Although each method is unique, the following description of the determination of the total chlorine residual in water provides an instructive example of a typical procedure. The description here is based on Method 4500-Cl B as published in *Standard Methods for the Examination of Water and Wastewater*, 20th Ed., American Public Health Association: Washington, D. C., 1998.

Description of the Method

The chlorination of a public water supply produces several chlorine-containing species, the combined concentration of which is called the total chlorine residual. Chlorine is present in a variety of chemical states, including the free residual chlorine, which consists of Cl_2, HOCl and OCl^-, and the combined chlorine residual, which consists of NH_2Cl, $NHCl_2$, and NCl_3. The total chlorine residual is determined by using the oxidizing power of chlorine to convert I^- to I_3^-. The amount of I_3^- formed is then determined by titrating with $Na_2S_2O_3$ using starch as an indicator. Regardless of its form, the total chlorine residual is reported as if Cl_2 is the only source of chlorine, and is reported as mg Cl/L.

Procedure

Select a volume of sample that requires less than 20 mL of $Na_2S_2O_3$ to reach the end point. Using glacial acetic acid, acidify the sample to a pH between 3 and 4, and add about 1 gram of KI. Titrate with $Na_2S_2O_3$ until the yellow color of I_3^- begins to disappear. Add 1 mL of a starch indicator solution and continue titrating until the blue color of the starch–I_3^- complex disappears (Figure 9.4.6). Use a blank titration to correct the volume of titrant needed to reach the end point for reagent impurities.

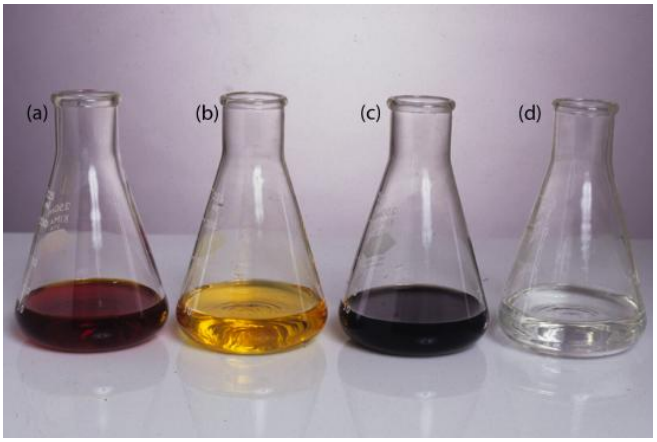


Figure 9.4.6 . Endpoint for the determination of the total chlorine residual. (a) Acidifying the sample and adding KI forms a brown solution of I_3^-. (b) Titrating with $Na_2S_2O_3$ converts I_3^- to I^- with the solution fading to a pale yellow color as we approach the end point. (c) Adding starch forms the deep purple starch–I_3^- complex. (d) As the titration continues, the end point is a sharp transition from a purple to a colorless solution. The change in color from (c) to (d) typically takes 1–2 drops of titrant.

Questions

1. Is this an example of a direct or an indirect analysis?

This is an indirect analysis because the chlorine-containing species do not react with the titrant. Instead, the total chlorine residual oxidizes I^- to I_3^-, and the amount of I_3^- is determined by titrating with $Na_2S_2O_3$.

2. Why does the procedure rely on an indirect analysis instead of directly titrating the chlorine-containing species using KI as a titrant?

Because the total chlorine residual consists of six different species, a titration with I^- does not have a single, well-defined equivalence point. By converting the chlorine residual to an equivalent amount of I_3^-, the indirect titration with $Na_2S_2O_3$ has a single, useful equivalence point. Even if the total chlorine residual is from a single species, such as HOCl, a direct titration with KI is impractical. Because the product of the titration, I_3^-, imparts a yellow color, the titrand's color would change with each addition of titrant, making it difficult to find a suitable indicator.

3. Both oxidizing and reducing agents can interfere with this analysis. Explain the effect of each type of interferent on the total chlorine residual.

An interferent that is an oxidizing agent converts additional I^- to I_3^-. Because this extra I_3^- requires an additional volume of $Na_2S_2O_3$ to reach the end point, we overestimate the total chlorine residual. If the interferent is a reducing agent, it reduces back to I^- some of the I_3^- produced by the reaction between the total chlorine residual and iodide; as a result, we underestimate the total chlorine residual.

QUANTITATIVE APPLICATIONS

Although many quantitative applications of redox titrimetry have been re- placed by other analytical methods, a few important applications continue to find relevance. In this section we review the general application of redox titrimetry with an emphasis on environmental, pharmaceutical, and industrial applications. We begin, however, with a brief discussion of selecting and characterizing redox titrants, and methods for controlling the titrand's oxidation state.

ADJUSTING THE TITRAND'S OXIDATION STATE

If a redox titration is to be used in a quantitative analysis, the titrand initially must be present in a single oxidation state. For example, iron is determined by a redox titration in which Ce^{4+} oxidizes Fe^{2+} to Fe^{3+}. Depending on the sample and the method of sample preparation, iron initially may be present in both the +2 and +3 oxidation states. Before titrating, we must reduce any Fe^{3+} to Fe^{2+} if we want to determine the total concentration of iron in the sample. This type of pretreatment is accomplished using an auxiliary reducing agent or oxidizing agent.

A metal that is easy to oxidize—such as Zn, Al, and Ag—can serve as an ***auxiliary reducing agent***. The metal, as a coiled wire or powder, is added to the sample where it reduces the titrand. Because any unreacted auxiliary reducing agent will react with the titrant, it is removed before we begin the titration by removing the coiled wire or by filtering.

An alternative method for using an auxiliary reducing agent is to immobilize it in a column. To prepare a reduction column an aqueous slurry of the finally divided metal is packed in a glass tube equipped with a porous plug at the bottom. The sample is placed at the top of the

column and moves through the column under the influence of gravity or vacuum suction. The length of the reduction column and the flow rate are selected to ensure the analyte's complete reduction.

Two common reduction columns are used. In the ***Jones reductor*** the column is filled with amalgamated zinc, Zn(Hg), which is prepared by briefly placing Zn granules in a solution of $HgCl_2$. Oxidation of zinc

$$Zn(Hg)(s) \rightarrow Zn^{2+}(aq) + Hg(l) + 2e^-$$

provides the electrons for reducing the titrand. In the ***Walden reductor*** the column is filled with granular Ag metal. The solution containing the titrand is acidified with HCl and passed through the column where the oxidation of silver

$$Ag(s) + Cl^-(aq) \rightarrow AgCl(s) + e^-$$

provides the necessary electrons for reducing the titrand. Table 9.4.3 provides a summary of several applications of reduction columns.

Table 9.4.3 . Examples of Reactions for Reducing a Titrand's Oxidation State Using a Reduction Column

oxidized titrand	Walden reductor	Jones reducator
Cr^{3+}	—	$Cr^{3+}(aq) + e^- \rightarrow Cr^{2+}(aq)$
Cu^{2+}	$Cu^{2+}(aq) + e^- \rightarrow Cu^+(aq)$	$Cu^{2+}(aq) + 2e^- \rightarrow Cu(s)$
Fe^{3+}	$Fe^{3+}(aq) + e^- \rightarrow Fe^{2+}(aq)$	$Fe^{3+}(aq) + e^- \rightarrow Fe^{2+}(aq)$
TiO^{2+}	—	$TiO^{2+}(aq) + 2H^+(aq) + e^- \rightarrow Ti^{3+}(aq) + H_2O(l)$
MoO_4^{2+}	$MoO_2^{2+}(aq) + e^- \rightarrow MoO_2^+(aq)$	$MoO_2^{2+}(aq) + 4H^+(aq) + 3e^- \rightarrow Mo^{3+}(aq) + 2H_2O(l)$
VO_4^+	$VO_2^+(aq) + 2H^+(aq) + e^- \rightarrow VO^{2+}(aq) + H_2O(l)$	$VO_2^+(aq) + 4H^+(aq) + 3e^- \rightarrow V^{2+}(aq) + 2H_2O(l)$

Several reagents are used as ***auxiliary oxidizing agents***, including ammonium peroxydisulfate, $(NH_4)_2S_2O_8$, and hydrogen peroxide, H_2O_2. Peroxydisulfate is a powerful oxidizing agent

$$S_2O_8^{2-}(aq) + 2e^- \rightarrow 2SO_4^{2-}(aq)$$

that is capable of oxidizing Mn^{2+} to MnO_4^-, Cr^{3+} to $Cr_2O_7^{2-}$, and Ce^{3+} to Ce^{4+}. Excess peroxydisulfate is destroyed by briefly boiling the solution. The reduction of hydrogen peroxide in an acidic solution

$$H_2O_2(aq) + 2H^+(aq) + 2e^- \rightarrow 2H_2O(l)$$

provides another method for oxidizing a titrand. Excess H_2O_2 is destroyed by briefly boiling the solution.

SELECTING AND STANDARDIZING A TITRANT

If it is to be used quantitatively, the titrant's concentration must remain stable during the analysis. Because a titrant in a reduced state is susceptible to air oxidation, most redox titrations use an oxidizing agent as the titrant. There are several common oxidizing titrants, including MnO_4^-, Ce^{4+}, $Cr_2O_7^{2-}$, and I_3^-. Which titrant is used often depends on how easily it oxidizes the titrand. A titrand that is a weak reducing agent needs a strong oxidizing titrant if the titration reaction is to have a suitable end point.

The two strongest oxidizing titrants are MnO_4^- and Ce^{4+}, for which the reduction half-reactions are

$$MnO_4^-(aq) + 8H^+(aq) + 5e^- \rightleftharpoons Mn^{2+}(aq) + 4H_2O(l)$$

$$Ce^{4+}(aq) + e^- \rightleftharpoons Ce^{3+}(aq)$$

A solution of Ce^{4+} in 1 M H_2SO_4 usually is prepared from the primary standard cerium ammonium nitrate, $Ce(NO_3)_4 \cdot 2NH_4NO_3$. When prepared using a reagent grade material, such as $Ce(OH)_4$, the solution is standardized against a primary standard reducing agent such as $Na_2C_2O_4$ or Fe^{2+} (prepared from iron wire) using ferroin as an indicator. Despite its availability as a primary standard and its ease of preparation, Ce^{4+} is not used as frequently as MnO_4^- because it is more expensive.

> The standardization reactions are
>
> $$Ce^{4+}(aq) + Fe^{2+}(aq) \rightarrow Fe^{3+}(aq) + Ce^{3+}(aq)$$
>
> $$2Ce^{4+}(aq) + H_2C_2O_4(aq) \rightarrow 2Ce^{3+}(aq) + 2CO_2(g) + 2H^+(aq)$$

A solution of MnO_4^- is prepared from $KMnO_4$, which is not available as a primary standard. An aqueous solution of permanganate is thermodynamically unstable due to its ability to oxidize water.

$$4MnO_4^-(aq) + 2H_2O(l) \rightleftharpoons 4MnO_2(s) + 3O_2(g) + 4OH^-(aq)$$

This reaction is catalyzed by the presence of MnO_2, Mn^{2+}, heat, light, and the presence of acids and bases. A moderately stable solution of permanganate is prepared by boiling it for an hour and filtering through a sintered glass filter to remove any solid MnO_2 that precipitates. Standardization is accomplished against a primary standard reducing agent such as $Na_2C_2O_4$ or Fe^{2+} (prepared from iron wire), with the pink color of excess MnO_4^- signaling the end point. A solution of MnO_4^- prepared in this fashion is stable for 1–2 weeks, although you should recheck the standardization periodically.

The standardization reactions are

$$MnO_4^-(aq) + 5Fe^{2+}(aq) + 8H^+(aq) \rightarrow Mn^{2+}(aq) + 5Fe^{3+}(aq) + 4H_2O(l)$$

$$2MnO_4^-(aq) + 5H_2C_2O_4(aq) + 6H^+(aq) \rightarrow 2Mn^{2+}(aq) + 10CO_2(g) + 8H_2O(l)$$

Potassium dichromate is a relatively strong oxidizing agent whose principal advantages are its availability as a primary standard and its long term stability when in solution. It is not, however, as strong an oxidizing agent as MnO_4^- or Ce^{4+}, which makes it less useful when the titrand is a weak reducing agent. Its reduction half-reaction is

$$Cr_2O_7^{2-}(aq) + 14H^+(aq) + 6e^- \rightleftharpoons 2Cr^{3+}(aq) + 7H_2O(l)$$

Although a solution of $Cr_2O_7^{2-}$ is orange and a solution of Cr^{3+} is green, neither color is intense enough to serve as a useful indicator. Diphenylamine sulfonic acid, whose oxidized form is red-violet and reduced form is colorless, gives a very distinct end point signal with $Cr_2O_7^{2-}$.

Iodine is another important oxidizing titrant. Because it is a weaker oxidizing agent than MnO_4^-, Ce^{4+}, and $Cr_2O_7^{2-}$, it is useful only when the titrand is a stronger reducing agent. This apparent limitation, however, makes I_2 a more selective titrant for the analysis of a strong reducing agent in the presence of a weaker reducing agent. The reduction half-reaction for I_2 is

$$I_2(aq) + 2e^- \rightleftharpoons 2I^-(aq)$$

Because iodine is not very soluble in water, solutions are prepared by adding an excess of I^-. The complexation reaction

$$I_2(aq) + I^-(aq) \rightleftharpoons I_3^-(aq)$$

increases the solubility of I_2 by forming the more soluble triiodide ion, I_3^-. Even though iodine is present as I_3^- instead of I_2, the number of electrons in the reduction half-reaction is unaffected.

$$I_3^-(aq) + 2e^-(aq) \rightleftharpoons 3I^-(aq)$$

Solutions of I_3^- normally are standardized against $Na_2S_2O_3$ using starch as a specific indicator for I_3^-.

The standardization reaction is

$$I_3^-(aq) + 2S_2O_3^{2-}(aq) \rightarrow 3I^-(aq) + 2S_4O_6^{2-}(aq)$$

An oxidizing titrant such as MnO_4^-, Ce^{4+}, $Cr_2O_7^{2-}$, and I_3^-, is used when the titrand is in a reduced state. If the titrand is in an oxidized state, we can first reduce it with an auxiliary reducing agent and then complete the titration using an oxidizing titrant. Alternatively, we can titrate it using a reducing titrant. Iodide is a relatively strong reducing agent that could serve as a reducing titrant except that its solutions are susceptible to the air-oxidation of I^- to I_3^-.

$$3I^-(aq) \rightleftharpoons I_3^-(aq) + 2e^-$$

A freshly prepared solution of KI is clear, but after a few days it may show a faint yellow coloring due to the presence of I_3^-.

Instead, adding an excess of KI reduces the titrand and releases a stoichiometric amount of I_3^-. The amount of I_3^- produced is then determined by a back titration using thiosulfate, $S_2O_3^{2-}$, as a reducing titrant.

$$2S_2O_3^{2-}(aq) \rightleftharpoons S_4O_6^{2-}(aq) + 2e^-$$

Solutions of $S_2O_3^{2-}$ are prepared using $Na_2S_2O_3$•$5H_2O$ and are standardized before use. Standardization is accomplished by dissolving a carefully weighed portion of the primary standard KIO_3 in an acidic solution that contains an excess of KI. The reaction between IO_3^- and I^-

$$IO_3^-(aq) + 8I^-(aq) + 6H^+(aq) \rightarrow 3I_3^-(aq) + 3H_2O(l)$$

liberates a stoichiometric amount of I-3 . By titrating this I_3^- with thiosulfate, using starch as a visual indicator, we can determine the concentration of $S_2O_3^{2-}$ in the titrant.

> The standardization titration is
>
> $$I_3^-(aq) + 2S_2O_3^{2-}(aq) \rightarrow 3I^-(aq) + S_4O_6^{2-}(aq)$$
>
> which is the same reaction used to standardize solutions of I_3^-. This approach to standardizing solutions of $S_2O_2^{3-}$ is similar to that used in the determination of the total chlorine residual outlined in Representative Method 9.4.1.

Although thiosulfate is one of the few reducing titrants that is not readily oxidized by contact with air, it is subject to a slow decomposition to bisulfite and elemental sulfur. If used over a period of several weeks, a solution of thiosulfate is restandardized periodically. Several forms of bacteria are able to metabolize thiosulfate, which leads to a change in its concentration. This problem is minimized by adding a preservative such as HgI_2 to the solution.

Another useful reducing titrant is ferrous ammonium sulfate, $Fe(NH_4)_2(SO_4)_2$•$6H_2O$, in which iron is present in the +2 oxidation state. A solution of Fe^{2+} is susceptible to air-oxidation, but when prepared in 0.5 M H_2SO_4 it remains stable for as long as a month. Periodic restandardization with $K_2Cr_2O_7$ is advisable. Ferrous ammonium sulfate is used as the titrant in a direct analysis of the titrand, or, it is added to the titrand in excess and the amount of Fe^{3+} produced determined by back titrating with a standard solution of Ce^{4+} or $Cr_2O_7^{2-}$.

INORGANIC ANALYSIS

One of the most important applications of redox titrimetry is evaluating the chlorination of public water supplies. Representative Method 9.4.1, for example, describes an approach for determining the total chlorine residual using the oxidizing power of chlorine to oxidize I^- to I_3^-. The amount of I_3^- is determined by back titrating with $S_2O_3^{2-}$.

The efficiency of chlorination depends on the form of the chlorinating species. There are two contributions to the total chlorine residual—the free chlorine residual and the combined chlorine residual. The free chlorine residual includes forms of chlorine that are available for disinfecting the water supply. Examples of species that contribute to the free chlorine residual include Cl_2, HOCl and OCl^-. The combined chlorine residual includes those species in which chlorine is in its reduced form and, therefore, no longer capable of providing disinfection. Species that contribute to the combined chlorine residual are NH_2Cl, $NHCl_2$ and NCl_3.

When a sample of iodide-free chlorinated water is mixed with an excess of the indicator *N*,*N*-diethyl-*p*-phenylenediamine (DPD), the free chlorine oxidizes a stoichiometric portion of DPD to its red-colored form. The oxidized DPD is then back-titrated to its colorless form using ferrous ammonium sulfate as the titrant. The volume of titrant is proportional to the free residual chlorine.

Having determined the free chlorine residual in the water sample, a small amount of KI is added, which catalyzes the reduction of monochloramine, NH_2Cl, and oxidizes a portion of the DPD back to its red-colored form. Titrating the oxidized DPD with ferrous ammonium sulfate yields the amount of NH_2Cl in the sample. The amount of dichloramine and trichloramine are determined in a similar fashion.

The methods described above for determining the total, free, or combined chlorine residual also are used to establish a water supply's chlorine demand. Chlorine demand is defined as the quantity of chlorine needed to react completely with any substance that can be oxidized by chlorine, while also maintaining the desired chlorine residual. It is determined by adding progressively greater amounts of chlorine to a set of samples drawn from the water supply and determining the total, free, or combined chlorine residual.

Another important example of redox titrimetry, which finds applications in both public health and environmental analysis, is the determination of dissolved oxygen. In natural waters, such as lakes and rivers, the level of dissolved O_2 is important for two reasons: it is the most readily available oxidant for the biological oxidation of inorganic and organic pollutants; and it is necessary for the support of aquatic life. In a wastewater treatment plant dissolved O_2 is essential for the aerobic oxidation of waste materials. If the concentration of dissolved O_2 falls below a critical value, aerobic bacteria are replaced by anaerobic bacteria, and the oxidation of organic waste produces undesirable gases, such as CH_4 and H_2S.

One standard method for determining dissolved O_2 in natural waters and wastewaters is the Winkler method. A sample of water is collected without exposing it to the atmosphere, which might change the concentration of dissolved O_2. The sample first is treated with a solution of $MnSO_4$ and then with a solution of NaOH and KI. Under these alkaline conditions the dissolved oxygen oxidizes Mn^{2+} to MnO_2.

$$2Mn^{2+}(aq) + 4OH^-(aq) + O_2(g) \rightarrow 2MnO_2(s) + 2H_2O(l)$$

After the reaction is complete, the solution is acidified with H_2SO_4. Under the now acidic conditions, I^- is oxidized to I_3^- by MnO_2.

$$MnO_2(s) + 3I^-(aq) + 4H^+(aq) \rightarrow Mn^{2+}(aq) + I_3^-(aq) + 2H_2O(l)$$

The amount of I_3^- that forms is determined by titrating with $S_2O_3^{2-}$ using starch as an indicator. The Winkler method is subject to a variety of interferences and several modifications to the original procedure have been proposed. For example, NO_2^- interferes because it reduces I_3^- to I^- under acidic conditions. This interference is eliminated by adding sodium azide, NaN_3, which reduces NO_2^- to N_2. Other reducing agents, such as Fe^{2+}, are eliminated by pretreating the sample with $KMnO_4$ and destroying any excess permanganate with $K_2C_2O_4$.

Another important example of redox titrimetry is the determination of water in nonaqueous solvents. The titrant for this analysis is known as the Karl Fischer reagent and consists of a mixture of iodine, sulfur dioxide, pyridine, and methanol. Because the concentration of pyridine is sufficiently large, I_2 and SO_2 react with pyridine (py) to form the complexes py•I_2 and py•SO_2. When added to a sample that contains water, I_2 is reduced to I^- and SO_2 is oxidized to SO_3.

$$\text{py} \cdot \text{I}_2 + \text{py} \cdot \text{SO}_2 + \text{H}_2\text{O} + 2\text{py} \rightarrow 2\text{py} \cdot \text{HI} + \text{py} \cdot \text{SO}_3$$

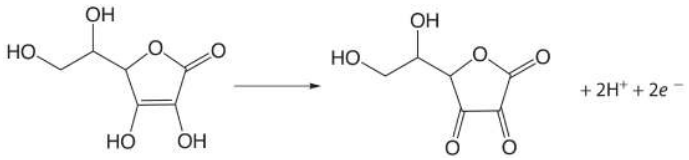
Methanol is included to prevent the further reaction of py•SO_3 with water. The titration's end point is signaled when the solution changes from the product's yellow color to the brown color of the Karl Fischer reagent.

ORGANIC ANALYSIS

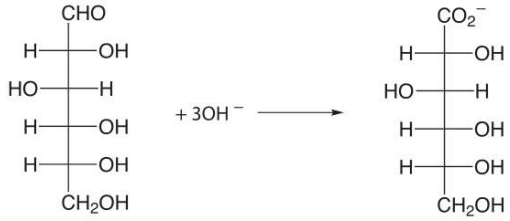
Redox titrimetry also is used for the analysis of organic analytes. One important example is the determination of the chemical oxygen demand (COD) of natural waters and wastewaters. The COD is a measure of the quantity of oxygen necessary to oxidize completely all the organic matter in a sample to CO_2 and H_2O. Because no attempt is made to correct for organic matter that is decomposed biologically, or for slow decomposition kinetics, the COD always overestimates a sample's true oxygen demand. The determination of COD is particularly important in the management of industrial wastewater treatment facilities where it is used to monitor the release of organic-rich wastes into municipal sewer systems or into the environment.

A sample's COD is determined by refluxing it in the presence of excess $K_2Cr_2O_7$, which serves as the oxidizing agent. The solution is acidified with H_2SO_4, using Ag_2SO_4 to catalyze the oxidation of low molecular weight fatty acids. Mercuric sulfate, $HgSO_4$, is added to complex any chloride that is present, which prevents the precipitation of the Ag^+ catalyst as AgCl. Under these conditions, the efficiency for oxidizing organic matter is 95–100%. After refluxing for two hours, the solution is cooled to room temperature and the excess $Cr_2O_7^{2-}$ determined by a back titration using ferrous ammonium sulfate as the titrant and ferroin as the indicator. Because it is difficult to remove completely all traces of organic matter from the reagents, a blank titration is performed. The difference in the amount of ferrous ammonium sulfate needed to titrate the sample and the blank is proportional to the COD.

Iodine has been used as an oxidizing titrant for a number of compounds of pharmaceutical interest. Earlier we noted that the reaction of $S_2O_3^{2-}$ with I_3^- produces the tetrathionate ion, $S_4O_6^{2-}$. The tetrathionate ion is actually a dimer that consists of two thiosulfate ions connected through a disulfide (–S–S–) linkage. In the same fashion, I_3^- is used to titrate mercaptans of the general formula RSH, forming the dimer RSSR as a product. The amino acid cysteine also can be titrated with I_3^-. The product of this titration is cystine, which is a dimer of cysteine. Triiodide also is used for the analysis of ascorbic acid (vitamin C) by oxidizing the enediol functional group to an alpha diketone



and for the analysis of reducing sugars, such as glucose, by oxidizing the aldehyde functional group to a carboxylate ion in a basic solution.



An organic compound that contains a hydroxyl, a carbonyl, or an amine functional group adjacent to an hydoxyl or a carbonyl group can be oxidized using metaperiodate, IO_4^-, as an oxidizing titrant.

$$IO_4^-(aq) + H_2O(l) + 2e^- \rightleftharpoons IO_3^-(aq) + 2OH^-(aq)$$

A two-electron oxidation cleaves the C–C bond between the two functional groups with hydroxyl groups oxidized to aldehydes or ketones, carbonyl groups oxidized to carboxylic acids, and amines oxidized to an aldehyde and an amine (ammonia if a primary amine). The analysis is conducted by adding a known excess of IO_4^- to the solution that contains the analyte and allowing the oxidation to take place for

approximately one hour at room temperature. When the oxidation is complete, an excess of KI is added, which converts any unreacted IO_4^- to IO_3^- and I_3^-.

$$IO_4^-(aq) + 3I^-(aq) + H_2O(l) \rightarrow IO_3^-(aq) + I_3^-(aq) + 2OH^-(aq)$$

The I_3^- is then determined by titrating with $S_2O_3^{2-}$ using starch as an indicator.

QUANTITATIVE CALCULATIONS

The quantitative relationship between the titrand and the titrant is determined by the stoichiometry of the titration reaction. If you are unsure of the balanced reaction, you can deduce its stoichiometry by remembering that the electrons in a redox reaction are conserved.

✔ EXAMPLE 9.4.2

The amount of Fe in a 0.4891-g sample of an ore is determined by titrating with $K_2Cr_2O_7$. After dissolving the sample in HCl, the iron is brought into a +2 oxidation state using a Jones reductor. Titration to the diphenylamine sulfonic acid end point requires 36.92 mL of 0.02153 M $K_2Cr_2O_7$. Report the ore's iron content as %w/w Fe_2O_3.

Solution

Because we are not provided with the titration reaction, we will use a conservation of electrons to deduce the stoichiometry. During the titration the analyte is oxidized from Fe^{2+} to Fe^{3+}, and the titrant is reduced from $Cr_2O_7^{2-}$ to Cr^{3+}. Oxidizing Fe^{2+} to Fe^{3+} requires a single electron. Reducing $Cr_2O_7^{2-}$, in which each chromium is in the +6 oxidation state, to Cr^{3+} requires three electrons per chromium, for a total of six electrons. A conservation of electrons for the titration, therefore, requires that each mole of $K_2Cr_2O_7$ reacts with six moles of Fe^{2+}.

The moles of $K_2Cr_2O_7$ used to reach the end point is

$$(0.02153\ \text{M})(0.03692\ \text{L}) = 7.949 \times 10^{-4}\ \text{mol}\ K_2Cr_2O_7$$

which means the sample contains

$$7.949 \times 10^{-4}\ \text{mol}\ K_2Cr_2O_7 \times \frac{6\ \text{mol}\ Fe^{2+}}{\text{mol}\ K_2Cr_2O_7} = 4.769 \times 10^{-3}\ \text{mol}\ Fe^{2+}$$

Thus, the %w/w Fe_2O_3 in the sample of ore is

$$4.769 \times 10^{-3}\ \text{mol}\ Fe^{2+} \times \frac{1\ \text{mol}\ Fe_2O_3}{2\ \text{mol}\ Fe^{2+}} \times \frac{159.69\text{g}\ Fe_2O_3}{\text{mol}\ Fe_2O_3} = 0.3808\ \text{g}\ Fe_2O_3$$

$$\frac{0.3808\ \text{g}\ Fe_2O_3}{0.4891\ \text{g sample}} \times 100 = 77.86\%\ \text{w/w}\ Fe_2O_3$$

Although we can deduce the stoichiometry between the titrant and the titrand in Example 9.4.2 without balancing the titration reaction, the balanced reaction

$$K_2Cr_2O_7(aq) + 6Fe^{2+}(aq) + 14H^+(aq) \rightarrow 2Cr^{3+}(aq) + 2K^+(aq) + 6Fe^{3+}(aq) + 7H_2O(l)$$

does provide useful information. For example, the presence of H^+ reminds us that the reaction must take place in an acidic solution.

? EXERCISE 9.4.4

The purity of a sample of sodium oxalate, $Na_2C_2O_4$, is determined by titrating with a standard solution of $KMnO_4$. If a 0.5116-g sample requires 35.62 mL of 0.0400 M $KMnO_4$ to reach the titration's end point, what is the %w/w $Na_2C_2O_4$ in the sample.

Answer

Because we are not provided with a balanced reaction, let's use a conservation of electrons to deduce the stoichiometry. Oxidizing $C_2O_4^{2-}$, in which each carbon has a +3 oxidation state, to CO_2, in which carbon has an oxidation state of +4, requires one electron per carbon or a total of two electrons for each mole of $C_2O_4^{2-}$. Reducing MnO_4^-, in which each manganese is in the +7 oxidation state, to Mn^{2+} requires five electrons. A conservation of electrons for the titration, therefore, requires that two moles of $KMnO_4$ (10 moles of e^-) react with five moles of $Na_2C_2O_4$ (10 moles of e^-).

The moles of $KMnO_4$ used to reach the end point is

$$(0.0400\ \text{M}\ KMnO_4)(0.03562\ \text{L}) = 1.42 \times 10^{-3}\ \text{mol}\ KMnO_4$$

which means the sample contains

$$1.42 \times 10^{-3} \text{ mol } KMnO_4 \times \frac{5 \text{ mol } Na_2C_2O_4}{2 \text{ mol } KMnO_4} = 3.55 \times 10^{-3} \text{ mol } Na_2C_2O_4$$

Thus, the %w/w $Na_2C_2O_4$ in the sample of ore is

$$3.55 \times 10^{-3} \text{ mol } Na_2C_2O_4 \times \frac{134.00 \text{ g } Na_2C_2O_4}{\text{mol } Na_2C_2O_4} = 0.476 \text{ g } Na_2C_2O_4$$

$$\frac{0.476 \text{ g } Na_2C_2O_4}{0.5116 \text{ g sample}} \times 100 = 93.0\% \text{ w/w } Na_2C_2O_4$$

As shown in the following two examples, we can easily extend this approach to an analysis that requires an indirect analysis or a back titration.

EXAMPLE 9.4.3

A 25.00-mL sample of a liquid bleach is diluted to 1000 mL in a volumetric flask. A 25-mL portion of the diluted sample is transferred by pipet into an Erlenmeyer flask that contains an excess of KI, reducing the OCl^- to Cl^- and producing I_3^-. The liberated I_3^- is determined by titrating with 0.09892 M $Na_2S_2O_3$, requiring 8.96 mL to reach the starch indicator end point. Report the %w/v NaOCl in the sample of bleach.

Solution

To determine the stoichiometry between the analyte, NaOCl, and the titrant, $Na_2S_2O_3$, we need to consider both the reaction between OCl^- and I^-, and the titration of I_3^- with $Na_2S_2O_3$.

First, in reducing OCl^- to Cl^- the oxidation state of chlorine changes from +1 to –1, requiring two electrons. The oxidation of three I^- to form I_3^- releases two electrons as the oxidation state of each iodine changes from –1 in I^- to –1⁄3 in I_3^-. A conservation of electrons, therefore, requires that each mole of OCl^- produces one mole of I_3^-.

Second, in the titration reaction, I_3^- is reduced to I^- and $S_2O_3^{2-}$ is oxidized to $S_4O_6^{2-}$. Reducing I_3^- to $3I^-$ requires two elections as each iodine changes from an oxidation state of –1⁄3 to –1. In oxidizing $S_2O_3^{2-}$ to $S_4O_6^{2-}$, each sulfur changes its oxidation state from +2 to +2.5, releasing one electron for each $S_2O_3^{2-}$. A conservation of electrons, therefore, requires that each mole of I_3^- reacts with two moles of $S_2O_3^{2-}$.

Finally, because each mole of OCl^- produces one mole of I_3^-, and each mole of I_3^- reacts with two moles of $S_2O_3^{2-}$, we know that every mole of NaOCl in the sample ultimately results in the consumption of two moles of $Na_2S_2O_3$.

The moles of $Na_2S_2O_3$ used to reach the titration's end point is

$$(0.09892 \text{ M})(0.00896 \text{ L}) = 8.86 \times 10^{-4} \text{ mol } Na_2S_2O_3$$

which means the sample contains

$$8.86 \times 10^{-4} \text{ mol } Na_2S_2O_3 \times \frac{1 \text{ mol NaOCl}}{\text{mol } Na_2S_2O_3} \times \frac{74.44 \text{ g NaOCl}}{\text{mol NaOCl}} = 0.03299 \text{ g NaOCl}$$

Thus, the %w/v NaOCl in the diluted sample is

$$\frac{0.03299 \text{ g NaOCl}}{25.00 \text{ mL}} \times 100 = 0.132\% \text{ w/v NaOCl}$$

Because the bleach was diluted by a factor of 40× (25 mL to 1000 mL), the concentration of NaOCl in the bleach is 5.28% w/v.

The balanced reactions for this analysis are:

$$OCl^-(aq) + 3I^-(aq) + 2H^+(aq) \rightarrow I_3^-(aq) + Cl^-(aq) + H_2O(l)$$

$$I_3^-(aq) + 2S_2O_3^{2-}(aq) \rightarrow S_4O_6^{2-}(aq) + 3I^-(aq)$$

EXAMPLE 9.4.4

The amount of ascorbic acid, $C_6H_8O_6$, in orange juice is determined by oxidizing ascorbic acid to dehydroascorbic acid, $C_6H_6O_6$, with a known amount of I_3^-, and back titrating the excess I_3^- with $Na_2S_2O_3$. A 5.00-mL sample of filtered orange juice is treated with 50.00

mL of 0.01023 M I_3^-. After the oxidation is complete, 13.82 mL of 0.07203 M $Na_2S_2O_3$ is needed to reach the starch indicator end point. Report the concentration ascorbic acid in mg/100 mL.

Solution

For a back titration we need to determine the stoichiometry between I_3^- and the analyte, $C_6H_8O_6$, and between I_3^- and the titrant, $Na_2S_2O_3$. The later is easy because we know from Example 9.4.3 that each mole of I_3^- reacts with two moles of $Na_2S_2O_3$.

In oxidizing ascorbic acid to dehydroascorbic acid, the oxidation state of carbon changes from +2⁄3 in $C_6H_8O_6$ to +1 in $C_6H_6O_6$. Each carbon releases 1⁄3 of an electron, or a total of two electrons per ascorbic acid. As we learned in Example 9.4.3 , reducing I_3^- requires two electrons; thus, a conservation of electrons requires that each mole of ascorbic acid consumes one mole of I_3^-.

The total moles of I_3^- that react with $C_6H_8O_6$ and with $Na_2S_2O_3$ is

$$(0.01023\ \text{M})(0.05000\ \text{L}) = 5.115 \times 10^{-4}\ \text{mol}\ I_3^-$$

The back titration consumes

$$0.01382\ \text{L}\ Na_2S_2O_3 \times \frac{0.07203\ \text{mol}\ Na_2S_2O_3}{\text{L}\ Na_2S_2O_3} \times \frac{1\ \text{mol}\ I_3^-}{2\ \text{mol}\ Na_2S_2O_3} = 4.977 \times 10^{-4}\ \text{mol}\ I_3^-$$

Subtracting the moles of I_3^- that react with $Na_2S_2O_3$ from the total moles of I_3^- gives the moles reacting with ascorbic acid.

$$5.115 \times 10^{-4}\ \text{mol}\ I_3^- - 4.977 \times 10^{-4}\ \text{mol}\ I_3^- = 1.38 \times 10^{-5}\ \text{mol}\ I_3^-$$

The grams of ascorbic acid in the 5.00-mL sample of orange juice is

$$1.38 \times 10^{-5}\ \text{mol}\ I_3^- \times \frac{1\ \text{mol}\ C_6H_8O_6}{\text{mol}\ I_3^-} \times \frac{176.12\ \text{g}\ C_6H_8O_6}{\text{mol}\ C_6H_8O_6} = 2.43 \times 10^{-3}\ \text{g}\ C_6H_8O_6$$

There are 2.43 mg of ascorbic acid in the 5.00-mL sample, or 48.6 mg per 100 mL of orange juice.

The balanced reactions for this analysis are:

$$C_6H_8O_6(aq) + I_3^-(aq) \rightarrow 3I^-(aq) + C_6H_6O_6(aq) + 2H^+(aq)$$

$$I_3^-(aq) + 2S_2O_3^{2-}(aq) \rightarrow S_4O_6^{2-}(aq) + 3I^-(aq)$$

? EXERCISE 9.4.5

A quantitative analysis for ethanol, C_2H_6O, is accomplished by a redox back titration. Ethanol is oxidized to acetic acid, $C_2H_4O_2$, using excess dichromate, $Cr_2O_7^{2-}$, which is reduced to Cr^{3+}. The excess dichromate is titrated with Fe^{2+}, giving Cr^{3+} and Fe^{3+} as products. In a typical analysis, a 5.00-mL sample of a brandy is diluted to 500 mL in a volumetric flask. A 10.00-mL sample is taken and the ethanol is removed by distillation and collected in 50.00 mL of an acidified solution of 0.0200 M K_2Cr_2O7. A back titration of the unreacted $Cr_2O_7^{2-}$ requires 21.48 mL of 0.1014 M Fe^{2+}. Calculate the %w/v ethanol in the brandy.

Answer

For a back titration we need to determine the stoichiometry between $Cr_2O_7^{2-}$ and the analyte, C_2H_6O, and between $Cr_2O_7^{2-}$ and the titrant, Fe^{2+}. In oxidizing ethanol to acetic acid, the oxidation state of carbon changes from –2 in C_2H_6O to 0 in $C_2H_4O_2$. Each carbon releases two electrons, or a total of four electrons per C_2H_6O. In reducing $Cr_2O_7^{2-}$, in which each chromium has an oxidation state of +6, to Cr^{3+}, each chromium loses three electrons, for a total of six electrons per $Cr_2O_7^{2-}$. Oxidation of Fe^{2+} to Fe^{3+} requires one electron. A conservation of electrons requires that each mole of $K_2Cr_2O_7$ (6 moles of e^-) reacts with six moles of Fe^{2+} (6 moles of e^-), and that four moles of $K_2Cr_2O_7$ (24 moles of e^-) react with six moles of C_2H_6O (24 moles of e^-).

The total moles of $K_2Cr_2O_7$ that react with C_2H_6O and with Fe^{2+} is

$$(0.0200\ \text{M}\ K_2Cr_2O_7)(0.05000\ \text{L}) = 1.00 \times 10^{-3}\ \text{mol}\ K_2Cr_2O_7$$

The back titration with Fe^{2+} consumes

$$(0.1014\ \text{M}\ Fe^{2+})(0.02148\ \text{L}) \times \frac{1\ \text{mol}\ K_2Cr_2O_7}{6\ \text{mol}\ Fe^{2+}} = 3.63 \times 10^{-4}\ \text{mol}\ K_2Cr_2O_7$$

Subtracting the moles of $K_2Cr_2O_7$ that react with Fe^{2+} from the total moles of $K_2Cr_2O_7$ gives the moles that react with the analyte.

$$(1.00 \times 10^{-3}\ \text{mol}\ K_2Cr_2O_7) - (3.63 \times 10^{-4}\ \text{mol}\ K_2Cr_2O_7) = 6.37 \times 10^{-4}\ \text{mol}\ K_2Cr_2O_7$$

The grams of ethanol in the 10.00-mL sample of diluted brandy is

$$6.37 \times 10^{-4}\ \text{mol}\ K_2Cr_2O_7 \times \frac{6\ \text{mol}\ C_2H_6O}{4\ \text{mol}\ K_2Cr_2O_7} \times \frac{46.07\ \text{g}\ C_2H_6O}{\text{mol}\ C_2H_6O} = 0.0440\ \text{g}\ C_2H_6O$$

The %w/v C_2H_6O in the brandy is

$$\frac{0.0440\ \text{g}\ C_2H_6O}{10.0\ \text{mL diluted brandy}} \times \frac{500.0\ \text{mL diluted brandy}}{5.00\ \text{mL brandy}} \times 100 = 44.0\%\ \text{w/v}\ C_2H_6O$$

EVALUATION OF REDOX TITRIMETRY

The scale of operations, accuracy, precision, sensitivity, time, and cost of a redox titration are similar to those described earlier in this chapter for an acid–base or a complexation titration. As with an acid–base titration, we can extend a redox titration to the analysis of a mixture of analytes if there is a significant difference in their oxidation or reduction potentials. Figure 9.4.7 shows an example of the titration curve for a mixture of Fe^{2+} and Sn^{2+} using Ce^{4+} as the titrant. A titration of a mixture of analytes is possible if their standard state potentials or formal potentials differ by at least 200 mV.

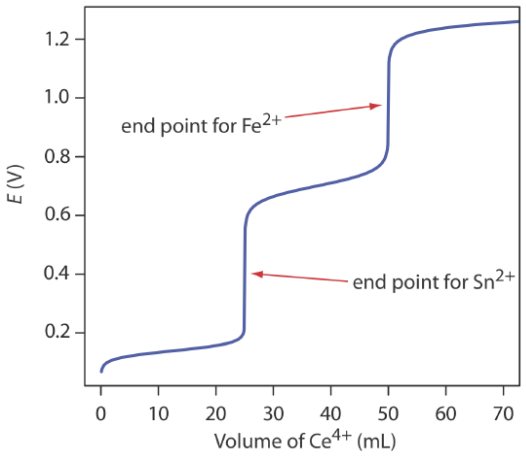


Figure 9.4.7 . Titration curve for the titration of 50.0 mL of 0.0125 M Sn^{2+} and 0.0250 M Fe^{2+} with 0.050 M Ce^{4+}. Both the titrand and the titrant are 1M in HCl.

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10.4: PROBLEMS

1. Identify the anode and the cathode for the following electrochemical cells, and identify the oxidation or the reduction reaction at each electrode.

(a) Pt| $FeCl_2$ (*aq*, 0.015), $FeCl_3$ (*aq*, 0.045) || $AgNO_3$ (*aq*, 0.1) | Ag

(b) Ag | AgBr(*s*), NaBr (*aq*, 1.0) || $CdCl_2$ (*aq*, 0.05) | Cd

(c) Pb | $PbSO_4$ (*s*), H_2SO_4 (*aq*, 1.5) || H_2SO_4 (*aq*, 2.0), $PbSO_4$ (*s*) | PbO_2

2. Calculate the potential for each electrochemical cell in problem 1. The values in parentheses are the activities of the associated species.

3. Calculate the activity of KI, *x*, in the following electrochemical cell if the potential is +0.294 V.

$$\text{Ag} \mid \text{AgCl}\ (s), \text{NaCl}\ (aq, 0.1) \parallel \text{KI}\ (\text{aq}, x), \text{I}_2\ (s) \mid \text{Pt}$$

4. What reaction prevents us from using Zn as an electrode of the first kind in an acidic solution? Which other metals do you expect to behave in the same manner as Zn when immersed in an acidic solution?

5. Creager and colleagues designed a salicylate ion-selective electrode using a PVC membrane impregnated with tetraalkylammonium salicylate [Creager, S. E.; Lawrence, K. D.; Tibbets, C. R. *J. Chem. Educ.* **1995**, *72*, 274–276]. To determine the ion-selective electrode's selectivity coefficient for benzoate, they prepared a set of salicylate calibration standards in which the concentration of benzoate was held constant at 0.10 M. Using the following data, determine the value of the selectivity coefficient.

[salicylate] (M)	potential (mV)
1.0	20.2
1.0×10^{-1}	73.5
1.0×10^{-2}	126
1.0×10^{-3}	168
1.0×10^{-4}	182
1.0×10^{-5}	182
1.0×10^{-6}	177

What is the maximum acceptable concentration of benzoate if you plan to use this ion-selective electrode to analyze a sample that contains as little as 10^{-5} M salicylate with an accuracy of better than 1%?

6. Watanabe and co-workers described a new membrane electrode for the determination of cocaine, a weak base alkaloid with a pK_a of 8.64 [Watanabe, K.; Okada, K.; Oda, H.; Furuno, K.; Gomita, Y.; Katsu, T. *Anal. Chim. Acta* **1995**, *316*, 371–375]. The electrode's response for a fixed concentration of cocaine is independent of pH in the range of 1–8, but decreases sharply above a pH of 8. Offer an explanation for this pH dependency.

7. Figure 11.2.14 shows a schematic diagram for an enzyme electrode that responds to urea by using a gas-sensing NH_3 electrode to measure the amount of ammonia released following the enzyme's reaction with urea. In turn, the NH_3 electrode uses a pH electrode to monitor the change in pH due to the ammonia. The response of the urea electrode is given by equation 11.2.12. Beginning with equation 11.2.19, which gives the potential of a pH electrode, show that equation 11.2.12 for the urea electrode is correct.

8. Explain why the response of an NH_3-based urea electrode (Figure 11.2.14 and equation 11.2.12) is different from the response of a urea electrode in which the enzyme is coated on the glass membrane of a pH electrode (Figure 11.2.15 and equation 11.2.13).

9. A potentiometric electrode for HCN uses a gas-permeable membrane, a buffered internal solution of 0.01 M $KAg(CN)_2$, and a Ag_2S ISE electrode that is immersed in the internal solution. Consider the equilibrium reactions that take place within the internal solution and derive an equation that relates the electrode's potential to the concentration of HCN in the sample. To check your work, search on-line for US Patent 3859191 and consult Figure 2.

10. Mifflin and associates described a membrane electrode for the quantitative analysis of penicillin in which the enzyme penicillinase is immobilized in a polyacrylamide gel coated on the glass membrane of a pH electrode [Mifflin, T. E.; Andriano, K. M.; Robbins, W. B. *J. Chem. Educ.* **1984**, *61*, 638–639]. The following data were collected using a set of penicillin standards.

[penicillin] (M)	potential (mV)
1.0×10^{-2}	220
2.0×10^{-3}	204
1.0×10^{-3}	190
2.0×10^{-4}	153
1.0×10^{-4}	135
1.0×10^{-5}	96
1.0×10^{-6}	80

(a) Over what range of concentrations is there a linear response?

(b) What is the calibration curve's equation for this concentration range?

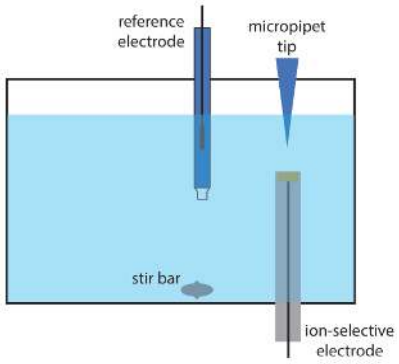
(c) What is the concentration of penicillin in a sample that yields a potential of 142 mV?

11. An ion-selective electrode can be placed in a flow cell into which we inject samples or standards. As the analyte passes through the cell, a potential spike is recorded instead of a steady-state potential. The concentration of K^+ in serum has been determined in this fashion using standards prepared in a matrix of 0.014 M NaCl [Meyerhoff, M. E.; Kovach, P. M. *J. Chem. Educ.* **1983**, *9*, 766–768].

$[K^+]$ (mM)	*E* (arb. units)	$[K^+]$ (mM)	*E* (arb. units)
0.10	25.5	0.60	58.7
0.20	37.2	0.80	64.0
0.40	50.8	1.00	66.8

A 1.00-mL sample of serum is diluted to volume in a 10-mL volumetric flask and analyzed, giving a potential of 51.1 (arbitrary units). Report the concentration of K^+ in the sample of serum.

12. Wang and Taha described an interesting application of potentiometry, which they call batch injection [Wang, J.; Taha, Z. *Anal. Chim. Acta* **1991**, *252*, 215–221]. As shown in the figure below, an ion-selective electrode is placed in an inverted position in a large volume tank, and a fixed volume of a sample or a standard solution is injected toward the electrode's surface using a micropipet. The response of the electrode is a spike in potential that is proportional to the analyte's concentration. The following data were collected using a pH electrode and a set of pH standards.



pH	potential (mV)
2.0	+300
3.0	+240
4.0	+168
5.0	+81
6.0	+35
8.0	–92
9.0	–168
10.0	–235
11.0	–279

Determine the pH of the following samples given the recorded peak potentials: tomato juice, 167 mV; tap water, –27 mV; coffee, 122 mV.

13. The concentration of NO_3^- in a water sample is determined by a one-point standard addition using a NO_3^- ion-selective electrode. A 25.00-mL sample is placed in a beaker and a potential of 0.102 V is measured. A 1.00-mL aliquot of a 200.0-mg/L standard solution of NO_3^- is added, after which the potential is 0.089 V. Report the mg NO_3^-/L in the water sample.

14. In 1977, when I was an undergraduate student at Knox College, my lab partner and I completed an experiment to determine the concentration of fluoride in tap water and the amount of fluoride in toothpaste. The data in this problem are from my lab notebook.

(a) To analyze tap water, we took three 25.0-mL samples and added 25.0 mL of TISAB to each. We measured the potential of each solution using a F^- ISE and an SCE reference electrode. Next, we made five 1.00-mL additions of a standard solution of 100.0 ppm F^- to each sample, and measured the potential after each addition, recording the potential three times.

mL of standard added	potential (mV), replicate 1	potential (mV), replicate 2	potential (mV), replicate 3
0.00	–79	–82	–83
1.00	–119	–119	–118
2.00	–133	–133	–133
3.00	–142	–142	–142
4.00	–149	–148	–148
5.00	–154	–153	–153

Report the parts-per-million of F^- in the tap water.

(b) To analyze the toothpaste, we measured 0.3619 g into a 100-mL volumetric flask, added 50.0 mL of TISAB, and diluted to volume with distilled water. After we ensured that the sample was thoroughly mixed, we transferred three 20.0-mL portions into separate beakers and measured the potential of each using a F^- ISE and an SCE reference electrode. Next, we made five 1.00-mL additions of a standard solution of 100.0 ppm F^- to each sample, and measured the potential after each addition, recording the potential three times.

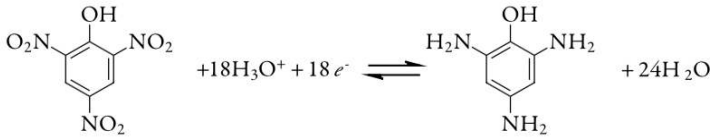
mL of standard added	potential (mV), replicate 1	potential (mV), replicate 2	potential (mV), replicate 3
0.00	–55	–54	–55
1.00	–82	–82	–83
2.00	–94	–94	–94
3.00	–102	–103	–102
4.00	–108	–108	–109
5.00	–112	–112	–113

Report the parts-per-million F^- in the toothpaste.

15. You are responsible for determining the amount of KI in iodized salt and decide to use an I^- ion-selective electrode. Describe how you would perform this analysis using external standards and how you would per-form this analysis using the method of standard additions.

16. Explain why each of the following decreases the analysis time in controlled-potential coulometry: a larger surface area for the working electrode; a smaller volume of solution; and a faster stirring rate.

17. The purity of a sample of picric acid, $C_6H_3N_3O_7$, is determined by controlled-potential coulometry, converting picric acid to triaminophenol, $C_6H_9N_3O$.



A 0.2917-g sample of picric acid is placed in a 1000-mL volumetric flask and diluted to volume. A 10.00-mL portion of this solution is transferred to a coulometric cell and sufficient water added so that the Pt cathode is immersed. An exhaustive electrolysis of the sample requires 21.67 C of charge. Report the purity of the picric acid.

18. The concentration of H_2S in the drainage from an abandoned mine is determined by a coulometric titration using KI as a mediator and I_3^- as the titrant.

$$H_2S(aq) + I_3^-(aq) + 2H_2O(l) \rightleftharpoons 2H_3O^+(aq) + 3I^-(aq) + S(s)$$

A 50.00-mL sample of water is placed in a coulometric cell, along with an excess of KI and a small amount of starch as an indicator. Electrolysis is carried out at a constant current of 84.6 mA, requiring 386 s to reach the starch end point. Report the concentration of H_2S in the sample in μg/mL.

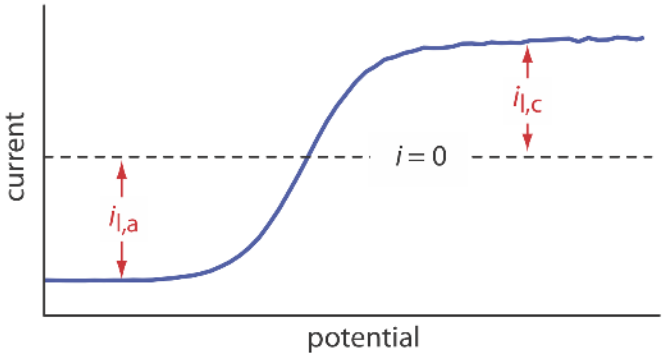
19. One method for the determination of a given mass of H_3AsO_3 is a coulometric titration using I_3^- as a titrant. The relevant standard-state reactions and potentials are summarized here

$$H_3AsO_4(aq) + 2H^+(aq) + 2e^- \rightleftharpoons H_3AsO_3(aq) + H_2O(l)$$
$$I_3^-(aq) + 2e^- \rightleftharpoons 3I^-(aq)$$

with standard state reduction potentials of, respectively, +0.559 V and +0.536 V. Explain why the coulometric titration is carried out in a neutral solution (pH ≈ 7) instead of in a strongly acidic solution (pH < 0).

20. The production of adiponitrile, $NC(CH_2)_4CN$, from acrylonitrile, CH_2=CHCN, is an important industrial process. A 0.594-g sample of acrylonitrile is placed in a 1-L volumetric flask and diluted to volume. An exhaustive controlled-potential electrolysis of a 1.00-mL portion of the diluted acrylonitrile requires 1.080 C of charge. What is the value of *n* for the reduction of acrylonitrile to adiponitrile?

21. The linear-potential scan hydrodynamic voltammogram for a mixture of Fe^{2+} and Fe^{3+} is shown in the figure below where $i_{l,a}$ and $i_{l,c}$ are the anodic and cathodic limiting currents.



(a) Show that the potential is given by

$$E = E^{\circ}_{Fe^{3+}/Fe^{2+}} - 0.05916 \log \frac{K_{Fe^{3+}}}{K_{Fe^{2+}}} - 0.05916 \log \frac{i - i_{l,a}}{i_{l,c} - i}$$

(b) What is the potential when i = 0 for a solution that is 0.100 mM Fe^{3+} and 0.050 mM Fe^{2+}?

22. The amount of sulfur in aromatic monomers is determined by differential pulse polarography. Standard solutions are prepared for analysis by dissolving 1.000 mL of the purified monomer in 25.00 mL of an electrolytic solvent, adding a known amount of sulfur, deaerating, and measuring the peak current. The following results were obtained for a set of calibration standards.

µg S added	peak current (µA)
0	0.14
28	0.70
56	1.23
112	2.41
168	3.42

Analysis of a 1.000-mL sample, treated in the same manner as the standards, gives a peak current of 1.77 µA. Report the mg S/mL in the sample.

23. The purity of a sample of $K_3Fe(CN)_6$ is determined using linear-potential scan hydrodynamic voltammetry at a glassy carbon electrode. The following data were obtained for a set of external calibration standards.

$[K_3Fe(CN)_6]$ (mM)	limiting current (µA)
2.0	127
4.0	252
6.0	376
8.0	500
10.0	624

A sample of impure $K_3Fe(CN)_6$ is prepared for analysis by diluting a 0.246-g portion to volume in a 100-mL volumetric flask. The limiting current for the sample is 444 µA. Report the purity of this sample of $K_3Fe(CN)_6$.

24. One method for determining whether an individual recently fired a gun is to look for traces of antimony in residue collected from the individual's hands. Anodic stripping voltammetry at a mercury film electrode is ideally suited for this analysis. In a typical analysis a sample is collected from a suspect using a cotton-tipped swab wetted with 5% v/v HNO_3. After returning to the lab, the swab is placed in a vial that contains 5.0 mL of 4 M HCl that is 0.02 M in hydrazine sulfate. After soaking the swab, a 4.0-mL portion of the solution is transferred to an electrochemical cell along with 100 µL of 0.01 M $HgCl_2$. After depositing the thin film of mercury and the antimony, the stripping step gives a peak current of 0.38 µA. After adding a standard addition of 100 µL of 5.00×10^2 ppb Sb, the peak current increases to 1.14 µA. How many nanograms of Sb were collected from the suspect's hand?

25. Zinc is used as an internal standard in an analysis of thallium by differential pulse polarography. A standard solution of 5.00×10^{-5} M Zn^{2+} and 2.50×10^{-5} M Tl^{+} has peak currents of 5.71 µA and 3.19 µA, respectively. An 8.713-g sample of a zinc-free alloy is dissolved in acid, transferred to a 500-mL volumetric flask, and diluted to volume. A 25.0-mL portion of this solution is mixed with 25.0 mL of 5.00×10^{-4} M Zn^{2+}. Analysis of this solution gives peak currents of 12.3 µA and of 20.2 µA for Zn^{2+} and Tl^{+}, respectively. Report the %w/w Tl in the alloy.

26. Differential pulse voltammetry at a carbon working electrode is used to determine the concentrations of ascorbic acid and caffeine in drug formulations [Lau, O.; Luk, S.; Cheung, Y. *Analyst* **1989**, *114*, 1047–1051]. In a typical analysis a 0.9183-g tablet is crushed and ground into a fine powder. A 0.5630-g sample of this powder is transferred to a 100-mL volumetric flask, brought into solution, and diluted to volume. A 0.500-mL portion of this solution is then transferred to a voltammetric cell that contains 20.00 mL of a suitable supporting electrolyte. The resulting voltammogram gives peak currents of 1.40 μA and 3.88 μA for ascorbic acid and for caffeine, respectively. A 0.500-mL aliquot of a standard solution that contains 250.0 ppm ascorbic acid and 200.0 ppm caffeine is then added. A voltammogram of this solution gives peak currents of 2.80 μA and 8.02 μA for ascorbic acid and caffeine, respectively. Report the milligrams of ascorbic acid and milligrams of caffeine in the tablet.

27. Ratana-ohpas and co-workers described a stripping analysis method for determining tin in canned fruit juices [Ratana-ohpas, R.; Kanatharana, P.; Ratana-ohpas, W.; Kongsawasdi, W. *Anal. Chim. Acta* **1996**, *333*, 115–118]. Standards of 50.0 ppb Sn^{4+}, 100.0 ppb Sn^{4+}, and 150.0 ppb Sn^{4+} were analyzed giving peak currents (arbitrary units) of 83.0, 171.6, and 260.2, respectively. A 2.00-mL sample of lychee juice is mixed with 20.00 mL of 1:1 HCl/HNO_3. A 0.500-mL portion of this mixture is added to 10 mL of 6 M HCl and the volume adjusted to 30.00 mL. Analysis of this diluted sample gave a signal of 128.2 (arbitrary units). Report the parts-per-million Sn^{4+} in the original sample of lychee juice.

28. Sittampalam and Wilson described the preparation and use of an amperometric sensor for glucose [Sittampalam, G.; Wilson, G. S. *J. Chem. Educ.* **1982**, *59*, 70–73]. The sensor is calibrated by measuring the steady-state current when it is immersed in standard solutions of glucose. A typical set of calibration data is shown here.

[glucose] (mg/100 mL)	current (arb. units)
2.0	17.2
4.0	32.9
6.0	52.1
8.0	68.0
10.0	85.8

A 2.00-mL sample is diluted to 10 mL in a volumetric flask and a steady-state current of 23.6 (arbitrary units) is measured. What is the concentration of glucose in the sample in mg/100 mL?

29. Differential pulse polarography is used to determine the concentrations of lead, thallium, and indium in a mixture. Because the peaks for lead and thallium, and for thallium and indium overlap, a simultaneous analysis is necessary. Peak currents (in arbitrary units) at –0.385 V, –0.455 V, and –0.557 V are measured for a single standard solution, and for a sample, giving the results shown in the following table. Report the mg/mL of Pb^{2+}, Tl^{+} and In^{3+} in the sample.

analyte	[standard] (μg/mL)	peak current at –0.385 V	peak current at –0.455 V	peak current at –0.557 V
Pb^{2+}	1.0	26.1	2.9	0
Tl^{+}	2.0	7.8	23.5	3.2
In^{3+}	0.4	0	0	22.9
sample		60.6	28.8	54.1

30. Abass and co-workers developed an amperometric biosensor for NH_4^+ that uses the enzyme glutamate dehydrogenase to catalyze the following reaction

$$2\text{-oxyglutarate}\,(aq) + \mathrm{NH_4^+}(aq) + \mathrm{NADH}(aq) \rightleftharpoons \text{glutamate}\,(aq) + \mathrm{NAD^+}(aq) + \mathrm{H_2O}(l)$$

where NADH is the reduced form of nicotinamide adenine dinucleotide [Abass, A. K.; Hart, J. P.; Cowell, D. C.; Chapell, A. *Anal. Chim. Acta* **1988**, *373*, 1–8]. The biosensor actually responds to the concentration of NADH, however, the rate of the reaction depends on the concentration of NH_4^+. If the initial concentrations of 2-oxyglutarate and NADH are the same for all samples and standards, then the signal is proportional to the concentration of NH_4^+. As shown in the following table, the sensitivity of the method is dependent on pH.

pH	sensitivity (nA S^{-1} M^{-1})
6.2	1.67×10^3
6.75	5.00×10^3
7.3	9.33×10^3
7.7	1.04×10^4
8.3	1.27×10^4
9.3	2.67×10^3

Two possible explanations for the effect of pH on the sensitivity of this analysis are the acid–base chemistry of NH_4^+ and the acid–base chemistry of the enzyme. Given that the pK_a for NH_4^+ is 9.244, explain the source of this pH-dependent sensitivity.

31. The speciation scheme for trace metals in Table 11.4.2 divides them into seven operationally defined groups by collecting and analyzing two samples following each of four treatments, requiring a total of eight samples and eight measurements. After removing insoluble particulates by filtration (treatment 1), the solution is analyzed for the concentration of ASV labile metals and for the total concentration of metals. A portion of the filtered solution is then passed through an ion-exchange column (treatment 2), and the concentrations of ASV metal and of total metal are determined. A second portion of the filtered solution is irradiated with UV light (treatment 3), and the concentrations of ASV metal and of total metal are measured. Finally, a third portion of the filtered solution is irradiated with UV light and passed through an ion-exchange column (treatment 4), and the concentrations of ASV labile metal and of total metal again are determined. The groups that are included in each measurement are summarized in the following table.

treatment	groups removed by treatement	groups contributing to ASV-labile metals	groups contributing to total metals
1	none	I, II, III	I, II, III, IV, V, VI, VII
2	I, IV, V	II, III	II, III, V1, VII
3	none	I, II, III, IV, VI	I, II, III, IV, V, VI, VII
4	I, II, IV, V, VI	III	III, VII

(a) Explain how you can use these eight measurements to determine the concentration of metals present in each of the seven groups identified in Table 11.4.2.

(b) Batley and Florence report the following results for the speciation of cadmium, lead, and copper in a sample of seawater [Batley, G. E.; Florence, T. M. *Anal. Lett.* **1976**, *9*, 379–388]. Determine the speciation of each metal in comment on your results.

measurement treatement: ASV-labile or total	ppb Cd^{2+}	ppb Pb^{2+}	ppb Cu^{2+}
1: ASV-labile	0.24	0.39	0.26
2: total	0.28	0.50	0.40
2: ASV-labile	0.21	0.33	0.17
2: total	0.26	0.43	0.24
3: ASV-labile	0.26	0.37	0.33
3: total	0.28	0.5	0.43
4: ASV-labile	0.00	0.00	0.00
4: total	0.02	0.12	0.10

32. The concentration of Cu^{2+} in seawater is determined by anodic stripping voltammetry at a hanging mercury drop electrode after first releasing any copper bound to organic matter. To a 20.00-mL sample of seawater is added 1 mL of 0.05 M HNO_3 and 1 mL of 0.1% H_2O_2. The sample is irradiated with UV light for 8 hr and then diluted to volume in a 25-mL volumetric flask. Deposition of Cu^{2+} takes place at –0.3 V versus an SCE for 10 min, producing a peak current of 26.1 (arbitrary units). A second 20.00-mL sample of the seawater is treated identically, except that 0.1 mL of a 5.00 μM solution of Cu^{2+} is added, producing a peak current of 38.4 (arbitrary units). Report the concentration of Cu^{2+} in the seawater in mg/L.

33. Thioamide drugs are determined by cathodic stripping analysis [Davidson, I. E.; Smyth, W. F. Anal. Chem. 1977, 49, 1195–1198]. Deposition occurs at +0.05 V versus an SCE. During the stripping step the potential is scanned cathodically and a stripping peak is observed at –0.52 V. In a typical application a 2.00-mL sample of urine is mixed with 2.00 mL of a pH 4.78 buffer. Following a 2.00 min deposition, a peak current of 0.562 μA is measured. A 0.10-mL addition of a 5.00 μM solution of the drug is added to the same solution. A peak current of 0.837 μA is recorded using the same deposition and stripping conditions. Report the drug's molar concentration in the urine sample.

34. The concentration of vanadium (V) in sea water is determined by adsorptive stripping voltammetry after forming a complex with catechol [van der Berg, C. M. G.; Huang, Z. Q. *Anal. Chem.* **1984**, *56*, 2383–2386]. The catechol-V(V) complex is deposited on a hanging mercury drop electrode at a potential of –0.1 V versus a Ag/AgCl reference electrode. A cathodic potential scan gives a stripping peak that is proportional to the concentration of V(V). The following standard additions are used to analyze a sample of seawater.

$[V(V)]_{added}$ (M)	peak current (μA)
2.0×10^{-8}	24
4.0×10^{-8}	33
8.0×10^{-8}	52
1.2×10^{-7}	69
1.8×10^{-7}	97
2.8×10^{-7}	140

Determine the molar concentration of V (V) in the sample of sea water, assuming that the standard additions result in a negligible change in the sample's volume.

35. The standard-state reduction potential for Cu^{2+} to Cu is +0.342 V versus the SHE. Given that Cu^{2+} forms a very stable complex with the ligand EDTA, do you expect that the standard-state reduction potential for $Cu(EDTA)^{2-}$ is greater than +0.342 V, less than +0.342 V, or equal to +0.342 V? Explain your reasoning.

36. The polarographic half-wave potentials (versus the SCE) for Pb^{2+} and for Tl^{+} in 1 M HCl are, respectively, –0.44 V and –0.45 V. In an electrolyte of 1 M NaOH, however, the half-wave potentials are –0.76 V for Pb^{2+} and –0.48 V for Tl^{+}. Why does the change in electrolyte have such a significant effect on the half-wave potential for Pb^{2+}, but not on the half-wave potential for Tl^{+}?

37. The following data for the reduction of Pb^{2+} were collected by normal-pulse polarography.

potential (V vs. SCE)	current (μA)
–0.345	0.16
–0.370	0.98
–0.383	2.05
–0.393	3.13
–0.409	4.62
–0.420	5.16

The limiting current was 5.67 μA. Verify that the reduction reaction is reversible and determine values for n and $E_{1/2}$. The half-wave potentials for the normal-pulse polarograms of Pb^{2+} in the presence of several different concentrations of OH^{-} are shown in the following table.

$[OH^{-}]$ (M)	$E_{1/2}$ (V vs. SCE)	$[OH^{-}]$ (M)	$E_{1/2}$ (V vs. SCE)
0.050	–0.646	0.150	–0.689
0.100	–0.673	0.300	–0.715

Determine the stoichiometry of the Pb-hydroxide complex and its formation constant.

38. In 1977, when I was an undergraduate student at Knox College, my lab partner and I completed an experiment to study the voltammetric behavior of Cd^{2+} (in 0.1 M KNO_3) and Ni^{2+} (in 0.2 M KNO_3) at a dropping mercury electrode. The data in this problem are from my lab notebook. All potentials are relative to an SCE reference electrode.

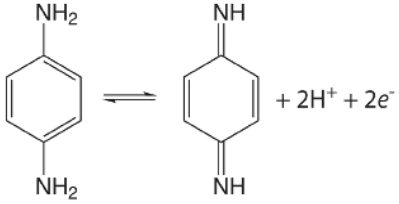
potential for Cd^{2+} (V)	current for Cd^{2+} (μA)	potential for Ni^{2+} (V)	current for Ni^{2+} (μA)
–0.60	4.5	–1.07	1.90
–0.58	3.4	–1.05	1.75
–0.56	2.1	–1.03	1.50
–0.54	0.6	–1.02	1.25
–0.52	0.2	–1.00	1.00

The limiting currents for Cd^{2+} was 4.8 μA and that for Ni^{2+} was 2.0 μA. Evaluate the electrochemical reversibility for each metal ion and comment on your results.

39. Baldwin and co-workers report the following data from a cyclic voltammetry study of the electrochemical behavior of *p*-phenylenediamine in a pH 7 buffer [Baldwin, R. P.; Ravichandran, K.; Johnson, R. K. *J. Chem. Educ.* **1984**, *61*, 820–823]. All potentials are measured relative to an SCE.

scan rate (mV/s)	$E_{p,a}$ (V)	$E_{p,c}$ (V)	$i_{p,a}$ (mA)	$i_{p,c}$ (mA)
2	0.148	0.104	0.34	0.30
5	0.149	0.098	0.56	0.53
10	0.152	0.095	1.00	0.04
20	0.161	0.095	1.44	1.44
50	0.167	0.082	2.12	1.81
100	0.180	0.063	2.50	2.19

The initial scan is toward more positive potentials, leading to the oxidation reaction shown here.



Use this data to show that the reaction is electrochemically irreversible. A reaction may show electrochemical irreversibility because of slow electron transfer kinetics or because the product of the oxidation reaction participates in a chemical reaction that produces an nonelectroactive species. Based on the data in this problem, what is the likely source of *p*-phenylenediamine's electrochemical irreversibility?

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10.5: ADDITIONAL RESOURCES

The following set of experiments introduce students to the applications of electrochemistry. Experiments are grouped into four categories: general electrochemistry, preparation of electrodes, potentiometry, coulometry, and voltammetry and amperometry.

General Electrochemistry

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Preparation of Electrodes

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Potentiometry

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Coulometry

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10.6: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

In this chapter we introduced three electrochemical methods of analysis: potentiometry, coulometry, and voltammetry. In potentiometry we measure the potential at an indicator electrode without allowing any significant current to pass through the electrochemical cell, and use the Nernst equation to calculate the analyte's activity after accounting for junction potentials.

There are two broad classes of potentiometric electrodes: metallic electrodes and membrane electrodes. The potential of a metallic electrode is the result of a redox reaction at the electrode's surface. An electrode of the first kind responds to the concentration of its cation in solution; thus, the potential of a Ag wire is determined by the activity of Ag^+ in solution. If another species is in equilibrium with the metal ion, the electrode's potential also responds to the concentration of that species. For example, the potential of a Ag wire in a solution of $Cl^–$ responds to the concentration of $Cl^–$ because the relative concentrations of Ag^+ and $Cl^–$ are fixed by the solubility product for AgCl. We call this an electrode of the second kind.

The potential of a membrane electrode is determined by a difference in the composition of the solution on each side of the membrane. Electrodes that use a glass membrane respond to ions that bind to negatively charged sites on the membrane's surface. A pH electrode is one example of a glass membrane electrode. Other kinds of membrane electrodes include those that use insoluble crystalline solids or liquid ion-exchangers incorporated into a hydrophobic membrane. The $F^–$ ion-selective electrode, which uses a single crystal of LaF_3 as the ion-selective membrane, is an example of a solid-state electrode. The Ca^{2+} ion-selective electrode, in which the chelating ligand di-(*n*-decyl)phosphate is immobilized in a PVC membrane, is an example of a liquid-based ion-selective electrode.

Potentiometric electrodes are designed to respond to molecules by using a chemical reaction that produces an ion whose concentration is determined using a traditional ion-selective electrode. A gas-sensing electrode, for example, includes a gas permeable membrane that isolates the ion-selective electrode from the gas. When a gas-phase analyte diffuses across the membrane it alters the composition of the inner solution, which is monitored with an ion-selective electrode. An enzyme electrodes operate in the same way.

Coulometric methods are based on Faraday's law that the total charge or current passed during an electrolysis is proportional to the amount of reactants and products participating in the redox reaction. If the electrolysis is 100% efficient—which means that only the analyte is oxidized or reduced—then we can use the total charge or total current to determine the amount of analyte in a sample. In controlled-potential coulometry we apply a constant potential and measure the resulting current as a function of time. In controlled-current coulometry the current is held constant and we measure the time required to completely oxidize or reduce the analyte.

In voltammetry we measure the current in an electrochemical cell as a function of the applied potential. There are several different voltammetric methods that differ in terms of the choice of working electrode, how we apply the potential, and whether we include convection (stirring) as a means for transporting of material to the working electrode.

Polarography is a voltammetric technique that uses a mercury electrode and an unstirred solution. Normal polarography uses a dropping mercury electrode, or a static mercury drop electrode, and a linear potential scan. Other forms of polarography include normal pulse polarography, differential pulse polarography, staircase polarography, and square-wave polarography, all of which use a series of potential pulses.

In hydrodynamic voltammetry the solution is stirred using either a magnetic stir bar or by rotating the electrode. Because the solution is stirred a dropping mercury electrode is not used; instead we use a solid electrode. Both linear potential scans and potential pulses can be applied.

In stripping voltammetry the analyte is deposited on the electrode, usually as the result of an oxidation or reduction reaction. The potential is then scanned, either linearly or using potential pulses, in a direction that removes the analyte by a reduction or oxidation reaction.

Amperometry is a voltammetric method in which we apply a constant potential to the electrode and measure the resulting current. Amperometry is most often used in the construction of chemical sensors for the quantitative analysis of single analytes. One important example is the Clark O_2 electrode, which responds to the concentration of dissolved O_2 in solutions such as blood and water.

KEY TERMS

amalgam	amperometry	anode
anodic current	asymmetry potential	auxiliary electrode
cathode	cathodic current	charging current
controlled-current coulometry	controlled-potential coulometry	convection
coulometric titrations	coulometry	counter electrode
current efficiency	cyclic voltammetry	diffusion
diffusion layer	dropping mercury electrode	electrical double layer
electrochemically irreversible	electrochemically reversible	electrode of the first kind
electrode of the second kind	electrochemistry	electrogravimetry
enzyme electrodes	faradaic current	Faraday's law
galvanostat	gas-sensing electrode	glass electrode
hanging mercury drop electrode	hydrodynamic voltammetry	indicator electrode
ionophore	ion selective electrode	junction potential
limiting current	liquid-based ion-selective electrode	mass transport
mediator	membrane potential	mercury film electrode
migration	nonfaradaic current	Ohm's law
overpotential	peak current	polarography
potentiometer	potentiostat	pulse polarography
redox electrode	reference electrode	residual current
salt bridge	saturated calomel electrode	selectivity coefficient
silver/silver chloride electrode	solid-state ion-selective electrodes	standard hydrogen electrode
static mercury drop electrode	stripping voltammetry	total ionic strength adjustment buffer
voltammetry	voltammogram	working electrode

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CHAPTER OVERVIEW

11: SPECTROSCOPIC METHODS

An early example of a colorimetric analysis is Nessler's method for ammonia, which was introduced in 1856. Nessler found that adding an alkaline solution of HgI_2 and KI to a dilute solution of ammonia produced a yellow-to-reddish brown colloid, in which the colloid's color depended on the concentration of ammonia. By visually comparing the color of a sample to the colors of a series of standards, Nessler was able to determine the concentration of ammonia. Colorimetry, in which a sample absorbs visible light, is one example of a spectroscopic method of analysis. At the end of the nineteenth century, spectroscopy was limited to the absorption, emission, and scattering of visible, ultraviolet, and infrared electromagnetic radiation. Since then, spectroscopy has expanded to include other forms of electromagnetic radiation—such as X-rays, microwaves, and radio waves—and other energetic particles—such as electrons and ions.

11.1: Overview of Spectroscopy
11.2: Spectroscopy Based on Absorption
11.3: UV/Vis and IR Spectroscopy
11.4: Atomic Absorption Spectroscopy
11.5: Emission Spectroscopy
11.6: Photoluminescent Spectroscopy
11.7: Atomic Emission Spectroscopy
11.8: Spectroscopy Based on Scattering
11.9: Problems
11.10: Additional Resources
11.11: Chapter Summary and Key Terms

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11.1: OVERVIEW OF SPECTROSCOPY

The focus of this chapter is on the interaction of ultraviolet, visible, and infrared radiation with matter. Because these techniques use optical materials to disperse and focus the radiation, they often are identified as optical spectroscopies. For convenience we will use the simpler term spectroscopy in place of optical ***spectroscopy***; however, you should understand we will consider only a limited piece of what is a much broader area of analytical techniques.

Despite the difference in instrumentation, all spectroscopic techniques share several common features. Before we consider individual examples in greater detail, let's take a moment to consider some of these similarities. As you work through the chapter, this overview will help you focus on the similarities between different spectroscopic methods of analysis. You will find it easier to understand a new analytical method when you can see its relationship to other similar methods.

WHAT IS ELECTROMAGNETIC RADIATION?

Electromagnetic radiation—light—is a form of energy whose behavior is described by the properties of both waves and particles. Some properties of electromagnetic radiation, such as its refraction when it passes from one medium to another (Figure 10.1.1), are explained best when we describe light as a wave. Other properties, such as absorption and emission, are better described by treating light as a particle. The exact nature of electromagnetic radiation remains unclear, as it has since the development of quantum mechanics in the first quarter of the 20th century [Home, D.; Gribbin, J. *New Scientist* 1991, 2 Nov. 30–33]. Nevertheless, this dual model of wave and particle behavior provide a useful description for electromagnetic radiation.



Figure 10.1.1 . The Golden Gate bridge as seen through rain drops. Refraction of light by the rain drops produces the distorted images. Source: Brocken Inaglory (commons. Wikipedia.org).

WAVE PROPERTIES OF ELECTROMAGNETIC RADIATION

Electromagnetic radiation consists of oscillating electric and magnetic fields that propagate through space along a linear path and with a constant velocity. In a vacuum, electromagnetic radiation travels at the speed of light, c, which is 2.99792×10^8 m/s. When electromagnetic radiation moves through a medium other than a vacuum, its velocity, v, is less than the speed of light in a vacuum. The difference between v and c is sufficiently small (<0.1%) that the speed of light to three significant figures, 3.00×10^8 m/s, is accurate enough for most purposes.

The oscillations in the electric field and the magnetic field are perpendicular to each other and to the direction of the wave's propagation. Figure 10.1.2 shows an example of plane-polarized electromagnetic radiation, which consists of a single oscillating electric field and a single oscillating magnetic field.

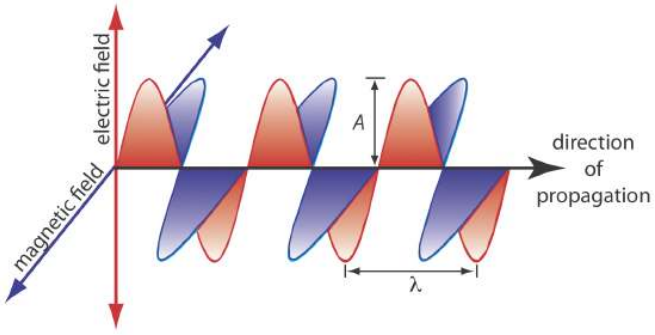


Figure 10.1.2 . Plane-polarized electromagnetic radiation showing the oscillating electric field in blue and the oscillating magnetic field in red. The radiation's amplitude, A, and its wavelength, λ, are shown. Normally, electromagnetic radiation is unpolarized, with oscillating electric and magnetic fields present in all possible planes perpendicular to the direction of propagation.

An electromagnetic wave is characterized by several fundamental properties, including its velocity, amplitude, frequency, phase angle, polarization, and direction of propagation [Ball, D. W. *Spectroscopy* **1994**, *9(5)*, 24–25]. For example, the amplitude of the oscillating

electric field at any point along the propagating wave is

$$A_t = A_e \sin(2\pi\nu t + \Phi)$$

where A_t is the magnitude of the electric field at time t, A_e is the electric field's maximum ***amplitude***, ν is the wave's ***frequency***—the number of oscillations in the electric field per unit time—and Φ is a ***phase angle*** that accounts for the fact that A_t need not have a value of zero at t = 0. The identical equation for the magnetic field is

$$A_t = A_m \sin(2\pi\nu t + \Phi)$$

where A_m is the magnetic field's maximum amplitude.

Other properties also are useful for characterizing the wave behavior of electromagnetic radiation. The ***wavelength***, λ, is defined as the distance between successive maxima (see Figure 10.1.2). For ultraviolet and visible electromagnetic radiation the wavelength usually is expressed in nanometers (1 nm = 10^{-9} m), and for infrared radiation it is expressed in microns (1 mm = 10^{-6} m). The relationship between wavelength and frequency is

$$\lambda = \frac{c}{\nu}$$

Another unit useful unit is the ***wavenumber***, $\bar{\nu}$, which is the reciprocal of wavelength

$$\bar{\nu} = \frac{1}{\lambda}$$

Wavenumbers frequently are used to characterize infrared radiation, with the units given in cm^{-1}.

When electromagnetic radiation moves between different media—for example, when it moves from air into water—its frequency, ν, remains constant. Because its velocity depends upon the medium in which it is traveling, the electromagnetic radiation's wavelength, λ, changes. If we replace the speed of light in a vacuum, c, with its speed in the medium, v, then the wavelength is

$$\lambda = \frac{v}{\nu}$$

This change in wavelength as light passes between two media explains the refraction of electromagnetic radiation shown in Figure 10.1.1 .

EXAMPLE 10.1.1

In 1817, Josef Fraunhofer studied the spectrum of solar radiation, observing a continuous spectrum with numerous dark lines. Fraunhofer labeled the most prominent of the dark lines with letters. In 1859, Gustav Kirchhoff showed that the D line in the sun's spectrum was due to the absorption of solar radiation by sodium atoms. The wavelength of the sodium D line is 589 nm. What are the frequency and the wavenumber for this line?

Solution

The frequency and wavenumber of the sodium D line are

$$\nu = \frac{c}{\lambda} = \frac{3.00 \times 10^8 \text{ m/s}}{589 \times 10^{-9} \text{ m}} = 5.09 \times 10^{14} \text{ s}^{-1}$$

$$\bar{\nu} = \frac{1}{\lambda} = \frac{1}{589 \times 10^{-9} \text{ m}} \times \frac{1 \text{ m}}{100 \text{ cm}} = 1.70 \times 10^4 \text{ cm}^{-1}$$

EXERCISE 10.1.1

Another historically important series of spectral lines is the Balmer series of emission lines from hydrogen. One of its lines has a wavelength of 656.3 nm. What are the frequency and the wavenumber for this line?

Answer

The frequency and wavenumber for the line are

$$\nu = \frac{c}{\lambda} = \frac{3.00 \times 10^8 \text{ m/s}}{656.3 \times 10^{-9} \text{ m}} = 4.57 \times 10^{14} \text{ s}^{-1}$$

$$\bar{\nu} = \frac{1}{\lambda} = \frac{1}{656.3 \times 10^{-9}\ \text{m}} \times \frac{1\ \text{m}}{100\ \text{cm}} = 1.524 \times 10^{4}\ \text{cm}^{-1}$$

PARTICLE PROPERTIES OF ELECTROMAGNETIC RADIATION

When matter absorbs electromagnetic radiation it undergoes a change in energy. The interaction between matter and electromagnetic radiation is easiest to understand if we assume that radiation consists of a beam of energetic particles called photons. When a ***photon*** is absorbed by a sample it is "destroyed" and its energy acquired by the sample [Ball, D. W. *Spectroscopy* **1994**, *9(6)* 20–21]. The energy of a photon, in joules, is related to its frequency, wavelength, and wavenumber by the following equalities

$$E = h\nu = \frac{hc}{\lambda} = hc\bar{\nu}$$

where *h* is Planck's constant, which has a value of 6.626×10^{-34} Js.

EXAMPLE 10.1.2

What is the energy of a photon from the sodium D line at 589 nm?

Solution

The photon's energy is

$$E = \frac{hc}{\lambda} = \frac{\left(6.626 \times 10^{-34}\ \text{Js}\right)\left(3.00 \times 10^{8}\ \text{m/s}\right)}{589 \times 10^{-7}\ \text{m}} = 3.37 \times 10^{-19}\ \text{J}$$

EXERCISE 10.1.2

What is the energy of a photon for the Balmer line at a wavelength of 656.3 nm?

Answer

The photon's energy is

$$E = \frac{hc}{\lambda} = \frac{\left(6.626 \times 10^{-34}\ \text{Js}\right)\left(3.00 \times 10^{8}\ \text{m/s}\right)}{656.3 \times 10^{-9}\ \text{m}} = 3.03 \times 10^{-19}\ \text{J}$$

THE ELECTROMAGNETIC SPECTRUM

The frequency and the wavelength of electromagnetic radiation vary over many orders of magnitude. For convenience, we divide electromagnetic radiation into different regions—the ***electromagnetic spectrum***—based on the type of atomic or molecular transitions that gives rise to the absorption or emission of photons (Figure 10.1.3). The boundaries between the regions of the electromagnetic spectrum are not rigid and overlap between spectral regions is possible.

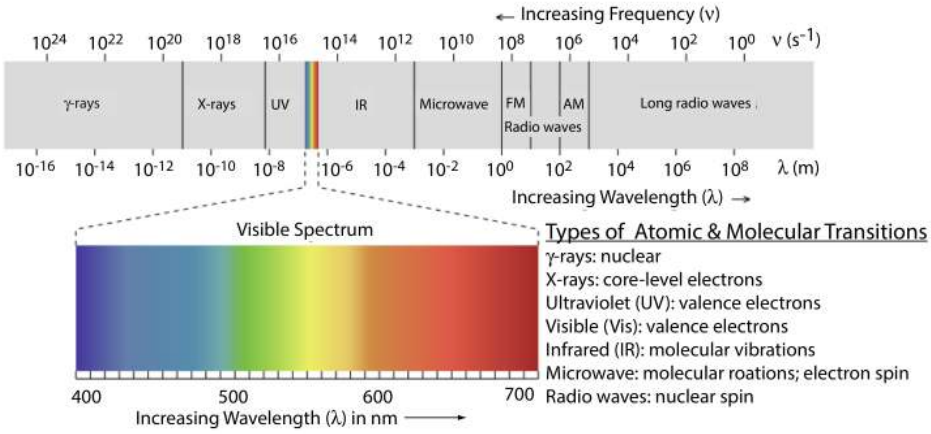


Figure 10.1.3 . The electromagnetic spectrum showing the boundaries between different regions and the type of atomic or molecular transitions responsible for the change in energy. The colored inset shows the visible spectrum. Source: modified from Zedh (www.commons.Wikipedia.org).

PHOTONS AS A SIGNAL SOURCE

In the previous section we defined several characteristic properties of electromagnetic radiation, including its energy, velocity, amplitude, frequency, phase angle, polarization, and direction of propagation. A spectroscopic measurement is possible only if the photon's interaction with the sample leads to a change in one or more of these characteristic properties.

We will divide spectroscopy into two broad classes of techniques. In one class of techniques there is a transfer of energy between the photon and the sample. Table 10.1.1 provides a list of several representative examples.

Table 10.1.1 . Examples of Spectroscopic Techniques That Involve an Exchange of Energy Between a Photon and the Sample

type of energy transfer	region of electromagnetic spectrum	spectroscopic technique
absorption	γ-ray	Mossbauer spectroscopy
	X-ray	X-ray absorption spectroscopy
	UV/Vis	*UV/Vis spectroscopy*
	IR	*infrared spectroscopy*
	microwave	raman spectroscopy
	radio wave	electron spin resonance nuclear magnetic resonance
emission (thermal excitation)	UV/Vis	*atomic emission spectroscopy*
photoluminescence	X-ray	X-ray fluorescence
	UV/Vis	*fluorescence spectroscopy* *phosphorescence spectroscopy* atomic fluorescence spectroscopy
chemiluminescence	UV/Vis	chemiluminescence spectroscopy
techniques discussed in this chapter are shown in *italics*		

In absorption spectroscopy a photon is absorbed by an atom or molecule, which undergoes a transition from a lower-energy state to a higher-energy, or excited state (Figure 10.1.4). The type of transition depends on the photon's energy. The electromagnetic spectrum in Figure 10.1.3 , for example, shows that absorbing a photon of visible light promotes one of the atom's or molecule's valence electrons to a higher-energy level. When an molecule absorbs infrared radiation, on the other hand, one of its chemical bonds experiences a change in vibrational energy.

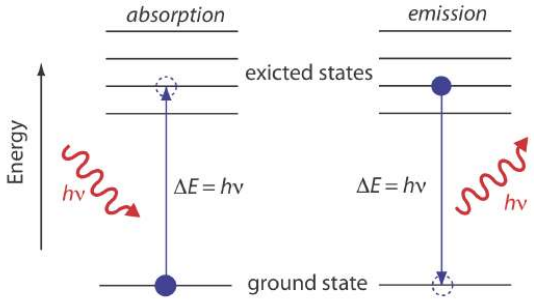


Figure 10.1.4 . A simplified energy diagram that shows the absorption and emission of a photon by an atom or a molecule. When a photon of energy $h\nu$ strikes the atom or molecule, absorption may occur if the difference in energy, ΔE, between the ground state and the excited state is equal to the photon's energy. An atom or molecule in an excited state may emit a photon and return to the ground state. The photon's energy, $h\nu$, equals the difference in energy, ΔE, between the two states.

When it absorbs electromagnetic radiation the number of photons passing through a sample decreases. The measurement of this decrease in photons, which we call ***absorbance***, is a useful analytical signal. Note that each energy level in Figure 10.1.4 has a well-defined value because each is quantized. Absorption occurs only when the photon's energy, $h\nu$, matches the difference in energy, ΔE, between two energy levels. A plot of absorbance as a function of the photon's energy is called an ***absorbance spectrum***. Figure 10.1.5 , for example, shows the absorbance spectrum of cranberry juice.

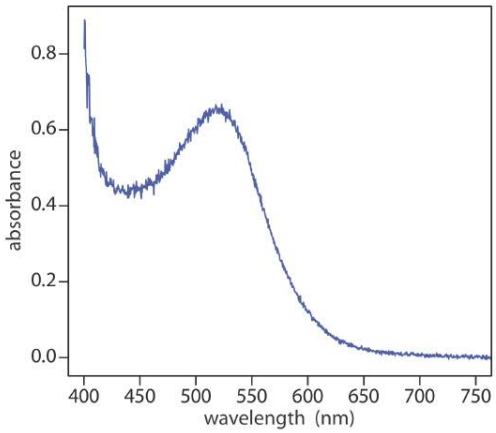


Figure 10.1.5 . Visible absorbance spectrum for cranberry juice. The anthocyanin dyes in cranberry juice absorb visible light with blue, green, and yellow wavelengths (see Figure 10.1.3). As a result, the juice appears red.

When an atom or molecule in an excited state returns to a lower energy state, the excess energy often is released as a photon, a process we call ***emission*** (Figure 10.1.4). There are several ways in which an atom or a molecule may end up in an excited state, including thermal energy, absorption of a photon, or as the result of a chemical reaction. Emission following the absorption of a photon is also called ***photoluminescence***, and that following a chemical reaction is called ***chemiluminescence***. A typical emission spectrum is shown in Figure 10.1.6 .

> Molecules also can release energy in the form of heat. We will return to this point later in the chapter.

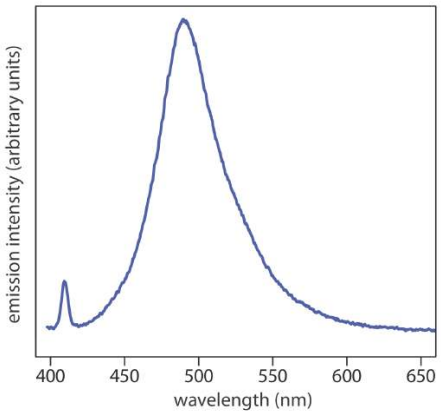


Figure 10.1.6 . Photoluminescence spectrum of the dye coumarin 343, which is incorporated in a reverse micelle suspended in cyclohexanol. The dye's absorbance spectrum (not shown) has a broad peak around 400 nm. The sharp peak at 409 nm is from the laser source used to excite coumarin 343. The broad band centered at approximately 500 nm is the dye's emission band. Because the dye absorbs blue light, a solution of coumarin 343 appears yellow in the absence of photoluminescence. Its photoluminescent emission is blue-green. Source: data from Bridget Gourley, Department of Chemistry & Biochemistry, DePauw University.

In the second broad class of spectroscopic techniques, the electromagnetic radiation undergoes a change in amplitude, phase angle, polarization, or direction of propagation as a result of its refraction, reflection, scattering, diffraction, or dispersion by the sample. Several representative spectroscopic techniques are listed in Table 10.1.2 .

Table 10.1.2 . Examples of Spectroscopic Techniques That Do Not Involve an Exchange of Energy Between a Photon and the Sample

region of electromagnetic spectrum	type of interaction	spectroscopic technique
X-ray	diffraction	X-ray diffraction
UV/Vis	refraction	refractrometry
	scattering	*nephelometry* *turbidimetry*
	dispersion	optical rotary dispersion
techniques discussed in this chapter are shown in *italics*		

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BASIC COMPONENTS OF SPECTROSCOPIC INSTRUMENTS

The spectroscopic techniques in Table 10.1.1 and Table 10.1.2 use instruments that share several common basic components, including a source of energy, a means for isolating a narrow range of wavelengths, a detector for measuring the signal, and a signal processor that displays the signal in a form convenient for the analyst. In this section we introduce these basic components. Specific instrument designs are considered in later sections.

> You will find a more detailed treatment of these components in the additional resources for this chapter.

SOURCES OF ENERGY

All forms of spectroscopy require a source of energy. In absorption and scattering spectroscopy this energy is supplied by photons. Emission and photoluminescence spectroscopy use thermal, radiant (photon), or chemical energy to promote the analyte to a suitable excited state.

Sources of Electromagnetic Radiation. A source of electromagnetic radiation must provide an output that is both intense and stable. Sources of electromagnetic radiation are classified as either continuum or line sources. A ***continuum source*** emits radiation over a broad range of wavelengths, with a relatively smooth variation in intensity (Figure 10.1.7). A ***line source***, on the other hand, emits radiation at selected wavelengths (Figure 10.1.8). Table 10.1.3 provides a list of the most common sources of electromagnetic radiation.

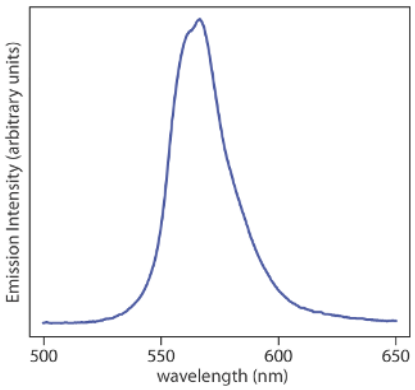


Figure 10.1.7 . Spectrum showing the emission from a green LED, which provides continuous emission over a wavelength range of approximately 530–640 nm.

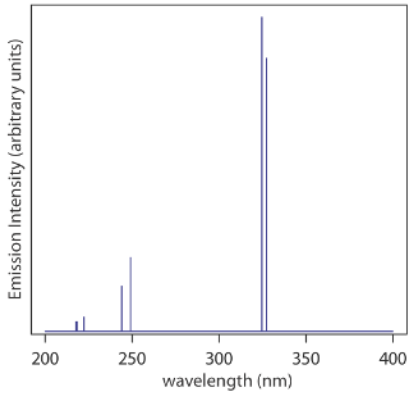


Figure 10.1.8 . Emission spectrum from a Cu hollow cathode lamp. This spectrum consists of seven distinct emission lines (the first two differ by only 0.4 nm and are not resolved at the scale shown in this spectrum). Each emission line has a width of approximately 0.01 nm at 1⁄2 of its maximum intensity.

Table 10.1.3 . Common Source of Electromagnetic Radiation

source	wavelength region	useful for...
H_2 and D_2 lamp	continuum source from 160–380 nm	molecular absorption
tungsten lamp	continuum source from 320–2400 nm	molecular absorption
Xe arc lamp	continuum source from 200–1000 nm	molecular fluorescence
nernst glower	continuum source from 0.4–20 μm	molecular absorption
globar	continuum source from 1–40 μm	molecular absorption
nichrome wire	continuum source from 0.75–20 μm	molecular absorption
hollow cathode lamp	line source in UV/Vis	atomic absorption
Hg vapor lamp	line source in UV/Vis	molecular fluorescence
laser	line source in UV/Vis/Ir	atomic and molecular absorption, fluorescence, and scattering

Sources of Thermal Radiation. The most common sources of thermal energy are flames and plasmas. A flame source uses a combustion of a fuel and an oxidant to achieve temperatures of 2000–3400 K. Plasmas, which are hot, ionized gases, provide temperatures of 6000–10000 K.

Chemical Sources of Energy. Exothermic reactions also may serve as a source of energy. In chemiluminescence the analyte is raised to a higher-energy state by means of a chemical reaction, emitting characteristic radiation when it returns to a lower-energy state. When the chemical reaction results from a biological or enzymatic reaction, the emission of radiation is called bioluminescence. Commercially available “light sticks” and the flash of light from a firefly are examples of chemiluminescence and bioluminescence.

WAVELENGTH SELECTION

In Nessler’s original colorimetric method for ammonia, which was described at the beginning of the chapter, the sample and several standard solutions of ammonia are placed in separate tall, flat-bottomed tubes. As shown in Figure 10.1.9 , after adding the reagents and allowing the color to develop, the analyst evaluates the color by passing ambient light through the bottom of the tubes and looking down through the solutions. By matching the sample’s color to that of a standard, the analyst is able to determine the concentration of ammonia in the sample.

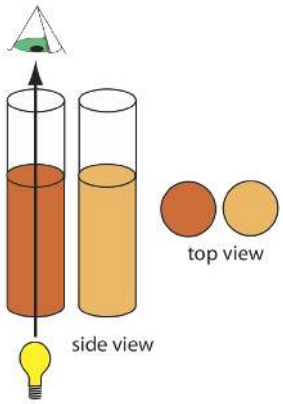


Figure 10.1.9 . Nessler’s original method for comparing the color of two solutions. Natural light passes upwards through the samples and standards and the analyst views the solutions by looking down toward the light source. The top view, shown on the right, is what the analyst sees. To determine the analyte’s concentration, the analyst exchanges standards until the two colors match.

In Figure 10.1.9 every wavelength of light from the source passes through the sample. This is not a problem if there is only one absorbing species in the sample. If the sample contains two components, then a quantitative analysis using Nessler’s original method is impossible unless the standards contains the second component at the same concentration it has in the sample.

To overcome this problem, we want to select a wavelength that only the analyte absorbs. Unfortunately, we can not isolate a single wavelength of radiation from a continuum source, although we can narrow the range of wavelengths that reach the sample. As seen in Figure 10.1.10 , a wavelength selector always passes a narrow band of radiation characterized by a ***nominal wavelength***, an ***effective bandwidth***, and a maximum throughput of radiation. The effective bandwidth is defined as the width of the radiation at half of its maximum throughput.

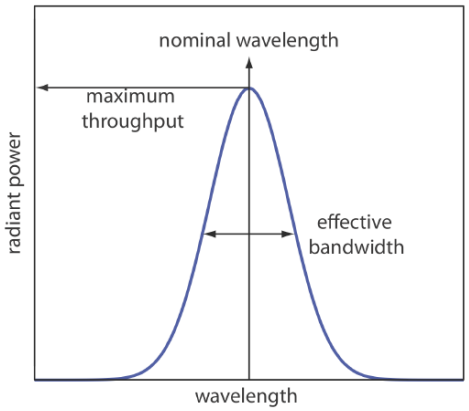


Figure 10.1.10 . Radiation exiting a wavelength selector showing the band's nominal wavelength and its effective bandwidth.

The ideal wavelength selector has a high throughput of radiation and a narrow effective bandwidth. A high throughput is desirable because the more photons that pass through the wavelength selector, the stronger the signal and the smaller the background noise. A narrow effective bandwidth provides a higher ***resolution***, with spectral features separated by more than twice the effective bandwidth being resolved. As shown in Figure 10.1.11 , these two features of a wavelength selector often are in opposition. A larger effective bandwidth favors a higher throughput of radiation, but provide less resolution. Decreasing the effective bandwidth improves resolution, but at the cost of a noisier signal [Jiang, S.; Parker, G. A. *Am. Lab.* **1981**, October, 38–43]. For a qualitative analysis, resolution usually is more important than noise and a smaller effective bandwidth is desirable; however, in a quantitative analysis less noise usually is desirable.

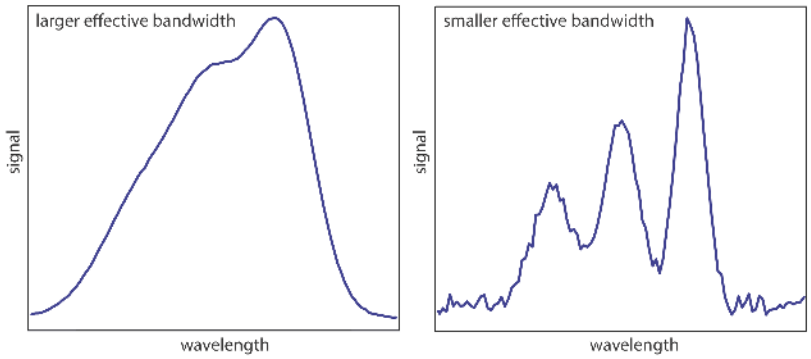


Figure 10.1.11 . Example showing the effect of the wavelength selector's effective bandwidth on resolution and noise. The spectrum with the smaller effective bandwidth (on the right) has a better resolution, allowing us to see the presence of three peaks, but at the expense of a noisier signal. The spectrum with the larger effective bandwidth (on the left) has less noise, but at the expense of less resolution between the three peaks.

Wavelength Selection Using Filters. The simplest method for isolating a narrow band of radiation is to use an absorption or interference ***filter***. Absorption filters work by selectively absorbing radiation from a narrow region of the electromagnetic spectrum. Interference filters use constructive and destructive interference to isolate a narrow range of wavelengths. A simple example of an absorption filter is a piece of colored glass. A purple filter, for example, removes the complementary color green from 500–560 nm.

Commercially available absorption filters provide effective bandwidths of 30–250 nm, although the throughput at the low end of this range often is only 10% of the source's emission intensity. Interference filters are more expensive than absorption filters, but have narrower effective bandwidths, typically 10–20 nm, with maximum throughputs of at least 40%.

Wavelength Selection Using Monochromators. A filter has one significant limitation—because a filter has a fixed nominal wavelength, if we need to make measurements at two different wavelengths, then we must use two different filters. A ***monochromator*** is an alternative method for selecting a narrow band of radiation that also allows us to continuously adjust the band's nominal wavelength.

The construction of a typical monochromator is shown in Figure 10.1.12 . Radiation from the source enters the monochromator through an entrance slit. The radiation is collected by a collimating mirror, which reflects a parallel beam of radiation to a diffraction grating. The diffraction grating is an optically reflecting surface with a large number of parallel grooves (see insert to Figure 10.1.12). The diffraction grating disperses the radiation and a second mirror focuses the radiation onto a planar surface that contains an exit slit. In some monochromators a prism is used in place of the diffraction grating.

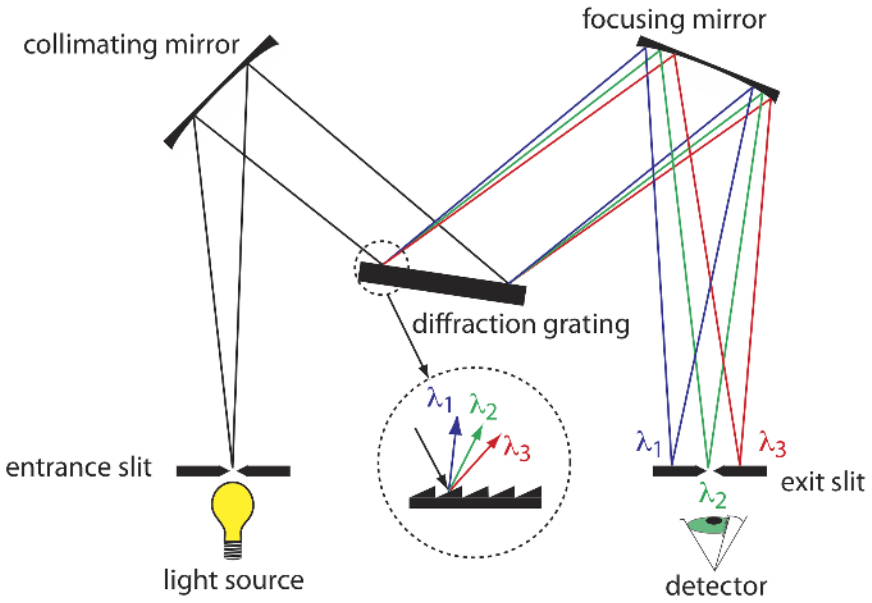


Figure 10.1.12 . Schematic diagram of a monochromator that uses a diffraction grating to disperse the radiation.

Radiation exits the monochromator and passes to the detector. As shown in Figure 10.1.12 , a monochromator converts a ***polychromatic*** source of radiation at the entrance slit to a ***monochromatic*** source of finite effective bandwidth at the exit slit. The choice of which wavelength exits the monochromator is determined by rotating the diffraction grating. A narrower exit slit provides a smaller effective bandwidth and better resolution than does a wider exit slit, but at the cost of a smaller throughput of radiation.

> Polychromatic means many colored. Polychromatic radiation contains many different wavelengths of light. Monochromatic means one color, or one wavelength. Although the light exiting a monochromator is not strictly of a single wavelength, its narrow effective bandwidth allows us to think of it as monochromatic.

Monochromators are classified as either fixed-wavelength or scanning. In a fixed-wavelength monochromator we manually select the wavelength by rotating the grating. Normally a fixed-wavelength monochromator is used for a quantitative analysis where measurements are made at one or two wavelengths. A scanning monochromator includes a drive mechanism that continuously rotates the grating, which allows successive wavelengths of light to exit from the monochromator. A scanning monochromator is used to acquire spectra, and, when operated in a fixed-wavelength mode, for a quantitative analysis.

Interferometers. An ***interferometer*** provides an alternative approach for wavelength selection. Instead of filtering or dispersing the electromagnetic radiation, an interferometer allows source radiation of all wavelengths to reach the detector simultaneously (Figure 10.1.13). Radiation from the source is focused on a beam splitter that reflects half of the radiation to a fixed mirror and transmits the other half to a moving mirror. The radiation recombines at the beam splitter, where constructive and destructive interference determines, for each wavelength, the intensity of light that reaches the detector. As the moving mirror changes position, the wavelength of light that experiences maximum constructive interference and maximum destructive interference also changes. The signal at the detector shows intensity as a function of the moving mirror's position, expressed in units of distance or time. The result is called an ***interferogram*** or a time domain spectrum. The time domain spectrum is converted mathematically, by a process called a Fourier transform, to a spectrum (a frequency domain spectrum) that shows intensity as a function of the radiation's energy.

> The mathematical details of the Fourier transform are beyond the level of this textbook. You can consult the chapter's additional resources for additional information.

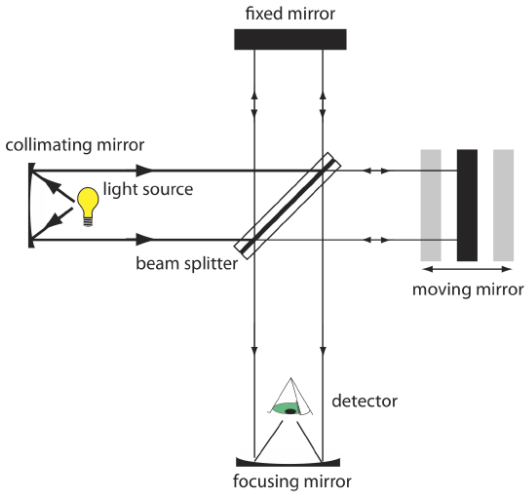


Figure 10.1.13 . Schematic diagram of an interferometers.

In comparison to a monochromator, an interferometer has two significant advantages. The first advantage, which is termed ***Jacquinot's advantage***, is the greater throughput of source radiation. Because an interferometer does not use slits and has fewer optical components from which radiation is scattered and lost, the throughput of radiation reaching the detector is $80-200\times$ greater than that for a monochromator. The result is less noise. The second advantage, which is called ***Fellgett's advantage***, is a savings in the time needed to obtain a spectrum. Because the detector monitors all frequencies simultaneously, a spectrum takes approximately one second to record, as compared to 10–15 minutes when using a scanning monochromator.

DETECTORS

In Nessler's original method for determining ammonia (Figure 10.1.9) the analyst's eye serves as the detector, matching the sample's color to that of a standard. The human eye, of course, has a poor range—it responds only to visible light—and it is not particularly sensitive or accurate. Modern detectors use a sensitive ***transducer*** to convert a signal consisting of photons into an easily measured electrical signal. Ideally the detector's signal, *S*, is a linear function of the electromagnetic radiation's power, *P*,

$$S = kP + D$$

where *k* is the detector's sensitivity, and *D* is the detector's ***dark current***, or the background current when we prevent the source's radiation from reaching the detector.

There are two broad classes of spectroscopic transducers: thermal transducers and photon transducers. Table 10.1.4 provides several representative examples of each class of transducers.

> Transducer is a general term that refers to any device that converts a chemical or a physical property into an easily measured electrical signal. The retina in your eye, for example, is a transducer that converts photons into an electrical nerve impulse; your eardrum is a transducer that converts sound waves into a different electrical nerve impulse.

Table 10.1.4 . Examples of Transducers for Spectroscopy

transducer	class	wavelength range	output signal
phototube	photon	200–1000 nm	current
photomultiplier	photon	110–1000 nm	current
Si photodiode	photon	250–1100 nm	current
photoconductor	photon	750–6000 nm	change in resistance
photovoltaic cell	photon	400–5000 nm	current or voltage
thermocouple	thermal	0.8–40 μm	voltage
thermistor	thermal	0.8–40 μm	change in resistance
pneumatic	thermal	0.8–1000 μm	membrane displacement
pyroelectric	thermal	0.3–1000 μm	current

Photon Transducers. Phototubes and photomultipliers use a photosensitive surface that absorbs radiation in the ultraviolet, visible, or near IR to produce an electrical current that is proportional to the number of photons reaching the transducer (Figure 10.1.14). Other photon detectors use a semiconductor as the photosensitive surface. When the semiconductor absorbs photons, valence electrons move to the semiconductor's conduction band, producing a measurable current. One advantage of the Si photodiode is that it is easy to miniaturize.

Groups of photodiodes are gathered together in a linear array that contains 64–4096 individual photodiodes. With a width of 25 μm per diode, a linear array of 2048 photodiodes requires only 51.2 mm of linear space. By placing a ***photodiode array*** along the monochromator's focal plane, it is possible to monitor simultaneously an entire range of wavelengths.

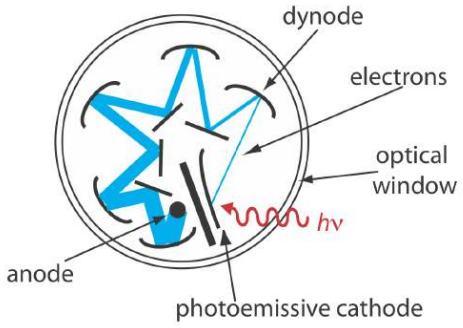


Figure 10.1.14 . Schematic of a photomultiplier. A photon strikes the photoemissive cathode producing electrons, which accelerate toward a positively charged dynode. Collision of these electrons with the dynode generates additional electrons, which accelerate toward the next dynode. A total of 10^6–10^7 electrons per photon eventually reach the anode, generating an electrical current.

Thermal Transducers. Infrared photons do not have enough energy to produce a measurable current with a photon transducer. A thermal transducer, therefore, is used for infrared spectroscopy. The absorption of infrared photons increases a thermal transducer's temperature, changing one or more of its characteristic properties. A pneumatic transducer, for example, is a small tube of xenon gas with an IR transparent window at one end and a flexible membrane at the other end. Photons enter the tube and are absorbed by a blackened surface, increasing the temperature of the gas. As the temperature inside the tube fluctuates, the gas expands and contracts and the flexible membrane moves in and out. Monitoring the membrane's displacement produces an electrical signal.

SIGNAL PROCESSORS

A transducer's electrical signal is sent to a ***signal processor*** where it is displayed in a form that is more convenient for the analyst. Examples of signal processors include analog or digital meters, recorders, and computers equipped with digital acquisition boards. A signal processor also is used to calibrate the detector's response, to amplify the transducer's signal, to remove noise by filtering, or to mathematically transform the signal.

> If the retina in your eye and the eardrum in your ear are transducers, then your brain is the signal processor.

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11.2: SPECTROSCOPY BASED ON ABSORPTION

In absorption spectroscopy a beam of electromagnetic radiation passes through a sample. Much of the radiation passes through the sample without a loss in intensity. At selected wavelengths, however, the radiation's intensity is attenuated. This process of attenuation is called absorption.

ABSORPTION SPECTRA

There are two general requirements for an analyte's absorption of electromagnetic radiation. First, there must be a mechanism by which the radiation's electric field or magnetic field interacts with the analyte. For ultraviolet and visible radiation, absorption of a photon changes the energy of the analyte's valence electrons. A bond's vibrational energy is altered by the absorption of infrared radiation.

> Figure 10.1.3 provides a list of the types of atomic and molecular transitions associated with different types of electromagnetic radiation.

The second requirement is that the photon's energy, $h\nu$, must exactly equal the difference in energy, ΔE, between two of the analyte's quantized energy states. Figure 10.1.4 shows a simplified view of a photon's absorption, which is useful because it emphasizes that the photon's energy must match the difference in energy between a lower-energy state and a higher-energy state. What is missing, however, is information about what types of energy states are involved, which transitions between energy states are likely to occur, and the appearance of the resulting spectrum.

We can use the energy level diagram in Figure 10.2.1 to explain an absorbance spectrum. The lines labeled E_0 and E_1 represent the analyte's ground (lowest) electronic state and its first electronic excited state. Superimposed on each electronic energy level is a series of lines representing vibrational energy levels.

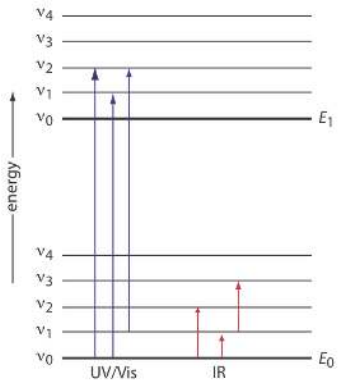


Figure 10.2.1 . Diagram showing two electronic energy levels (E_0 and E_1), each with five vibrational energy levels ν_{0-4}. Absorption of ultraviolet and visible radiation (shown by the blue arrows) leads to a change in the analyte's electronic energy levels and, possibly, a change in vibrational energy as well. A change in vibrational energy without a change in electronic energy levels occurs with the absorption of infrared radiation (shown by the red arrows).

INFRARED SPECTRA FOR MOLECULES AND POLYATOMIC IONS

The energy of infrared radiation produces a change in a molecule's or a polyatomic ion's vibrational energy, but is not sufficient to effect a change in its electronic energy. As shown in Figure 10.2.1 , vibrational energy levels are quantized; that is, a molecule or polyatomic ion has only certain, discrete vibrational energies. The energy for an allowed vibrational mode, E_ν, is

$$E_\nu = \nu + \frac{1}{2} h\nu_0$$

where ν is the vibrational quantum number, which has values of 0, 1, 2, ..., and ν_0 is the bond's fundamental vibrational frequency. The value of ν_0, which is determined by the bond's strength and by the mass at each end of the bond, is a characteristic property of a bond. For example, a carbon-carbon single bond (C–C) absorbs infrared radiation at a lower energy than a carbon-carbon double bond (C=C) because a single bond is weaker than a double bond.

At room temperature most molecules are in their ground vibrational state ($\nu = 0$) . A transition from the ground vibrational state to the first vibrational excited state ($\nu = 1$) requires absorption of a photon with an energy of $h\nu_0$. Transitions in which $\Delta\nu = \pm 1$ give rise to the fundamental absorption lines. Weaker absorption lines, called overtones, result from transitions in which $\Delta\nu$ is ±2 or ±3. The number of possible normal vibrational modes for a linear molecule is $3N - 5$, and for a non-linear molecule is $3N - 6$, where N is the number of atoms in the molecule. Not surprisingly, infrared spectra often show a considerable number of absorption bands. Even a relatively simple

molecule, such as ethanol (C_2H_6O), for example, has $3 \times 9 - 6$, or 21 possible normal modes of vibration, although not all of these vibrational modes give rise to an absorption. The IR spectrum for ethanol is shown in Figure 10.2.2 .

> Why does a non-linear molecule have $3N - 6$ vibrational modes? Consider a molecule of methane, CH_4. Each of methane's five atoms can move in one of three directions (x, y, and z) for a total of $5 \times 3 = 15$ different ways in which the molecule's atoms can move. A molecule can move in three ways: it can move from one place to another, which we call translational motion; it can rotate around an axis, which we call rotational motion; and its bonds can stretch and bend, which we call vibrational motion. Because the entire molecule can move in the x, y, and z directions, three of methane's 15 different motions are translational. In addition, the molecule can rotate about its x, y, and z axes, accounting for three additional forms of motion. This leaves 15 – 3 – 3 = 9 vibrational modes. A linear molecule, such as CO_2, has $3N - 5$ vibrational modes because it can rotate around only two axes.

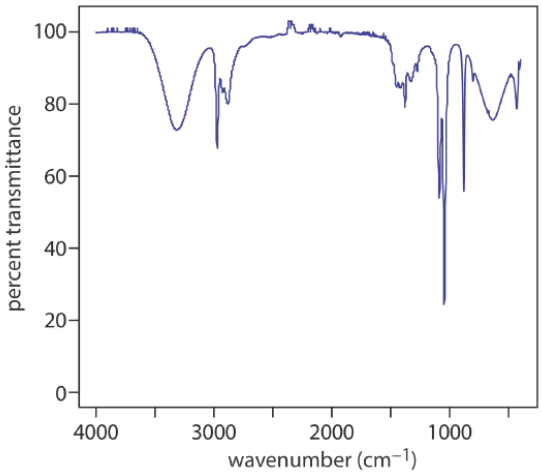


Figure 10.2.2 . Infrared spectrum of ethanol.

UV/VIS SPECTRA FOR MOLECULES AND IONS

The valence electrons in organic molecules and polyatomic ions, such as CO_3^{2-}, occupy quantized sigma bonding (σ), pi bonding (π), and non-bonding (n) molecular orbitals (MOs). Unoccupied sigma antibonding (σ^*) and pi antibonding (π^*) molecular orbitals are slightly higher in energy. Because the difference in energy between the highest-energy occupied MOs and the lowest-energy unoccupied MOs corresponds to ultraviolet and visible radiation, absorption of a photon is possible.

Four types of transitions between quantized energy levels account for most molecular UV/Vis spectra. Table 10.2.1 lists the approximate wavelength ranges for these transitions, as well as a partial list of bonds, functional groups, or molecules responsible for these transitions. Of these transitions, the most important are $n \rightarrow \pi^*$ and $\pi \rightarrow \pi^*$ because they involve important functional groups that are characteristic of many analytes and because the wavelengths are easily accessible. The bonds and functional groups that give rise to the absorption of ultraviolet and visible radiation are called ***chromophores***.

Table 10.2.1 . Electronic Transitions Involving n, σ, and π Molecular Orbitals

transition	wavelength range	examples
$\sigma \rightarrow \sigma^*$	<200 nm	C—C, C—H
$n \rightarrow \sigma^*$	160–260 nm	H_2O, CH_3OH, CH_3Cl
$\pi \rightarrow \pi^*$	200–500 nm	C=C, C=O, C=N, C≡C
$n \rightarrow \pi^*$	250–600 nm	C=O, C=N, N=N, N=O

Many transition metal ions, such as Cu^{2+} and Co^{2+}, form colorful solutions because the metal ion absorbs visible light. The transitions that give rise to this absorption are valence electrons in the metal ion's d-orbitals. For a free metal ion, the five d-orbitals are of equal energy. In the presence of a complexing ligand or solvent molecule, however, the d-orbitals split into two or more groups that differ in energy. For example, in an octahedral complex of $Cu(H_2O)_6^{2+}$ the six water molecules perturb the d-orbitals into the two groups shown in Figure 10.2.3 . The resulting $d \rightarrow d$ transitions for transition metal ions are relatively weak.

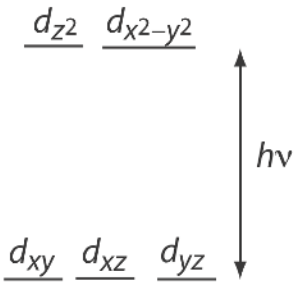


Figure 10.2.3 . Splitting of the *d*-orbitals in an octahedral field.

A more important source of UV/Vis absorption for inorganic metal–ligand complexes is charge transfer, in which absorption of a photon produces an excited state in which there is transfer of an electron from the metal, *M*, to the ligand, *L*.

$$M - L + h\nu \rightarrow \left(M^{+} - L^{-}\right)^{*}$$

Charge-transfer absorption is important because it produces very large absorbances. One important example of a charge-transfer complex is that of *o*-phenanthroline with Fe^{2+}, the UV/Vis spectrum for which is shown in Figure 10.2.4 . Charge-transfer absorption in which an electron moves from the ligand to the metal also is possible.

Why is a larger absorbance desirable? An analytical method is more sensitive if a smaller concentration of analyte gives a larger signal.

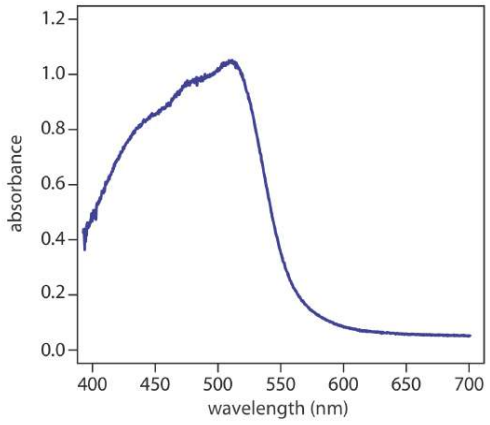


Figure 10.2.4 . UV/Vis spectrum for the metal–ligand complex $\mathrm{Fe(phen)}_3^{2+}$, where phen is the ligand *o*-phenanthroline.

Comparing the IR spectrum in Figure 10.2.2 to the UV/Vis spectrum in Figure 10.2.4 shows us that UV/Vis absorption bands are often significantly broader than those for IR absorption. We can use Figure 10.2.1 to explain why this is true. When a species absorbs UV/Vis radiation, the transition between electronic energy levels may also include a transition between vibrational energy levels. The result is a number of closely spaced absorption bands that merge together to form a single broad absorption band.

UV/VIS SPECTRA FOR ATOMS

The energy of ultraviolet and visible electromagnetic radiation is sufficient to cause a change in an atom's valence electron configuration. Sodium, for example, has a single valence electron in its 3*s* atomic orbital. As shown in Figure 10.2.5 , unoccupied, higher energy atomic orbitals also exist.

The valence shell energy level diagram in Figure 10.2.5 might strike you as odd because it shows that the 3*p* orbitals are split into two groups of slightly different energy. The reasons for this splitting are unimportant in the context of our treatment of atomic absorption. For further information about the reasons for this splitting, consult the chapter's additional resources.

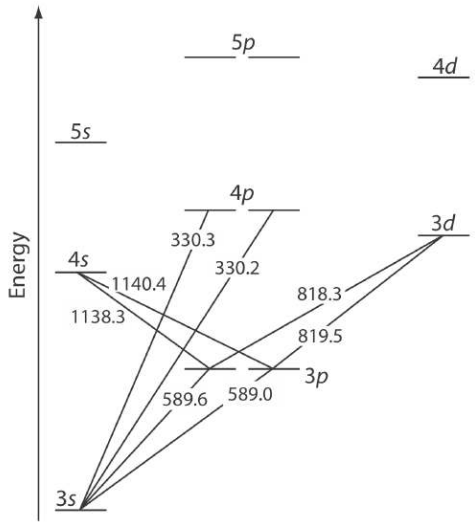


Figure 10.2.5 . Valence shell energy level diagram for sodium. The wavelengths (in wavenumbers) corresponding to several transitions are shown.

Absorption of a photon is accompanied by the excitation of an electron from a lower-energy atomic orbital to an atomic orbital of higher energy. Not all possible transitions between atomic orbitals are allowed. For sodium the only allowed transitions are those in which there is a change of ±1 in the orbital quantum number (l); thus transitions from $s \rightarrow p$ orbitals are allowed, but transitions from $s \rightarrow s$ and from $s \rightarrow d$ orbitals are forbidden.

The atomic absorption spectrum for Na is shown in Figure 10.2.6 , and is typical of that found for most atoms. The most obvious feature of this spectrum is that it consists of a small number of discrete absorption lines that correspond to transitions between the ground state (the 3*s* atomic orbital) and the 3*p* and the 4*p* atomic orbitals. Absorption from excited states, such as the $3p \rightarrow 4s$ and the $3p \rightarrow 3d$ transitions included in Figure 10.2.5 , are too weak to detect. Because an excited state's lifetime is short—an excited state atom typically returns to a lower energy state in 10^{-7} to 10^{-8} seconds—an atom in the exited state is likely to return to the ground state before it has an opportunity to absorb a photon.

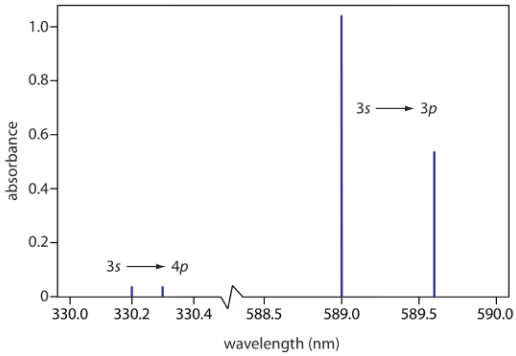


Figure 10.2.6 . Atomic absorption spectrum for sodium. Note that the scale on the *x*-axis includes a break.

Another feature of the atomic absorption spectrum in Figure 10.2.6 is the narrow width of the absorption lines, which is a consequence of the fixed difference in energy between the ground state and the excited state, and the lack of vibrational and rotational energy levels. Natural line widths for atomic absorption, which are governed by the uncertainty principle, are approximately 10^{-5} nm. Other contributions to broadening increase this line width to approximately 10^{-3} nm.

TRANSMITTANCE AND ABSORBANCE

As light passes through a sample, its power decreases as some of it is absorbed. This attenuation of radiation is described quantitatively by two separate, but related terms: transmittance and absorbance. As shown in Figure 10.2.7 a, transmittance is the ratio of the source radiation's power as it exits the sample, P_T, to that incident on the sample, P_0.

$$T = \frac{P_T}{P_0} \tag{11.2.1}$$

Multiplying the transmittance by 100 gives the percent transmittance, %*T*, which varies between 100% (no absorption) and 0% (complete absorption). All methods of detecting photons—including the human eye and modern photoelectric transducers—measure the transmittance of electromagnetic radiation.

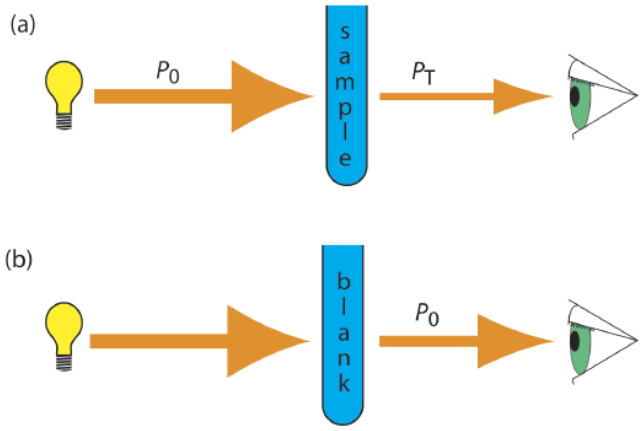


Figure 10.2.7 . (a) Schematic diagram showing the attenuation of radiation passing through a sample; P_0 is the source's radiant power and P_T is the radiant power transmitted by the sample. (b) Schematic diagram showing how we redefine P_0 as the radiant power transmitted by the blank. Redefining P_0 in this way corrects the transmittance in (a) for the loss of radiation due to scattering, reflection, absorption by the sample's container, and absorption by the sample's matrix.

Equation 11.2.1 does not distinguish between different mechanisms that prevent a photon emitted by the source from reaching the detector. In addition to absorption by the analyte, several additional phenomena contribute to the attenuation of radiation, including reflection and absorption by the sample's container, absorption by other components in the sample's matrix, and the scattering of radiation. To compensate for this loss of the radiation's power, we use a method blank. As shown in Figure 10.2.7 b, we redefine P_0 as the power exiting the method blank.

An alternative method for expressing the attenuation of electromagnetic radiation is absorbance, A, which we define as

$$A = -\log T = -\log \frac{P_T}{P_0} \tag{11.2.2}$$

Absorbance is the more common unit for expressing the attenuation of radiation because it is a linear function of the analyte's concentration.

> We will show that this is true in the next section when we introduce Beer's law.

EXAMPLE 10.2.1

A sample has a percent transmittance of 50%. What is its absorbance?

Solution

A percent transmittance of 50.0% is the same as a transmittance of 0.500. Substituting into Equation 11.2.2 gives

$$A = -\log T = -\log(0.500) = 0.301$$

EXERCISE 10.2.1

What is the %T for a sample if its absorbance is 1.27?

Answer

To find the transmittance, T, we begin by noting that

$$A = 1.27 = -\log T$$

Solving for T

$$-1.27 = \log T$$
$$10^{-1.27} = T$$

gives a transmittance of 0.054, or a %T of 5.4%.

Equation 11.2.1 has an important consequence for atomic absorption. As we learned from Figure 10.2.6 , atomic absorption lines are very narrow. Even with a high quality monochromator, the effective bandwidth for a continuum source is $100 - 1000\times$ greater than the width of

an atomic absorption line. As a result, little radiation from a continuum source is absorbed when it passes through a sample of atoms; because $P_0 \approx P_T$ the measured absorbance effectively is zero. For this reason, atomic absorption requires that we use a line source instead of a continuum source.

ABSORBANCE AND CONCENTRATION: BEER'S LAW

When monochromatic electromagnetic radiation passes through an infinitesimally thin layer of sample of thickness *dx*, it experiences a decrease in its power of *dP* (Figure 10.2.8).

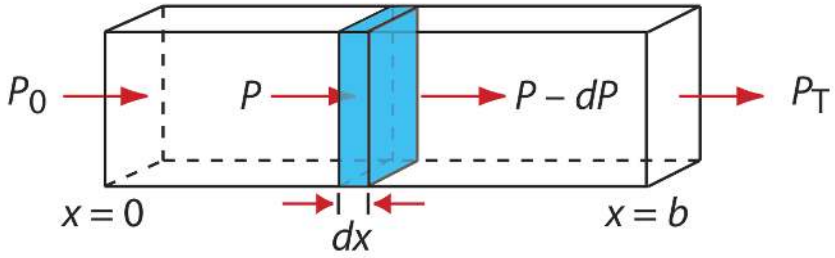


Figure 10.2.8 . Factors used to derive the Beer's law.

This fractional decrease in power is proportional to the sample's thickness and to the analyte's concentration, *C*; thus

$$-\frac{dP}{P} = \alpha C dx \tag{11.2.3}$$

where *P* is the power incident on the thin layer of sample and α is a proportionality constant. Integrating the left side of Equation 11.2.3 over the sample's full thickness

$$-\int_{P=P_0}^{P=P_t} \frac{dP}{P} = \alpha C \int_{x=0}^{x=b} dx$$

$$\ln \frac{P_0}{P_T} = \alpha b C$$

converting from ln to log, and substituting into Equation 11.2.2, gives

$$A = abC \tag{11.2.4}$$

where *a* is the analyte's ***absorptivity*** with units of cm^{-1} $conc^{-1}$. If we express the concentration using molarity, then we replace *a* with the ***molar absorptivity***, ε, which has units of cm^{-1} M^{-1}.

$$A = \varepsilon bC \tag{11.2.5}$$

The absorptivity and the molar absorptivity are proportional to the probability that the analyte absorbs a photon of a given energy. As a result, values for both *a* and ε depend on the wavelength of the absorbed photon.

EXAMPLE 10.2.2

A 5.00×10^{-4} M solution of analyte is placed in a sample cell that has a pathlength of 1.00 cm. At a wavelength of 490 nm, the solution's absorbance is 0.338. What is the analyte's molar absorptivity at this wavelength?

Solution

Solving Equation 11.2.5 for ϵ and making appropriate substitutions gives

$$\varepsilon = \frac{A}{bC} = \frac{0.338}{(1.00\text{ cm})\left(5.00 \times 10^{-4}\text{ M}\right)} = 676\text{ cm}^{-1}\text{ M}^{-1}$$

EXERCISE 10.2.2

A solution of the analyte from Example 10.2.2 has an absorbance of 0.228 in a 1.00-cm sample cell. What is the analyte's concentration?

Answer

Making appropriate substitutions into Beer's law

$$A = 0.228 = \varepsilon bC = \left(676\ \text{M}^{-1}\ \text{cm}^{-1}\right)(1\ \text{cm})C$$

and solving for C gives a concentration of 3.37×10^{-4} M.

Equation 11.2.4 and Equation 11.2.5, which establish the linear relationship between absorbance and concentration, are known as Beer's law. Calibration curves based on Beer's law are common in quantitative analyses.

As is often the case, the formulation of a law is more complicated than its name suggests. This is the case, for example, with Beer's law, which also is known as the Beer-Lambert law or the Beer-Lambert-Bouguer law. Pierre Bouguer, in 1729, and Johann Lambert, in 1760, noted that the transmittance of light decreases exponentially with an increase in the sample's thickness.

$$T \propto e^{-b}$$

Later, in 1852, August Beer noted that the transmittance of light decreases exponentially as the concentration of the absorbing species increases.

$$T \propto e^{-C}$$

Together, and when written in terms of absorbance instead of transmittance, these two relationships make up what we know as Beer's law.

BEER'S LAW AND MULTICOMPONENT SAMPLES

We can extend Beer's law to a sample that contains several absorbing components. If there are no interactions between the components, then the individual absorbances, A_i, are additive. For a two-component mixture of analyte's X and Y, the total absorbance, A_{tot}, is

$$A_{tot} = A_X + A_Y = \varepsilon_X bC_X + \varepsilon_Y bC_Y$$

Generalizing, the absorbance for a mixture of n components, A_{mix}, is

$$A_{mix} = \sum_{i=1}^{n} A_i = \sum_{i=1}^{n} \varepsilon_i bC_i \tag{11.2.6}$$

LIMITATIONS TO BEER'S LAW

Beer's law suggests that a plot of absorbance vs. concentration—we will call this a Beer's law plot—is a straight line with a y-intercept of zero and a slope of ab or εb. In some cases a Beer's law plot deviates from this ideal behavior (see Figure 10.2.9), and such deviations from linearity are divided into three categories: fundamental, chemical, and instrumental.

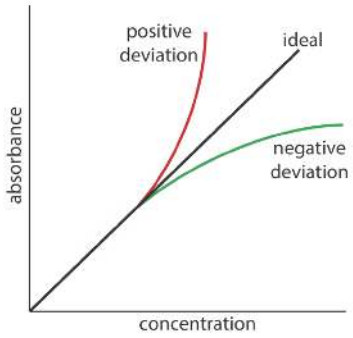


Figure 10.2.9 . Plots of absorbance vs. concentration showing positive and negative deviations from the ideal Beer's law relationship, which is a straight line.

FUNDAMENTAL LIMITATIONS TO BEER'S LAW

Beer's law is a limiting law that is valid only for low concentrations of analyte. There are two contributions to this fundamental limitation to Beer's law. At higher concentrations the individual particles of analyte no longer are independent of each other. The resulting interaction between particles of analyte may change the analyte's absorptivity. A second contribution is that an analyte's absorptivity depends on the solution's refractive index. Because a solution's refractive index varies with the analyte's concentration, values of a and ε may change. For sufficiently low concentrations of analyte, the refractive index essentially is constant and a Beer's law plot is linear.

CHEMICAL LIMITATIONS TO BEER'S LAW

A chemical deviation from Beer's law may occur if the analyte is involved in an equilibrium reaction. Consider, for example, the weak acid, HA. To construct a Beer's law plot we prepare a series of standard solutions—each of which contains a known total concentration of HA—and then measure each solution's absorbance at the same wavelength. Because HA is a weak acid, it is in equilibrium with its conjugate weak base, A^-.

> In the equations that follow, the conjugate weak base A^- is written as A as it is easy to mistake the symbol for anionic charge as a minus sign.

$$HA(aq) + H_2O(l) \rightleftharpoons H_3O^+(aq) + A^-(aq)$$

If both HA and A^- absorb at the selected wavelength, then Beer's law is

$$A = \varepsilon_{HA} b C_{HA} + \varepsilon_A b C_A \tag{11.2.7}$$

Because the weak acid's total concentration, C_{total}, is

$$C_{total} = C_{HA} + C_A$$

we can write the concentrations of HA and A^- as

$$C_{HA} = \alpha_{HA} C_{total} \tag{11.2.8}$$

$$C_A = (1 - \alpha_{HA}) C_{total} \tag{11.2.9}$$

where α_{HA} is the fraction of weak acid present as HA. Substituting Equation 11.2.8 and Equation 11.2.9 into Equation 11.2.7 and rearranging, gives

$$A = (\varepsilon_{HA}\alpha_{HA} + \varepsilon_A - \varepsilon_A\alpha_A)\, b C_{total} \tag{11.2.10}$$

To obtain a linear Beer's law plot, we must satisfy one of two conditions. If ε_{HA} and ε_A have the same value at the selected wavelength, then Equation 11.2.10 simplifies to

$$A = \varepsilon_A b C_{total} = \varepsilon_{HA} b C_{total}$$

Alternatively, if α_{HA} has the same value for all standard solutions, then each term within the parentheses of Equation 11.2.10 is constant—which we replace with *k*—and a linear calibration curve is obtained at any wavelength.

$$A = k b C_{total}$$

Because HA is a weak acid, the value of α_{HA} varies with pH. To hold α_{HA} constant we buffer each standard solution to the same pH. Depending on the relative values of α_{HA} and α_A, the calibration curve has a positive or a negative deviation from Beer's law if we do not buffer the standards to the same pH.

INSTRUMENTAL LIMITATIONS TO BEER'S LAW

There are two principal instrumental limitations to Beer's law. The first limitation is that Beer's law assumes that radiation reaching the sample is of a single wavelength—that is, it assumes a purely monochromatic source of radiation. As shown in Figure 10.1.10, even the best wavelength selector passes radiation with a small, but finite effective bandwidth. Polychromatic radiation always gives a negative deviation from Beer's law, but the effect is smaller if the value of ε essentially is constant over the wavelength range passed by the wavelength selector. For this reason, as shown in Figure 10.2.10 , it is better to make absorbance measurements at the top of a broad absorption peak. In addition, the deviation from Beer's law is less serious if the source's effective bandwidth is less than one-tenth of the absorbing species' natural bandwidth [(a) Strong, F. C., III *Anal. Chem.* **1984**, *56*, 16A–34A; Gilbert, D. D. *J. Chem. Educ.* **1991**, *68*, A278–A281]. When measurements must be made on a slope, linearity is improved by using a narrower effective bandwidth.

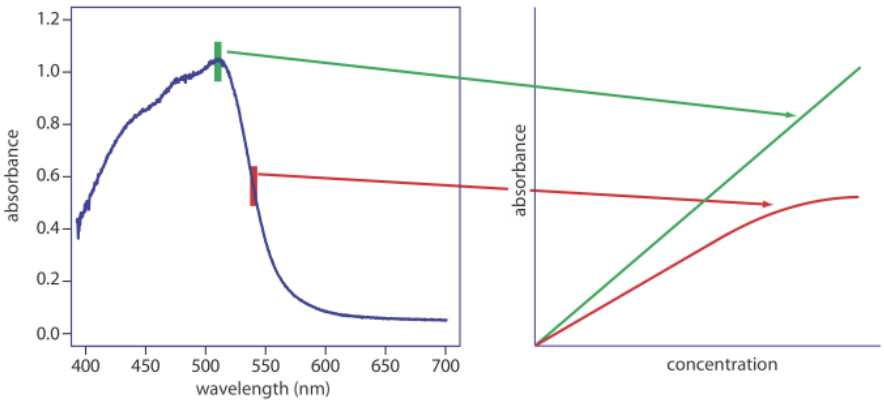


Figure 10.2.10 . Effect of wavelength selection on the linearity of a Beer's law plot. Another reason for measuring absorbance at the top of an absorbance peak is that it provides for a more sensitive analysis. Note that the green Beer's law plot has a steeper slope—and, therefore, a greater sensitivity—than the red Beer's law plot. A Beer's law plot, of course, is equivalent to a calibration curve.

Stray radiation is the second contribution to instrumental deviations from Beer's law. Stray radiation arises from imperfections in the wavelength selector that allow light to enter the instrument and to reach the detector without passing through the sample. Stray radiation adds an additional contribution, P_{stray}, to the radiant power that reaches the detector; thus

$$A = -\log \frac{P_{\text{T}} + P_{\text{stray}}}{P_0 + P_{\text{stray}}}$$

For a small concentration of analyte, P_{stray} is significantly smaller than P_0 and P_{T}, and the absorbance is unaffected by the stray radiation. For higher concentrations of analyte, less light passes through the sample and P_{T} and P_{stray} become similar in magnitude. This results is an absorbance that is smaller than expected, and a negative deviation from Beer's law.

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11.3: UV/VIS AND IR SPECTROSCOPY

In Figure 10.1.9 we examined Nessler's original method for matching the color of a sample to the color of a standard. Matching colors is a labor intensive process for the analyst and, not surprisingly, spectroscopic methods of analysis were slow to find favor. The 1930s and 1940s saw the introduction of photoelectric transducers for ultraviolet and visible radiation, and thermocouples for infrared radiation. As a result, modern instrumentation for absorption spectroscopy routinely became available in the 1940s—further progress has been rapid ever since.

INSTRUMENTATION

Frequently an analyst must select from among several instruments of different design, the one instrument best suited for a particular analysis. In this section we examine several different instruments for molecular absorption spectroscopy, with an emphasis on their advantages and limitations. Methods of sample introduction also are covered in this section.

INSTRUMENT DESIGNS FOR MOLECULAR UV/VIS ABSORPTION

Filter Photometer. The simplest instrument for molecular UV/Vis absorption is a ***filter photometer*** (Figure 10.3.1), which uses an absorption or interference filter to isolate a band of radiation. The filter is placed between the source and the sample to prevent the sample from decomposing when exposed to higher energy radiation. A filter photometer has a single optical path between the source and detector, and is called a ***single-beam*** instrument. The instrument is calibrated to 0% T while using a shutter to block the source radiation from the detector. After opening the shutter, the instrument is calibrated to 100% T using an appropriate blank. The blank is then replaced with the sample and its transmittance measured. Because the source's incident power and the sensitivity of the detector vary with wavelength, the photometer is recalibrated whenever the filter is changed. Photometers have the advantage of being relatively inexpensive, rugged, and easy to maintain. Another advantage of a photometer is its portability, making it easy to take into the field. Disadvantages of a photometer include the inability to record an absorption spectrum and the source's relatively large effective bandwidth, which limits the calibration curve's linearity.

> The percent transmittance varies between 0% and 100%. As we learned from Figure 10.2.7, we use a blank to determine P_0, which corresponds to 100%T. Even in the absence of light the detector records a signal. Closing the shutter allows us to assign 0%T to this signal. Together, setting 0% T and 100%T calibrates the instrument. The amount of light that passes through a sample produces a signal that is greater than or equal to 0%T and smaller than or equal to 100%T.

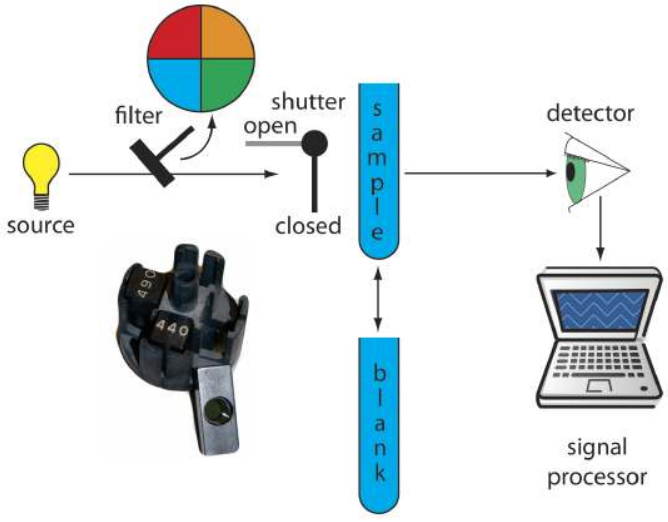


Figure 10.3.1 . Schematic diagram of a filter photometer. The analyst either inserts a removable filter or the filters are placed in a carousel, an example of which is shown in the photographic inset. The analyst selects a filter by rotating it into place.

Single-Beam Spectrophotometer. An instrument that uses a monochromator for wavelength selection is called a ***spectrophotometer***. The simplest spectrophotometer is a single-beam instrument equipped with a fixed-wavelength monochromator (Figure 10.3.2). Single-beam spectrophotometers are calibrated and used in the same manner as a photometer. One example of a single-beam spectrophotometer is Thermo Scientific's Spectronic 20D+, which is shown in the photographic insert to Figure 10.3.2 . The Spectronic 20D+ has a wavelength range of 340–625 nm (950 nm when using a red-sensitive detector), and a fixed effective bandwidth of 20 nm. Battery-operated, hand-held single-beam spectrophotometers are available, which are easy to transport into the field. Other single-beam spectrophotometers also are

available with effective bandwidths of 2–8 nm. Fixed wavelength single-beam spectrophotometers are not practical for recording spectra because manually adjusting the wavelength and recalibrating the spectrophotometer is awkward and time-consuming. The accuracy of a single-beam spectrophotometer is limited by the stability of its source and detector over time.

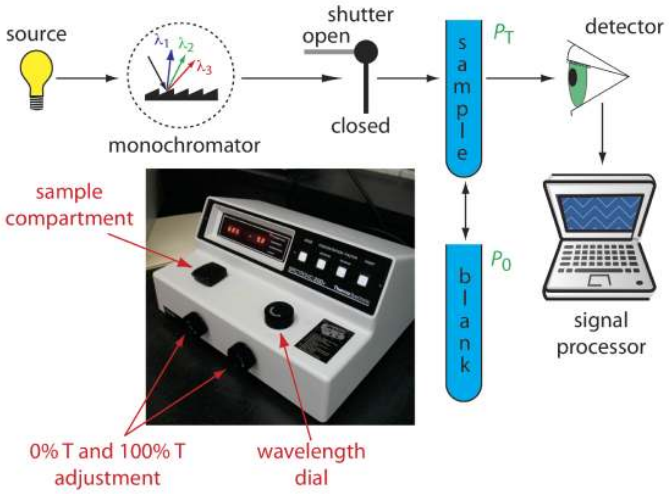


Figure 10.3.2 . Schematic diagram of a fixed-wavelength, single-beam spectrophotometer. The photographic inset shows a typical instrument. The shutter remains closed until the sample or blank is placed in the sample compartment. The analyst manually selects the wavelength by adjusting the wavelength dial. Inset photo modified from: Adi (www.commons.Wikipedia.org).

Double-Beam Spectrophotometer. The limitations of a fixed-wavelength, single-beam spectrophotometer is minimized by using a ***double-beam*** spectrophotometer (Figure 10.3.3). A chopper controls the radiation's path, alternating it between the sample, the blank, and a shutter. The signal processor uses the chopper's speed of rotation to resolve the signal that reaches the detector into the transmission of the blank, P_0, and the sample, P_T. By including an opaque surface as a shutter, it also is possible to continuously adjust 0%T. The effective bandwidth of a double-beam spectrophotometer is controlled by adjusting the monochromator's entrance and exit slits. Effective bandwidths of 0.2–3.0 nm are common. A scanning monochromator allows for the automated recording of spectra. Double-beam instruments are more versatile than single-beam instruments, being useful for both quantitative and qualitative analyses, but also are more expensive and not particularly portable.

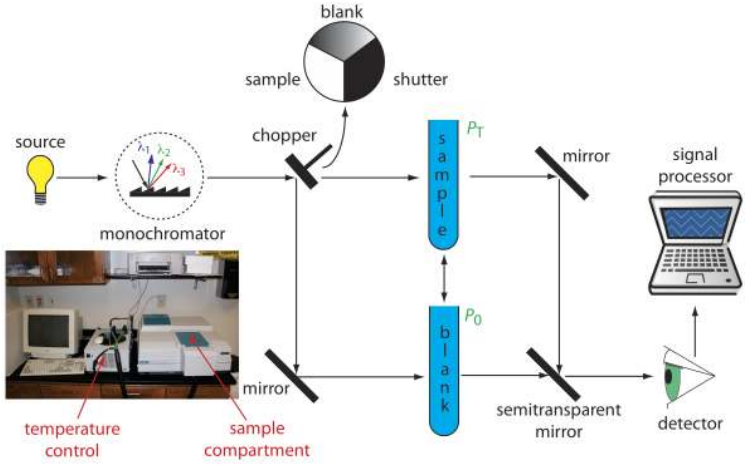


Figure 10.3.3 . Schematic diagram of a scanning, double-beam spectrophotometer. A chopper directs the source's radiation, using a transparent window to pass radiation to the sample and a mirror to reflect radiation to the blank. The chopper's opaque surface serves as a shutter, which allows for a constant adjustment of the spectrophotometer's 0%T. The photographic insert shows a typical instrument. The module in the middle of the photo is a temperature control unit that makes it possible to heat or cool the sample to a constant temperature.

Diode Array Spectrometer. An instrument with a single detector can monitor only one wavelength at a time. If we replace a single photomultiplier with an array of photodiodes, we can use the resulting detector to record a full spectrum in as little as 0.1 s. In a diode array spectrometer the source radiation passes through the sample and is dispersed by a grating (Figure 10.3.4). The photodiode array detector is situated at the grating's focal plane, with each diode recording the radiant power over a narrow range of wavelengths. Because we replace a full monochromator with just a grating, a diode array spectrometer is small and compact.

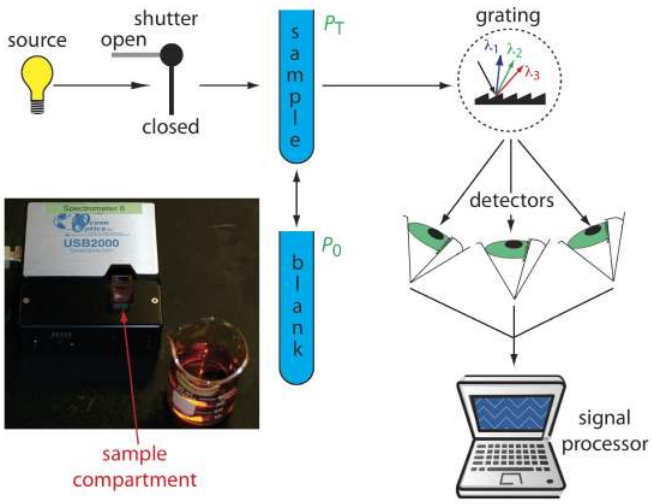


Figure 10.3.4 . Schematic diagram of a diode array spectrophotometer. The photographic insert shows a typical instrument. Note that the 50-mL beaker provides a sense of scale. Because the spectrometer is small and compact, it is easy to transport into the field.

One advantage of a diode array spectrometer is the speed of data acquisition, which allows us to collect multiple spectra for a single sample. Individual spectra are added and averaged to obtain the final spectrum. This ***signal averaging*** improves a spectrum's signal-to-noise ratio. If we add together n spectra, the sum of the signal at any point, x, increases as nS_x, where S_x is the signal. The noise at any point, N_x, is a random event, which increases as $\sqrt{n}N_x$ when we add together n spectra. The ***signal-to-noise ratio*** after n scans, $(S/N)_n$ is

$$\left(\frac{S}{N}\right)_n = \frac{nS_x}{\sqrt{n}N_x} = \sqrt{n}\frac{S_x}{N_x}$$

where S_x/N_x is the signal-to-noise ratio for a single scan. The impact of signal averaging is shown in Figure 10.3.5 . The first spectrum shows the signal after one scan, which consists of a single, noisy peak. Signal averaging using 4 scans and 16 scans decreases the noise and improves the signal-to-noise ratio. One disadvantage of a photodiode array is that the effective bandwidth per diode is roughly an order of magnitude larger than that for a high quality monochromator.

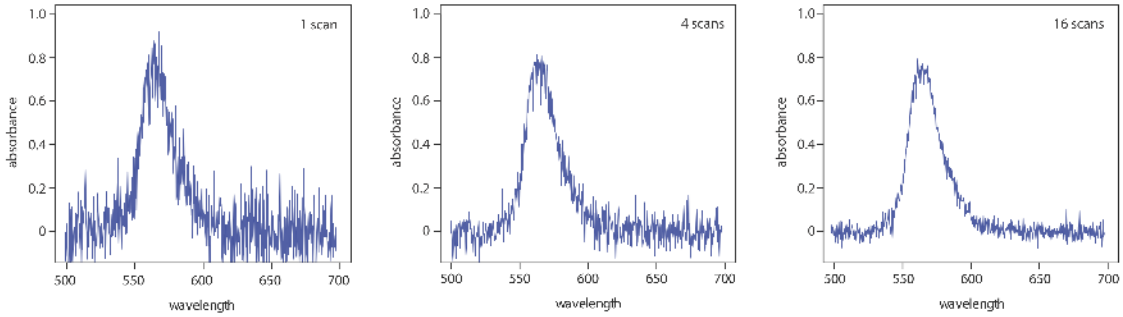


Figure 10.3.5 . Effect of signal averaging on a spectrum's signal-to-noise ratio. From top to bottom: spectrum for a single scan; average spectrum after four scans; and average spectrum after adding 16 scans.

For more details on signals and noise, see Introduction to Signals and Noise by Steven Petrovic, an on-line resource that is part of the Analytical Sciences Digital Library.

Sample Cells. The sample compartment provides a light-tight environment that limits stray radiation. Samples normally are in a liquid or solution state, and are placed in cells constructed with UV/Vis transparent materials, such as quartz, glass, and plastic (Figure 10.3.6). A quartz or fused-silica cell is required when working at a wavelength <300 nm where other materials show a significant absorption. The most common pathlength is 1 cm (10 mm), although cells with shorter (as little as 0.1 cm) and longer pathlengths (up to 10 cm) are available. Longer pathlength cells are useful when analyzing a very dilute solution or for gas samples. The highest quality cells allow the radiation to strike a flat surface at a 90° angle, minimizing the loss of radiation to reflection. A test tube often is used as a sample cell with simple, single-beam instruments, although differences in the cell's pathlength and optical properties add an additional source of error to the analysis.

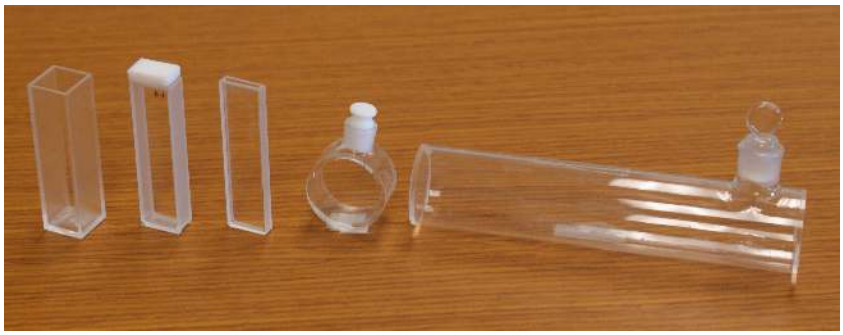


Figure 10.3.6 . Examples of sample cells for UV/Vis spectroscopy. From left to right (with path lengths in parentheses): rectangular plastic cuvette (10.0 mm), rectangular quartz cuvette (5.000 mm), rectangular quartz cuvette (1.000 mm), cylindrical quartz cuvette (10.00 mm), cylindrical glass cuvette with quartz windows (100.0 mm). Cells often are available as a matched pair, which is important when using a double-beam instrument.

If we need to monitor an analyte's concentration over time, it may not be possible to remove samples for analysis. This often is the case, for example, when monitoring an industrial production line or waste line, when monitoring a patient's blood, or when monitoring an environmental system, such as stream. With a ***fiber-optic probe*** we can analyze samples *in situ*. An example of a remote sensing fiber-optic probe is shown in Figure 10.3.7 . The probe consists of two bundles of fiber-optic cable. One bundle transmits radiation from the source to the probe's tip, which is designed to allow the sample to flow through the sample cell. Radiation from the source passes through the solution and is reflected back by a mirror. The second bundle of fiber-optic cable transmits the nonabsorbed radiation to the wavelength selector. Another design replaces the flow cell shown in Figure 10.3.7 with a membrane that contains a reagent that reacts with the analyte. When the analyte diffuses into the membrane it reacts with the reagent, producing a product that absorbs UV or visible radiation. The nonabsorbed radiation from the source is reflected or scattered back to the detector. Fiber optic probes that show chemical selectivity are called optrodes [(a) Seitz, W. R. *Anal. Chem.* **1984**, *56*, 16A–34A; (b) Angel, S. M. *Spectroscopy* **1987**, *2(2)*, 38–48].

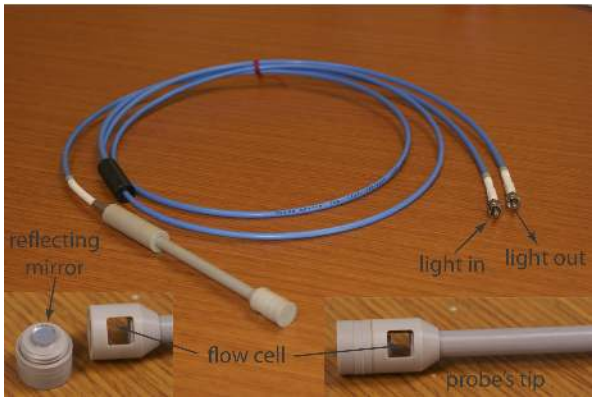


Figure 10.3.7 . Example of a fiber-optic probe. The inset photographs at the bottom of the figure provide close-up views of the probe's flow cell and the reflecting mirror.

INSTRUMENT DESIGNS FOR INFRARED ADSORPTION

Filter Photometer. The simplest instrument for IR absorption spectroscopy is a filter photometer similar to that shown in Figure 10.3.1 for UV/Vis absorption. These instruments have the advantage of portability and typically are used as dedicated analyzers for gases such as HCN and CO.

Double-beam spectrophotometer. Infrared instruments using a monochromator for wavelength selection use double-beam optics similar to that shown in Figure 10.3.3 . Double-beam optics are preferred over single-beam optics because the sources and detectors for infrared radiation are less stable than those for UV/Vis radiation. In addition, it is easier to correct for the absorption of infrared radiation by atmospheric CO_2 and H_2O vapor when using double-beam optics. Resolutions of 1–3 cm^{-1} are typical for most instruments.

Fourier transform spectrometer. In a Fourier transform infrared spectrometer, or FT–IR, the monochromator is replaced with an interferometer (Figure 10.1.13). Because an FT-IR includes only a single optical path, it is necessary to collect a separate spectrum to compensate for the absorbance of atmospheric CO_2 and H_2O vapor. This is done by collecting a background spectrum without the sample and storing the result in the instrument's computer memory. The background spectrum is removed from the sample's spectrum by taking the ratio the two signals. In comparison to other instrument designs, an FT–IR provides for rapid data acquisition, which allows for an enhancement in signal-to-noise ratio through signal-averaging.

Sample Cells. Infrared spectroscopy routinely is used to analyze gas, liquid, and solid samples. Sample cells are made from materials, such as NaCl and KBr, that are transparent to infrared radiation. Gases are analyzed using a cell with a pathlength of approximately 10 cm. Longer pathlengths are obtained by using mirrors to pass the beam of radiation through the sample several times.

A liquid sample may be analyzed using a variety of different sample cells (Figure 10.3.8). For non-volatile liquids a suitable sample is prepared by placing a drop of the liquid between two NaCl plates, forming a thin film that typically is less than 0.01 mm thick. Volatile liquids are placed in a sealed cell to prevent their evaporation.

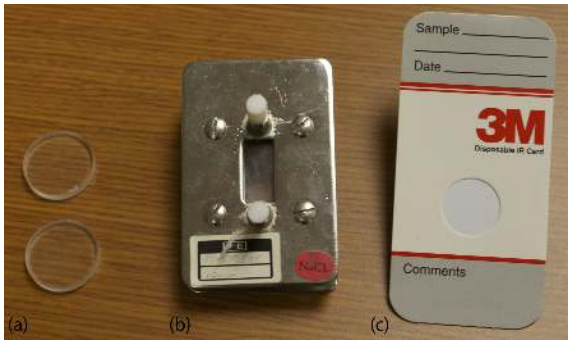


Figure 10.3.8 . Three examples of IR sample cells: (a) NaCl salts plates; (b) fixed pathlength (0.5 mm) sample cell with NaCl windows; (c) disposable card with a polyethylene window that is IR transparent with the exception of strong absorption bands at 2918 cm^{-1} and 2849 cm^{-1}.

The analysis of solution samples is limited by the solvent's IR absorbing properties, with CCl_4, CS_2, and $CHCl_3$ being the most common solvents. Solutions are placed in cells that contain two NaCl windows separated by a Teflon spacer. By changing the Teflon spacer, pathlengths from 0.015–1.0 mm are obtained.

Transparent solid samples are analyzed by placing them directly in the IR beam. Most solid samples, however, are opaque, and are first dispersed in a more transparent medium before recording the IR spectrum. If a suitable solvent is available, then the solid is analyzed by preparing a solution and analyzing as described above. When a suitable solvent is not available, solid samples are analyzed by preparing a mull of the finely powdered sample with a suitable oil. Alternatively, the powdered sample is mixed with KBr and pressed into an optically transparent pellet.

The analysis of an aqueous sample is complicated by the solubility of the NaCl cell window in water. One approach to obtaining an infrared spectrum of an aqueous solution is to use ***attenuated total reflectance*** instead of transmission. Figure 10.3.9 shows a diagram of a typical attenuated total reflectance (ATR) FT–IR instrument. The ATR cell consists of a high refractive index material, such as ZnSe or diamond, sandwiched between a low refractive index substrate and a lower refractive index sample. Radiation from the source enters the ATR crystal where it undergoes a series of internal reflections before exiting the crystal. During each reflection the radiation penetrates into the sample to a depth of a few microns, which results in a selective attenuation of the radiation at those wavelengths where the sample absorbs. ATR spectra are similar, but not identical, to those obtained by measuring the transmission of radiation.

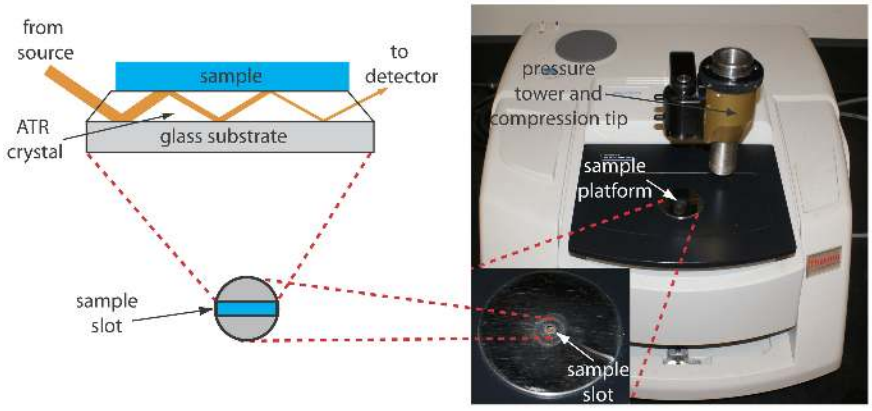


Figure 10.3.9 . FT-IR spectrometer equipped with a diamond ATR sample cell. The inserts show a close-up photo of the sample platform, a sketch of the ATR's sample slot, and a schematic showing how the source's radiation interacts with the sample. The pressure tower is used to ensure proper contact of a solid sample with the ATR crystal.

Solid samples also can be analyzed using an ATR sample cell. After placing the solid in the sample slot, a compression tip ensures that it is in contact with the ATR crystal. Examples of solids analyzed by ATR include polymers, fibers, fabrics, powders, and biological tissue samples. Another reflectance method is diffuse reflectance, in which radiation is reflected from a rough surface, such as a powder. Powdered samples are mixed with a non-absorbing material, such as powdered KBr, and the reflected light is collected and analyzed. As

with ATR, the resulting spectrum is similar to that obtained by conventional transmission methods. Further details about these, and other methods for preparing solids for infrared analysis can be found in this chapter's additional resources.

QUANTITATIVE APPLICATIONS

The determination of an analyte's concentration based on its absorption of ultraviolet or visible radiation is one of the most frequently encountered quantitative analytical methods. One reason for its popularity is that many organic and inorganic compounds have strong absorption bands in the UV/Vis region of the electromagnetic spectrum. In addition, if an analyte does not absorb UV/Vis radiation—or if its absorbance is too weak—we often can react it with another species that is strongly absorbing. For example, a dilute solution of Fe^{2+} does not absorb visible light. Reacting Fe^{2+} with *o*-phenanthroline, however, forms an orange–red complex of $Fe(phen)_3^{2+}$ that has a strong, broad absorbance band near 500 nm. An additional advantage to UV/Vis absorption is that in most cases it is relatively easy to adjust experimental and instrumental conditions so that Beer's law is obeyed.

A quantitative analysis based on the absorption of infrared radiation, although important, is encountered less frequently than with UV/Vis absorption. One reason is the greater tendency for instrumental deviations from Beer's law when using infrared radiation. Because an infrared absorption band is relatively narrow, any deviation due to the lack of monochromatic radiation is more pronounced. In addition, infrared sources are less intense than UV/Vis sources, which makes stray radiation more of a problem. Differences between the pathlengths for samples and for standards when using thin liquid films or KBr pellets are a problem, although an internal standard can correct for any difference in pathlength. Finally, establishing a 100%T ($A = 0$) baseline often is difficult because the optical properties of NaCl sample cells may change significantly with wavelength due to contamination and degradation. We can minimize this problem by measuring absorbance relative to a baseline established for the absorption band. Figure 10.3.10 shows how this is accomplished.

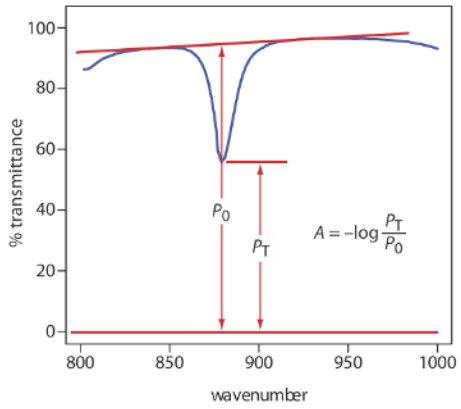


Figure 10.3.10 . Method for determining absorbance from an IR spectrum.

> Another approach is to use a cell with a fixed pathlength, such as that shown in Figure 10.3.8 b.

ENVIRONMENTAL APPLICATIONS

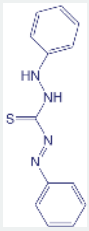
The analysis of waters and wastewaters often relies on the absorption of ultraviolet and visible radiation. Many of these methods are outlined in Table 10.3.1 . Several of these methods are described here in more detail.

Table 10.3.1 . Examples of Molecular UV/Vis Analysis of Waters and Wastewaters

analyte	method	λ (nm)
	trace metals	
aluminum	react with Eriochrome cyanide R dye at pH 6; forms red to pink complex	535
arsenic	reduce to AsH_3 using Zn and react with silver diethyldithiocarbamate; forms red complex	535
cadmium	extract into $CHCl_3$ containing dithizone from a sample made basic with NaOH; forms pink to red complex	518
chromium	oxidize to Cr(VI) and react with diphenylcarbazide; forms 540 red-violet product	540
copper	react with neocuprine in neutral to slightly acid solution and extract into $CHCl_3/CH_3OH$; forms yellow complex	457
iron	reduce to Fe^{2+} and react with *o*-phenanthroline; forms orange-red complex	510
lead	extract into $CHCl_3$ containing dithizone from sample made basic with NH_3/ NH_4^+ buffer; forms cherry red complex	510
manganese	oxidize to MnO_4^- with persulfate; forms purple solution	525
mercury	extract into $CHCl_3$ containing dithizone from acidic sample; forms orange complex	492
zinc	react with zincon at pH 9; forms blue complex	620
	inorganic nonmetals	
ammonia	reaction with hypochlorite and phenol using a manganous 630 salt catalyst; forms blue indophenol as product	630
cyanide	react with chloroamine-T to form CNCl and then with a pyridine-barbituric acid; forms a red-blue dye	578
fluoride	react with red Zr-SPADNS lake; formation of ZrF_6^{2-} decreases color of the red lake	570
chlorine (residual)	react with leuco crystal violet; forms blue product	592
nitrate	react with Cd to form NO_2^- and then react with sulfanilamide and *N*-(1-napthyl)-ethylenediamine; forms red azo 543 dye	543
phosphate	react with ammonium molybdate and then reduce with $SnCl_2$; forms molybdenum blue	690
	organics	
phenol	react with 4-aminoantipyrine and $K_3Fe(CN)_6$; forms yellow antipyrine dye	460
anionic surfactants	react with cationic methylene blue dye and extract into $CHCl_3$; forms blue ion pair	652

Although the quantitative analysis of metals in waters and wastewaters is accomplished primarily by atomic absorption or atomic emission spectroscopy, many metals also can be analyzed following the formation of a colored metal–ligand complex. One advantage to these spectroscopic methods is that they easily are adapted to the analysis of samples in the field using a filter photometer. One ligand used for the analysis of several metals is diphenylthiocarbazone, also known as dithizone. Dithizone is not soluble in water, but when a solution of dithizone in $CHCl_3$ is shaken with an aqueous solution that contains an appropriate metal ion, a colored metal–dithizonate complex forms that is soluble in $CHCl_3$. The selectivity of dithizone is controlled by adjusting the sample's pH. For example, Cd^{2+} is extracted from solutions made strongly basic with NaOH, Pb^{2+} from solutions made basic with an NH_3/ NH_4^+ buffer, and Hg^{2+} from solutions that are slightly acidic.

The structure of dithizone is shown below. See Chapter 7 for a discussion of extracting metal ions using dithizone.

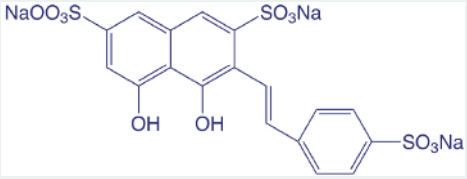


When chlorine is added to water the portion available for disinfection is called the chlorine residual. There are two forms of chlorine residual. The free chlorine residual includes Cl_2, HOCl, and OCl^-. The combined chlorine residual, which forms from the reaction of NH_3 with HOCl, consists of monochloramine, NH_2Cl, dichloramine, $NHCl_2$, and trichloramine, NCl_3. Because the free chlorine residual is more efficient as a disinfectant, there is an interest in methods that can distinguish between the total chlorine residual's different forms. One such method is the leuco crystal violet method. The free residual chlorine is determined by adding leuco crystal violet to the sample, which instantaneously oxidizes to give a blue-colored compound that is monitored at 592 nm. Completing the analysis in less than five minutes prevents a possible interference from the combined chlorine residual. The total chlorine residual (free + combined) is determined by reacting a separate sample with iodide, which reacts with both chlorine residuals to form HOI. When the reaction is complete, leuco crystal violet is added and oxidized by HOI, giving the same blue-colored product. The combined chlorine residual is determined by difference.

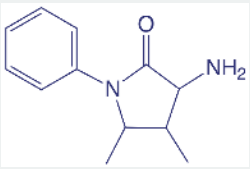
In Chapter 9 we explored how the total chlorine residual can be determined by a redox titration; see Representative Method 9.4.1 for further details. The method described here allows us to divide the total chlorine residual into its component parts.

The concentration of fluoride in drinking water is determined indirectly by its ability to form a complex with zirconium. In the presence of the dye SPADNS, a solution of zirconium forms a red colored compound, called a lake, that absorbs at 570 nm. When fluoride is added, the formation of the stable ZrF_6^{2-} complex causes a portion of the lake to dissociate, decreasing the absorbance. A plot of absorbance versus the concentration of fluoride, therefore, has a negative slope.

SPADNS, the structure of which is shown below, is an abbreviation for the sodium salt of 2-(4-sulfophenylazo)-1,8-dihydroxy-3,6-napthalenedisulfonic acid, which is a mouthful to say.



Spectroscopic methods also are used to determine organic constituents in water. For example, the combined concentrations of phenol and ortho- and meta-substituted phenols are determined by using steam distillation to separate the phenols from nonvolatile impurities. The distillate reacts with 4-aminoantipyrine at pH 7.9 ± 0.1 in the presence of $K_3Fe(CN)_6$ to a yellow colored antipyrine dye. After extracting the dye into $CHCl_3$, its absorbance is monitored at 460 nm. A calibration curve is prepared using only the unsubstituted phenol, C_6H_5OH. Because the molar absorptivity of substituted phenols generally are less than that for phenol, the reported concentration represents the minimum concentration of phenolic compounds.



4-aminoantipyrene

Molecular absorption also is used for the analysis of environmentally significant airborne pollutants. In many cases the analysis is carried out by collecting the sample in water, converting the analyte to an aqueous form that can be analyzed by methods such as those described in Table 10.3.1 . For example, the concentration of NO_2 is determined by oxidizing NO_2 to NO_3^-. The concentration of NO_3^- is then determined by first reducing it to NO_2^- with Cd, and then reacting NO_2^- with sulfanilamide and *N*-(1-naphthyl)-ethylenediamine to form a red azo dye. Another important application is the analysis for SO_2, which is determined by collecting the sample in an aqueous solution of $HgCl_4^{2-}$ where it reacts to form $Hg(SO_3)_2^{2-}$. Addition of *p*-rosaniline and formaldehyde produces a purple complex that is monitored at 569 nm. Infrared absorption is useful for the analysis of organic vapors, including HCN, SO_2, nitrobenzene, methyl mercaptan, and vinyl chloride. Frequently, these analyses are accomplished using portable, dedicated infrared photometers.

CLINICAL APPLICATIONS

The analysis of clinical samples often is complicated by the complexity of the sample's matrix, which may contribute a significant background absorption at the desired wavelength. The determination of serum barbiturates provides one example of how this problem is overcome. The barbiturates are first extracted from a sample of serum with $CHCl_3$ and then extracted from the $CHCl_3$ into 0.45 M NaOH (pH ≈ 13). The absorbance of the aqueous extract is measured at 260 nm, and includes contributions from the barbiturates as well as other components extracted from the serum sample. The pH of the sample is then lowered to approximately 10 by adding NH_4Cl and the absorbance remeasured. Because the barbiturates do not absorb at this pH, we can use the absorbance at pH 10, $A_{\text{pH 10}}$, to correct the absorbance at pH 13, $A_{\text{pH 13}}$

$$A_{\text{barb}} = A_{\text{pH 13}} - \frac{V_{\text{samp}} + V_{\text{NH}_4\text{Cl}}}{V_{\text{samp}}} \times A_{\text{pH 10}}$$

where A_{barb} is the absorbance due to the serum barbiturates and V_{samp} and $V_{\text{NH}_4\text{Cl}}$ are the volumes of sample and NH_4Cl, respectively. Table 10.3.2 provides a summary of several other methods for analyzing clinical samples.

Table 10.3.2 . Examples of the Molecular UV/Vis Analysis of Clinical Samples

analyte	method	λ (nm)
total serum protein	react with NaOH and Cu^{2+}; forms blue-violet complex	540
serum cholesterol	react with Fe^{3+} in presence of isopropanol, acetic acid, and H_2SO_4; forms blue-violet complex	540
uric acid	react with phosphotungstic acid; forms tungsten blue	710
serum barbituates	extract into $CHCl_3$ to isolate from interferents and then extract into 0.45 M NaOH	260
glucose	react with *o*-toludine at 100ºC; forms blue-green complex	630
protein-bound iodine	decompose protein to release iodide, which catalyzes redox reaction between Ce^{3+} and As^{3+}; forms yellow colored Ce^{4+}	420

INDUSTRIAL APPLICATIONS

UV/Vis molecular absorption is used for the analysis of a diverse array of industrial samples including pharmaceuticals, food, paint, glass, and metals. In many cases the methods are similar to those described in Table 10.3.1 and in Table 10.3.2 . For example, the amount of iron in food is determined by bringing the iron into solution and analyzing using the *o*-phenanthroline method listed in Table 10.3.1 .

Many pharmaceutical compounds contain chromophores that make them suitable for analysis by UV/Vis absorption. Products analyzed in this fashion include antibiotics, hormones, vitamins, and analgesics. One example of the use of UV absorption is in determining the purity of aspirin tablets, for which the active ingredient is acetylsalicylic acid. Salicylic acid, which is produced by the hydrolysis of acetylsalicylic acid, is an undesirable impurity in aspirin tablets, and should not be present at more than 0.01% w/w. Samples are screened for unacceptable levels of salicylic acid by monitoring the absorbance at a wavelength of 312 nm. Acetylsalicylic acid absorbs at 280 nm, but absorbs poorly at 312 nm. Conditions for preparing the sample are chosen such that an absorbance of greater than 0.02 signifies an unacceptable level of salicylic acid.

FORENSIC APPLICATIONS

UV/Vis molecular absorption routinely is used for the analysis of narcotics and for drug testing. One interesting forensic application is the determination of blood alcohol using the Breathalyzer test. In this test a 52.5-mL breath sample is bubbled through an acidified solution of $K_2Cr_2O_7$, which oxidizes ethanol to acetic acid. The concentration of ethanol in the breath sample is determined by a decrease in the absorbance at 440 nm where the dichromate ion absorbs. A blood alcohol content of 0.10%, which is above the legal limit, corresponds to 0.025 mg of ethanol in the breath sample.

DEVELOPING A QUANTITATIVE METHOD FOR A SINGLE COMPONENT

To develop a quantitative analytical method, the conditions under which Beer's law is obeyed must be established. First, the most appropriate wavelength for the analysis is determined from an absorption spectrum. In most cases the best wavelength corresponds to an absorption maximum because it provides greater sensitivity and is less susceptible to instrumental limitations. Second, if the instrument has adjustable slits, then an appropriate slit width is chosen. The absorption spectrum also aids in selecting a slit width by choosing a width that is narrow enough to avoid instrumental limita- tions to Beer's law, but wide enough to increase the throughput of source radiation. Finally, a calibration curve is constructed to determine the range of concentrations for which Beer's law is valid. Additional considerations that are important in any quantitative method are the effect of potential interferents and establishing an appropriate blank.

REPRESENTATIVE METHOD 10.3.1: DETERMINATION OF IRON IN WATER AND WASTEWATER

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of iron in water and waste- water provides an instructive example of a typical procedure. The description here is based on Method 3500-Fe B as published in *Standard Methods for the Examination of Water and Wastewater*, 20th Ed., American Public Health Association: Washington, D. C., 1998.

Description of Method

Iron in the +2 oxidation state reacts with *o*-phenanthroline to form the orange-red $Fe(phen)_3^{2+}$ complex. The intensity of the complex's color is independent of the solution's acidity between a pH of 3 and 9. Because the complex forms more rapidly at lower pH levels, the reaction usually is carried out within a pH range of 3.0–3.5. Any iron present in the +3 oxidation state is reduced with hydroxylamine before adding *o*-phenanthroline. The most important interferents are strong oxidizing agents, polyphosphates, and metal ions such as Cu^{2+}, Zn^{2+}, Ni^{2+}, and Cd^{2+}. An interference from oxidizing agents is minimized by adding an excess of hydroxylamine, and an interference from polyphosphate is minimized by boiling the sample in the presence of acid. The absorbance of samples and standards are measured at a wavelength of 510 nm using a 1-cm cell (longer pathlength cells also may be used). Beer's law is obeyed for concentrations of within the range of 0.2–4.0 mg Fe/L.

Procedure

For a sample that contains less than 2 mg Fe/L, directly transfer a 50-mL portion to a 125-mL Erlenmeyer flask. Samples that contain more than 2 mg Fe/L are diluted before acquiring the 50-mL portion. Add 2 mL of concentrated HCl and 1 mL of hydroxylamine to the sample. Bring the solution to a boil and continue boiling until the solution's volume is reduced to between 15 and 20 mL. After cooling to room temperature, transfer the solution to a 50-mL volumetric flask, add 10 mL of an ammonium acetate buffer, 2 mL of a 1000 ppm solution of

o-phenanthroline, and dilute to volume. Allow 10–15 minutes for color development before measuring the absorbance, using distilled water to set 100% T. Calibration standards, including a blank, are prepared by the same procedure using a stock solution that contains a known concentration of Fe^{2+}.

Questions

1. Explain why strong oxidizing agents are interferents and why an excess of hydroxylamine prevents the interference.

A strong oxidizing agent will oxidize some Fe^{2+} to Fe^{3+}. Because $Fe(phen)_3^{3+}$ does not absorb as strongly as $Fe(phen)_3^{2+}$, the absorbance is smaller than expected, which produces a negative determinate error. The excess hydroxylamine reacts with the oxidizing agents, removing them from the solution.

2. The color of the complex is stable between pH levels of 3 and 9. What are some possible complications at more acidic or at more basic pH's?

Because *o*-phenanthroline is a weak base, its conditional formation constant for $Fe(phen)_3^{2+}$ becomes smaller at more acidic pH levels, where *o*-phenanthroline is present in its protonated form. The result is a decrease in absorbance and a less sensitive analytical method. When the pH is greater than 9, competition between OH^- and *o*-phenanthroline for Fe^{2+} also decreases the absorbance. In addition, if the pH is sufficiently basic there is a risk that the iron will precipitate as $Fe(OH)_2$.

3. Cadmium is an interferent because it forms a precipitate with *o*-phenanthroline. What effect does the formation of precipitate have on the determination of iron?

Because *o*-phenanthroline is present in large excess (2000 µg of *o*-phenanthroline for 100 µg of $Fe2^+$), it is not likely that the interference is due to an insufficient amount of *o*-phenanthroline being available to react with the Fe^{2+}. The presence of a precipitate in the sample cell results in the scattering of radiation, which causes an apparent increase in absorbance. Because the measured absorbance increases, the reported concentration is too high. Although scattering is a problem here, it can serve as the basis of a useful analytical method. See Chapter 10.8 for further details.

4. Even high quality ammonium acetate contains a significant amount of iron. Why is this source of iron not a problem?

Because all samples and standards are prepared using the same volume of ammonium acetate buffer, the contribution of this source of iron is accounted for by the calibration curve's reagent blank.

QUANTITATIVE ANALYSIS FOR A SINGLE SAMPLE

To determine the concentration of an analyte we measure its absorbance and apply Beer's law using any of the standardization methods described in Chapter 5. The most common methods are a normal calibration curve using external standards and the method of standard additions. A single point standardization also is possible, although we must first verify that Beer's law holds for the concentration of analyte in the samples and the standard.

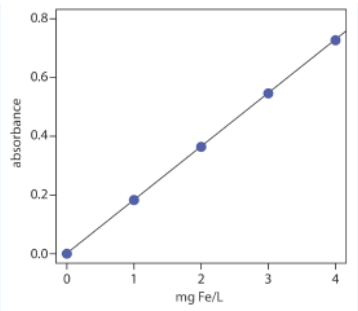
EXAMPLE 10.3.1

The determination of iron in an industrial waste stream is carried out by the *o*-phenanthroline described in Representative Method 10.3.1. Using the data in the following table, determine the mg Fe/L in the waste stream.

mg Fe/L	absorbance
0.00	0.000
1.00	0.183
2.00	0.364
3.00	0.546
4.00	0.727
sample	0.269

Solution

Linear regression of absorbance versus the concentration of Fe in the standards gives the calibration curve and calibration equation shown here



$$A = 0.0006 + \left(0.1817\ \text{mg}^{-1}\text{L}\right) \times (\text{mgFe/L})$$

Substituting the sample's absorbance into the calibration equation gives the concentration of Fe in the waste stream as 1.48 mg Fe/L

? EXERCISE 10.3.1

The concentration of Cu^{2+} in a sample is determined by reacting it with the ligand cuprizone and measuring its absorbance at 606 nm in a 1.00-cm cell. When a 5.00-mL sample is treated with cuprizone and diluted to 10.00 mL, the resulting solution has an absorbance of 0.118. A second 5.00-mL sample is mixed with 1.00 mL of a 20.00 mg/L standard of Cu^{2+}, treated with cuprizone and diluted to 10.00 mL, giving an absorbance of 0.162. Report the mg Cu^{2+}/L in the sample.

Answer

For this standard addition we write equations that relate absorbance to the concentration of Cu^{2+} in the sample before the standard addition

$$0.118 = \varepsilon b \left[C_{\text{Cu}} \times \frac{5.00\ \text{mL}}{10.00\ \text{mL}} \right]$$

and after the standard addition

$$0.162 = \varepsilon b \left(C_{\text{Cu}} \times \frac{5.00\ \text{mL}}{10.00\ \text{mL}} + \frac{20.00\ \text{mg Cu}}{\text{L}} \times \frac{1.00\ \text{mL}}{10.00\ \text{mL}} \right)$$

in each case accounting for the dilution of the original sample and for the standard. The value of εb is the same in both equation. Solving each equation for εb and equating

$$\frac{0.162}{C_{\text{Cu}} \times \frac{5.00\ \text{mL}}{10.00\ \text{mL}} + \frac{20.00\ \text{mg Cu}}{\text{L}} \times \frac{1.00\ \text{mL}}{10.00\ \text{mL}}} = \frac{0.118}{C_{\text{Cu}} \times \frac{5.00\ \text{mL}}{10.00\ \text{mL}}}$$

leaves us with an equation in which C_{Cu} is the only variable. Solving for C_{Cu} gives its value as

$$\frac{0.162}{0.500 \times C_{\text{Cu}} + 2.00\ \text{mg Cu/L}} = \frac{0.118}{0.500 \times C_{\text{Cu}}}$$

$$0.0810 \times C_{\text{Cu}} = 0.0590 \times C_{\text{Ca}} + 0.236\ \text{mg Cu/L}$$

$$0.0220 \times C_{\text{Cu}} = 0.236\ \text{mg Cu/L}$$

$$C_{\text{Cu}} = 10.7\ \text{mg Cu/L}$$

QUANTITATIVE ANALYSIS OF MIXTURES

Suppose we need to determine the concentration of two analytes, *X* and *Y*, in a sample. If each analyte has a wavelength where the other analyte does not absorb, then we can proceed using the approach in Example 10.3.5 . Unfortunately, UV/Vis absorption bands are so broad that frequently it is not possible to find suitable wavelengths. Because Beer's law is additive the mixture's absorbance, A_{mix}, is

$$(A_{mix})_{\lambda_1} = (\varepsilon_x)_{\lambda_1} bC_X + (\varepsilon_Y)_{\lambda_1} bC_Y \tag{11.3.1}$$

where λ_1 is the wavelength at which we measure the absorbance. Because Equation 11.3.1 includes terms for the concentration of both *X* and *Y*, the absorbance at one wavelength does not provide enough information to determine either C_X or C_Y. If we measure the absorbance at a second wavelength

$$(A_{mix})_{\lambda_2} = (\varepsilon_x)_{\lambda_2} bC_X + (\varepsilon_Y)_{\lambda_2} bC_Y \tag{11.3.2}$$

then we can determine C_X and C_Y by solving simultaneously Equation 11.3.1 and Equation 11.3.2. Of course, we also must determine the value for ε_X and ε_Y at each wavelength. For a mixture of *n* components, we must measure the absorbance at *n* different wavelengths.

EXAMPLE 10.3.2

The concentrations of Fe^{3+} and Cu^{2+} in a mixture are determined following their reaction with hexacyanoruthenate (II), $Ru(CN)_6^{4-}$, which forms a purple-blue complex with Fe^{3+} (λ_{max} = 550 nm) and a pale-green complex with Cu^{2+} (λ_{max} = 396 nm) [DiTusa, M. R.; Schlit, A. A. *J. Chem. Educ.* **1985**, *62*, 541–542]. The molar absorptivities (M^{-1} cm^{-1}) for the metal complexes at the two wavelengths are summarized in the following table.

analyte	ε_{550}	ε_{396}
Fe^{3+}	9970	84
Cu^{2+}	34	856

When a sample that contains Fe^{3+} and Cu^{2+} is analyzed in a cell with a pathlength of 1.00 cm, the absorbance at 550 nm is 0.183 and the absorbance at 396 nm is 0.109. What are the molar concentrations of Fe^{3+} and Cu^{2+} in the sample?

Solution

Substituting known values into Equation 11.3.1 and Equation 11.3.2 gives

$$\begin{aligned} A_{550} &= 0.183 = 9970C_{Fe} + 34C_{Cu} \\ A_{396} &= 0.109 = 84C_{Fe} + 856C_{Cu} \end{aligned}$$

To determine C_{Fe} and C_{Cu} we solve the first equation for C_{Cu}

$$C_{Cu} = \frac{0.183 - 9970C_{Fe}}{34}$$

and substitute the result into the second equation.

$$\begin{aligned} 0.109 &= 84C_{Fe} + 856 \times \frac{0.183 - 9970C_{Fe}}{34} \\ &= 4.607 - \left(2.51 \times 10^5\right) C_{Fe} \end{aligned}$$

Solving for C_{Fe} gives the concentration of Fe^{3+} as 1.8×10^{-5} M. Substituting this concentration back into the equation for the mixture's absorbance at 396 nm gives the concentration of Cu^{2+} as 1.3×10^{-4} M.

Another approach to solving Example 10.3.2 is to multiply the first equation by 856/34 giving

$$4.607 = 251009C_{Fe} + 856C_{Cu}$$

Subtracting the second equation from this equation

$$\begin{aligned} 4.607 &= 251009C_{Fe} + 856C_{Cu} \\ -0.109 &= 84C_{Fe} + 856C_{Cu} \end{aligned}$$

gives

$$4.498 = 250925C_{Fe}$$

and we find that C_{Fe} is 1.8×10^{-5}. Having determined C_{Fe} we can substitute back into one of the other equations to solve for C_{Cu}, which is 1.3×10^{-5}.

EXERCISE 10.3.2

The absorbance spectra for Cr^{3+} and Co^{2+} overlap significantly. To determine the concentration of these analytes in a mixture, its absorbance is measured at 400 nm and at 505 nm, yielding values of 0.336 and 0.187, respectively. The individual molar absorptivities (M^{-1} cm^{-1}) for $Cr3^{+}$ are 15.2 at 400 nm and 0.533 at 505 nm; the values for Co^{2+} are 5.60 at 400 nm and 5.07 at 505 nm.

Answer

Substituting into Equation 11.3.1 and Equation 11.3.2 gives

$$A_{400} = 0.336 = 15.2C_{Cr} + 5.60C_{Co}$$

$$A_{400} = 0187 = 0.533C_{Cr} + 5.07C_{Co}$$

To determine C_{Cr} and C_{Co} we solve the first equation for C_{Co}

$$C_{Co} = \frac{0.336 - 15.2C_{Co}}{5.60}$$

and substitute the result into the second equation.

$$0.187 = 0.533C_{Cr} + 5.07 \times \frac{0.336 - 15.2C_{Co}}{5.60}$$

$$0.187 = 0.3042 - 13.23C_{Cr}$$

Solving for C_{Cr} gives the concentration of Cr^{3+} as 8.86×10^{-3} M. Substituting this concentration back into the equation for the mixture's absorbance at 400 nm gives the concentration of Co^{2+} as 3.60×10^{-2} M.

To obtain results with good accuracy and precision the two wavelengths should be selected so that $\varepsilon_X > \varepsilon_Y$ at one wavelength and $\varepsilon_X < \varepsilon_Y$ at the other wavelength. It is easy to appreciate why this is true. Because the absorbance at each wavelength is dominated by one analyte, any uncertainty in the concentration of the other analyte has less of an impact. Figure 10.3.11 shows that the choice of wavelengths for Practice Exercise 10.3.2 are reasonable. When the choice of wavelengths is not obvious, one method for locating the optimum wavelengths is to plot $\varepsilon_X/\varepsilon_y$ as function of wavelength, and determine the wavelengths where $\varepsilon_X/\varepsilon_y$ reaches maximum and minimum values [Mehra, M. C.; Rioux, J. *J. Chem. Educ.* **1982**, *59*, 688–689].

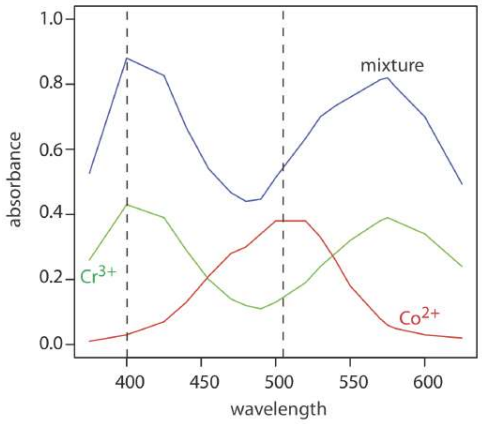


Figure 10.3.11 . Visible absorption spectra for 0.0250 M Cr^{3+}, 0.0750 M Co^{2+}, and for a mixture of Cr^{3+} and Co^{2+}. The two wavelengths used to analyze the mixture of Cr^{3+} and Co^{2+} are shown by the dashed lines. The data for the two standards are from Brewer, S. *Solving Problems in Analytical Chemistry*, John Wiley & Sons: New York, 1980.

When the analyte's spectra overlap severely, such that $\varepsilon_X \approx \varepsilon_Y$ at all wavelengths, other computational methods may provide better accuracy and precision. In a multiwavelength linear regression analysis, for example, a mixture's absorbance is compared to that for a set of standard solutions at several wavelengths [Blanco, M.; Iturriaga, H.; Maspoch, S.; Tarin, P. *J. Chem. Educ.* **1989**, *66*, 178–180]. If A_{SX} and A_{SY} are the absorbance values for standard solutions of components *X* and *Y* at any wavelength, then

$$A_{SX} = \varepsilon_X b C_{SX} \tag{11.3.3}$$

$$A_{SY} = \varepsilon_Y b C_{SY} \tag{11.3.4}$$

where C_{SX} and C_{SY} are the known concentrations of *X* and *Y* in the standard solutions. Solving Equation 11.3.3 and Equation 11.3.4 for ε_X and for ε_Y, substituting into Equation 11.3.1, and rearranging, gives

$$\frac{A_{mix}}{A_{SX}} = \frac{C_X}{C_{SX}} + \frac{C_Y}{C_{SY}} \times \frac{A_{SY}}{A_{SX}}$$

To determine C_X and C_Y the mixture's absorbance and the absorbances of the standard solutions are measured at several wavelengths. Graphing A_{mix}/A_{SX} versus A_{SY}/A_{SX} gives a straight line with a slope of C_Y/C_{SY} and a *y*-intercept of C_X/C_{SX}. This approach is particularly helpful when it is not possible to find wavelengths where $\varepsilon_X > \varepsilon_Y$ and $\varepsilon_X < \varepsilon_Y$.

The approach outlined here for a multiwavelength linear regression uses a single standard solution for each analyte. A more rigorous approach uses multiple standards for each analyte. The math behind the analysis of such data—which we call a multiple linear regression—is beyond the level of this text. For more details about multiple linear regression see Brereton, R. G. *Chemometrics: Data Analysis for the Laboratory and Chemical Plant*, Wiley: Chichester, England, 2003.

EXAMPLE 10.3.3

Figure $PageIndex{10.11}$ shows visible absorbance spectra for a standard solution of 0.0250 M Cr^{3+}, a standard solution of 0.0750 M Co^{2+}, and a mixture that contains unknown concentrations of each ion. The data for these spectra are shown here.

λ (nm)	A_{Cr}	A_{Cu}	A_{mix}	λ (nm)	A_{Cr}	A_{Cu}	A_{mix}
375	0.26	0.01	0.53	520	0.19	0.38	0.63
400	0.43	0.03	0.88	530	0.24	0.33	0.70
425	0.39	0.07	0.83	540	0.28	0.26	0.73
440	0.29	0.13	0.67	550	0.32	0.18	0.76
455	0.20	0.21	0.54	570	0.38	0.08	0.81
470	0.14	0.28	0.47	575	0.39	0.06	0.82
480	0.12	0.30	0.44	580	0.38	0.05	0.79
490	0.11	0.34	0.45	600	0.34	0.03	0.70
500	0.13	0.38	0.51	625	0.24	0.02	0.49

Use a multiwavelength regression analysis to determine the composition of the unknown.

Solution

First we need to calculate values for A_{mix}/A_{SX} and for A_{SY}/A_{SX}. Let's define X as Co^{2+} and Y as Cr^{3+}. For example, at a wavelength of 375 nm A_{mix}/A_{SX} is 0.53/0.01, or 53 and A_{SY}/A_{SX} is 0.26/0.01, or 26. Completing the calculation for all wavelengths and graphing A_{mix}/A_{SX} versus A_{SY}/A_{SX} gives the calibration curve shown in Figure 10.3.12 . Fitting a straight-line to the data gives a regression model of

$$\frac{A_{\text{mix}}}{A_{SX}} = 0.636 + 2.01 \times \frac{A_{SY}}{A_{SX}}$$

Using the *y*-intercept, the concentration of Co^{2+} is

$$\frac{C_X}{C_{SX}} = \frac{\left[\text{Co}^{2+}\right]}{0.0750\text{M}} = 0.636$$

or $[Co^{2+}]$ = 0.048 M; using the slope the concentration of Cr^{3+} is

$$\frac{C_Y}{C_{SY}} = \frac{\left[\text{Cr}^{3+}\right]}{0.0250\text{M}} = 2.01$$

or $[Cr^{3+}]$ = 0.050 M.

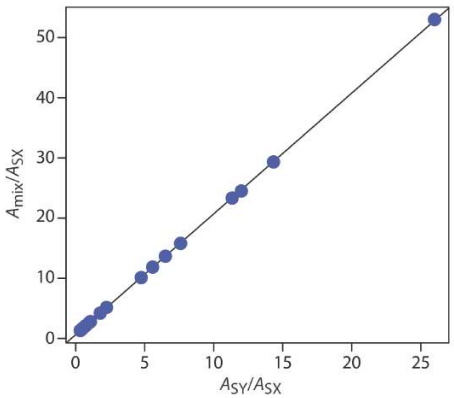


Figure 10.3.12 . Multiwavelength linear regression analysis for the data in Example 10.3.3 .

EXERCISE 10.3.3

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A mixture of MnO_4^- and $Cr_2O_7^{2-}$, and standards of 0.10 mM $KMnO_4$ and of 0.10 mM $K_2Cr_2O_7$ give the results shown in the following table. Determine the composition of the mixture. The data for this problem is from Blanco, M. C.; Iturriaga, H.; Maspoch, S.; Tarin, P. *J. Chem. Educ.* **1989**, *66*, 178–180.

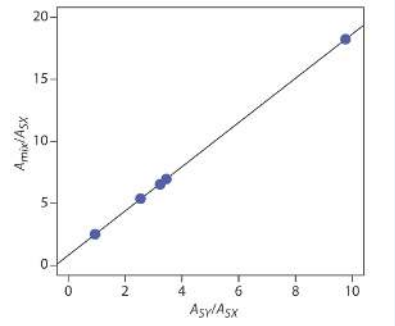
λ (nm)	A_{Mn}	A_{Cr}	A_{mix}
266	0.042	0.410	0.766
288	0.082	0.283	0.571
320	0.168	0.158	0.422
350	0.125	0.318	0.672
360	0.036	0.181	0.366

Answer

Letting *X* represent MnO_4^- and letting *Y* represent $Cr_2O_7^{2-}$, we plot the equation

$$\frac{A_{mix}}{A_{SX}} = \frac{C_X}{C_{SX}} + \frac{C_Y}{C_{SY}} \times \frac{A_{SY}}{A_{SX}}$$

placing A_{mix}/A_{SX} on the *y*-axis and A_{SY}/A_{SX} on the *x*-axis. For example, at a wavelength of 266 nm the value A_{mix}/A_{SX} of is 0.766/0.042, or 18.2, and the value of A_{SY}/A_{SX} is 0.410/0.042, or 9.76. Completing the calculations for all wavelengths and plotting the data gives the result shown here



Fitting a straight-line to the data gives a regression model of

$$\frac{A_{\text{mix}}}{A_{\text{SX}}} = 0.8147 + 1.7839 \times \frac{A_{SY}}{A_{SX}}$$

Using the *y*-intercept, the concentration of MnO_4^- is

$$\frac{C_X}{C_{SX}} = 0.8147 = \frac{[MnO_4^-]}{1.0 \times 10^{-4}\ \text{M}\ MnO_4^-}$$

or 8.15×10^{-5} M MnO_4^-, and using the slope, the concentration of $Cr_2O_7^{2-}$ is

$$\frac{C_Y}{C_{SY}} = 1.7839 = \frac{[Cr_2O_7^{2-}]}{1.00 \times 10^{-4}\ \text{M}\ Cr_2O_7^{2-}}$$

or 1.78×10^{-4} M $Cr_2O_7^{2-}$.

QUALITATIVE APPLICATIONS

As discussed in Chapter 10.2, ultraviolet, visible, and infrared absorption bands result from the absorption of electromagnetic radiation by specific valence electrons or bonds. The energy at which the absorption occurs, and the intensity of that absorption, is determined by the chemical environment of the absorbing moiety. For example, benzene has several ultraviolet absorption bands due to $\pi \rightarrow \pi^*$ transitions. The position and intensity of two of these bands, 203.5 nm (ε = 7400 M^{-1} cm^{-1}) and 254 nm (ε = 204 M^{-1} cm^{-1}), are sensitive to substitution. For benzoic acid, in which a carboxylic acid group replaces one of the aromatic hydrogens, the two bands shift to 230 nm (ε = 11600 M^{-1} cm^{-1}) and 273 nm (ε = 970 M^{-1} cm^{-1}). A variety of rules have been developed to aid in correlating UV/Vis absorption bands to chemical structure. Similar correlations are available for infrared absorption bands. For example a carbonyl's C=O stretch is sensitive to adjacent functional groups, appearing at 1650 cm^{-1} for acids, 1700 cm^{-1} for ketones, and 1800 cm^{-1} for acid chlorides. The interpretation of UV/ Vis and IR spectra receives adequate coverage elsewhere in the chemistry curriculum, notably in organic chemistry, and is not considered further in this text.

With the availability of computerized data acquisition and storage it is possible to build digital libraries of standard reference spectra. The identity of an a unknown compound often can be determined by comparing its spectrum against a library of reference spectra, a process known as ***spectral searching***. Comparisons are made using an algorithm that calculates the cumulative difference between the sample's spectrum and a reference spectrum. For example, one simple algorithm uses the following equation

$$D = \sum_{i=1}^{n} |(A_{sample})_i - (A_{reference})_i|$$

where D is the cumulative difference, A_{sample} is the sample's absorbance at wavelength or wavenumber i, $A_{reference}$ is the absorbance of the reference compound at the same wavelength or wavenumber, and n is the number of digitized points in the spectra. The cumulative difference is calculated for each reference spectrum. The reference compound with the smallest value of D is the closest match to the unknown compound. The accuracy of spectral searching is limited by the number and type of compounds included in the library, and by the effect of the sample's matrix on the spectrum.

Another advantage of computerized data acquisition is the ability to subtract one spectrum from another. When coupled with spectral searching it is possible to determine the identity of several components in a sample without the need of a prior separation step by repeatedly searching and sub- tracting reference spectra. An example is shown in Figure 10.3.13 in which the composition of a two-component mixture is determined by successive searching and subtraction. Figure 10.3.13 a shows the spectrum of the mixture. A search of the spectral library selects cocaine•HCl (Figure 10.3.13 b) as a likely component of the mixture. Subtracting the reference spectrum for cocaine•HCl from the mixture's spectrum leaves a result (Figure 10.3.13 c) that closely matches mannitol's reference spectrum (Figure 10.3.13 d). Subtracting the reference spectrum for mannitol leaves a small residual signal (Figure 10.3.13 e).

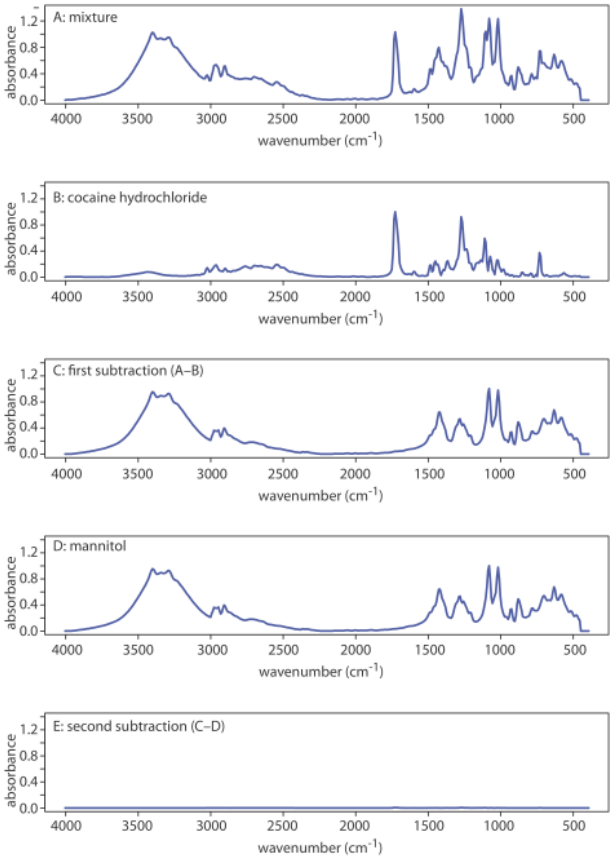


Figure 10.3.13 . Identifying the components of a mixture by spectral searching and subtracting. (a) IR spectrum of the mixture; (b) Reference IR spectrum of cocaine•HCl; (c) Result of subtracting the spectrum of cocaine•HCl from the mixture's spectrum; (d) Reference IR spectrum of mannitol; and (e) The residual spectrum after removing mannitol's contribution to the mixture's spectrum. IR spectra traditionally are displayed using percent transmittance, %T, along the *y*-axis (for example, see Figure 10.2.2). Because absorbance—not percent transmittance—is a linear function of concentration, spectral searching and spectral subtraction, is easier to do when displaying absorbance on the *y*-axis.

CHARACTERIZATION APPLICATIONS

Molecular absorption, particularly in the UV/Vis range, has been used for a variety of different characterization studies, including determining the stoichiometry of metal–ligand complexes and determining equilibrium constants. Both of these examples are examined in

this section.

STOICHIOMETRY OF A METAL-LIGAND COMPLEX

We can determine the stoichiometry of the metal–ligand complexation reaction

$$\mathrm{M} + y\mathrm{L} \rightleftharpoons \mathrm{ML}_y$$

using one of three methods: the method of continuous variations, the mole-ratio method, and the slope-ratio method. Of these approaches, the ***method of continuous variations***, also called Job's method, is the most popular. In this method a series of solutions is prepared such that the total moles of metal and of ligand, n_{total}, in each solution is the same. If $(n_{\mathrm{M}})_i$ and $(n_{\mathrm{L}})_i$ are, respectively, the moles of metal and ligand in solution i, then

$$n_{\text{total}} = (n_{\mathrm{M}})_i + (n_{\mathrm{L}})_i$$

The relative amount of ligand and metal in each solution is expressed as the mole fraction of ligand, $(X_{\mathrm{L}})i$, and the mole fraction of metal, $(X_{\mathrm{M}})_i$,

$$(X_{\mathrm{L}})_i = \frac{(n_{\mathrm{L}})_i}{n_{\text{total}}}$$

$$(X_M)_i = 1 - \frac{(n_{\mathrm{L}})_i}{n_{\text{total}}} = \frac{(n_{\mathrm{M}})_i}{n_{\text{total}}}$$

The concentration of the metal–ligand complex in any solution is determined by the limiting reagent, with the greatest concentration occurring when the metal and the ligand are mixed stoichiometrically. If we monitor the complexation reaction at a wavelength where only the metal–ligand complex absorbs, a graph of absorbance versus the mole fraction of ligand has two linear branches—one when the ligand is the limiting reagent and a second when the metal is the limiting reagent. The intersection of the two branches represents a stoichiometric mixing of the metal and the ligand. We use the mole fraction of ligand at the intersection to determine the value of y for the metal–ligand complex ML_y.

$$y = \frac{n_{\mathrm{L}}}{n_{\mathrm{M}}} = \frac{X_{\mathrm{L}}}{X_{\mathrm{M}}} = \frac{X_{\mathrm{L}}}{1 - X_{\mathrm{L}}}$$

> You also can plot the data as absorbance versus the mole fraction of metal. In this case, y is equal to $(1 - X_{\mathrm{M}})/X_{\mathrm{M}}$.

EXAMPLE 10.3.4

To determine the formula for the complex between Fe^{2+} and *o*-phenanthroline, a series of solutions is prepared in which the total concentration of metal and ligand is held constant at 3.15×10^{-4} M. The absorbance of each solution is measured at a wavelength of 510 nm. Using the following data, determine the formula for the complex.

X_{L}	absorbance	X_{L}	absorbance
0.000	0.000	0.600	0.693
0.100	0.116	0.700	0.809
0.200	0.231	0.800	0.693
0.300	0.347	0.900	0.347
0.400	0.462	1.000	0.000
0.500	0.578		

Solution

A plot of absorbance versus the mole fraction of ligand is shown in Figure 10.3.14 . To find the maximum absorbance, we extrapolate the two linear portions of the plot. The two lines intersect at a mole fraction of ligand of 0.75. Solving for y gives

$$y = \frac{X_L}{1 - X_L} = \frac{0.75}{1 - 0.75} = 3$$

The formula for the metal–ligand complex is $\mathrm{Fe(phen)}_3^{2+}$.

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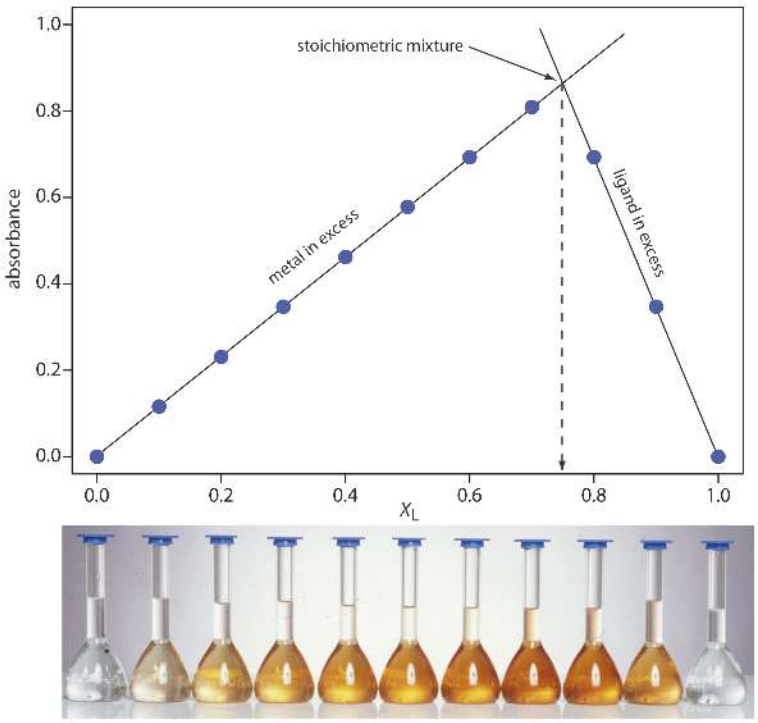


Figure 10.3.14 . Continuous variations plot for Example 10.3.4 . The photo shows the solutions used to gather the data. Each solution is displayed directly below its coresponding point on the continuous variations plot. To prepare these solutions I first prepared a solution of 3.15×10^{-4} M Fe^{2+} and a solution of 3.15×10^{-4} M *o*-phenanthroline. Because the two stock solutions have the same concentration, diluting a portion of one solution with the other solution gives a mixture in which the combined concentration of *o*-phenanthroline and Fe^{2+} is 3.15×10^{-4} M. Because each solution has the same volume, each solution also contains the same total moles of metal and ligand.

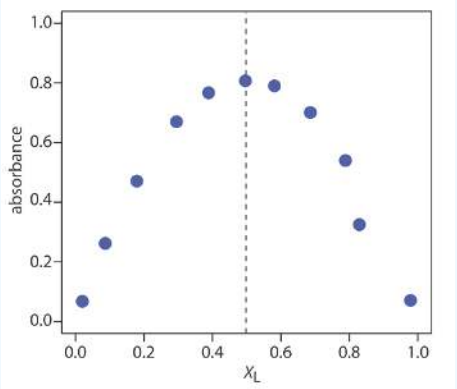
? EXERCISE 10.3.4

Use the continuous variations data in the following table to determine the formula for the complex between Fe^{2+} and SCN^-. The data for this problem is adapted from Meloun, M.; Havel, J.; Högfeldt, E. *Computation of Solution Equilibria*, Ellis Horwood: Chichester, England, 1988, p. 236.

X_L	absorbance	X_L	absorbance	X_L	absorbance	X_L	absorbance
0.0200	0.068	0.2951	0.670	0.5811	0.790	0.8923	0.324
0.0870	0.262	0.3887	0.767	0.6860	0.701	0.9787	0.071
0.1792	0.471	0.4964	0.807	0.7885	0.540		

Answer

The figure below shows a continuous variations plot for the data in this exercise. Although the individual data points show substantial curvature—enough curvature that there is little point in trying to draw linear branches for excess metal and excess ligand —the maximum absorbance clearly occurs at $X_L \approx 0.5$. The complex's stoichiometry, therefore, is $Fe(SCN)^{2+}$.



Several precautions are necessary when using the method of continuous variations. First, the metal and the ligand must form only one metal–ligand complex. To determine if this condition is true, plots of absorbance versus X_L are constructed at several different wavelengths and for several different values of n_{total}. If the maximum absorbance does not occur at the same value of X_L for each set of conditions, then more than one metal–ligand complex is present. A second precaution is that the metal–ligand complex's absorbance must obey Beer's law. Third, if the metal–ligand complex's formation constant is relatively small, a plot of absorbance versus X_L may show significant curvature. In this case it often is difficult to determine the stoichiometry by extrapolation. Finally, because the stability of a metal–ligand complex may be influenced by solution conditions, it is necessary to control carefully the composition of the solutions. When the ligand is a weak base, for example, each solutions must be buffered to the same pH.

In the ***mole-ratio method*** the moles of one reactant, usually the metal, is held constant, while the moles of the other reactant is varied. The absorbance is monitored at a wavelength where the metal–ligand complex absorbs. A plot of absorbance as a function of the ligand-to-metal mole ratio, n_L/n_M, has two linear branches that intersect at a mole–ratio corresponding to the complex's formula. Figure 10.3.15 a shows a mole-ratio plot for the formation of a 1:1 complex in which the absorbance is monitored at a wavelength where only the complex absorbs. Figure 10.3.15 b shows a mole-ratio plot for a 1:2 complex in which all three species—the metal, the ligand, and the complex—absorb at the selected wavelength. Unlike the method of continuous variations, the mole-ratio method can be used for complexation reactions that occur in a stepwise fashion if there is a difference in the molar absorptivities of the metal–ligand complexes, and if the formation constants are sufficiently different. A typical mole-ratio plot for the step-wise formation of ML and ML_2 is shown in Figure 10.3.15 c.

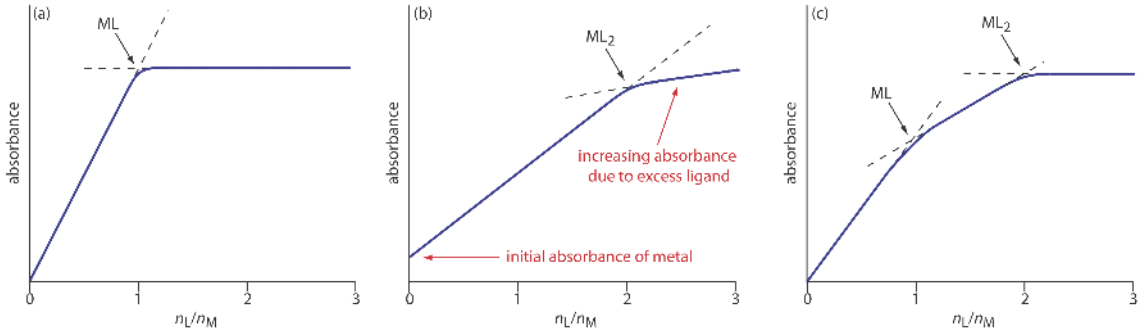


Figure 10.3.15 . Mole-ratio plots for: (a) a 1:1 metal–ligand complex in which only the complex absorbs; (b) a 1:2 metal–ligand complex in which the metal, the ligand, and the complex absorb; and (c) the stepwise formation of a 1:1 and a 1:2 metal–ligand complex.

For both the method of continuous variations and the mole-ratio method, we determine the complex's stoichiometry by extrapolating absorbance data from conditions in which there is a linear relationship between absorbance and the relative amounts of metal and ligand. If a metal–ligand complex is very weak, a plot of absorbance versus X_L or n_L/n_M becomes so curved that it is impossible to determine the stoichiometry by extrapolation. In this case the slope-ratio is used.

In the ***slope-ratio method*** two sets of solutions are prepared. The first set of solutions contains a constant amount of metal and a variable amount of ligand, chosen such that the total concentration of metal, C_M, is much larger than the total concentration of ligand, C_L. Under these conditions we may assume that essentially all the ligand reacts to form the metal–ligand complex. The concentration of the complex, which has the general form M_xL_y, is

$$[M_xL_y] = \frac{C_L}{y}$$

If we monitor the absorbance at a wavelength where only M_xL_y absorbs, then

$$A = \varepsilon b [M_xL_y] = \frac{\varepsilon b C_L}{y}$$

and a plot of absorbance versus C_L is linear with a slope, s_L, of

$$s_L = \frac{\varepsilon b}{y}$$

A second set of solutions is prepared with a fixed concentration of ligand that is much greater than a variable concentration of metal; thus

$$[M_xL_y] = \frac{C_M}{x}$$

$$A = \varepsilon b [M_xL_y] = \frac{\varepsilon b C_M}{x}$$

$$s_M = \frac{\varepsilon b}{x}$$

A ratio of the slopes provides the relative values of *x* and *y*.

$$\frac{s_M}{s_L} = \frac{\varepsilon b/x}{\varepsilon b/y} = \frac{y}{x}$$

An important assumption in the slope-ratio method is that the complexation reaction continues to completion in the presence of a sufficiently large excess of metal or ligand. The slope-ratio method also is limited to systems in which only a single complex forms and for which Beer's law is obeyed.

DETERMINATION OF EQUILIBRIUM CONSTANTS

Another important application of molecular absorption spectroscopy is the determination of equilibrium constants. Let's consider, as a simple example, an acid–base reaction of the general form

$$\mathrm{HIn}(aq) + \mathrm{H_2O}(l) \rightleftharpoons \mathrm{H_3O^+}(aq) + \mathrm{In^-}(aq)$$

where HIn and In^- are the conjugate weak acid and weak base forms of an acid–base indicator. The equilibrium constant for this reaction is

$$K_a = \frac{[\mathrm{H_3O^+}]\,[\mathrm{A^-}]}{[\mathrm{HA}]}$$

To determine the equilibrium constant's value, we prepare a solution in which the reaction is in a state of equilibrium and determine the equilibrium concentration for H_3O^+, HIn, and In^-. The concentration of H_3O^+ is easy to determine by measuring the solution's pH. To determine the concentration of HIn and In^- we can measure the solution's absorbance.

If both HIn and In^- absorb at the selected wavelength, then, from Beer's law, we know that

$$A = \varepsilon_{\mathrm{Hln}} b[\mathrm{HIn}] + \varepsilon_{\mathrm{ln}} b[\mathrm{In^-}] \tag{11.3.5}$$

where ε_{HIn} and ε_{In} are the molar absorptivities for HIn and In^-. The indicator's total concentration, *C*, is given by a mass balance equation

$$C = [\mathrm{HIn}] + [\mathrm{In^-}] \tag{11.3.6}$$

Solving Equation 11.3.6 for [HIn] and substituting into Equation 11.3.5 gives

$$A = \varepsilon_{\mathrm{Hln}} b\left(C - \left[\mathrm{In^-}\right]\right) + \varepsilon_{\mathrm{ln}} b\left[\mathrm{In^-}\right]$$

which we simplify to

$$A = \varepsilon_{\mathrm{Hln}} bC - \varepsilon_{\mathrm{Hln}} b\left[\mathrm{In^-}\right] + \varepsilon_{\mathrm{ln}} b\left[\mathrm{In^-}\right]$$

$$A = A_{\mathrm{HIn}} + b\left[\mathrm{In^-}\right]\left(\varepsilon_{\mathrm{ln}} - \varepsilon_{\mathrm{HIn}}\right) \tag{11.3.7}$$

where A_{HIn}, which is equal to $\varepsilon_{HIn}bC$, is the absorbance when the pH is acidic enough that essentially all the indicator is present as HIn. Solving Equation 11.3.7 for the concentration of In^- gives

$$\left[\mathrm{In^-}\right] = \frac{A - A_{\mathrm{Hln}}}{b\left(\varepsilon_{\mathrm{ln}} - \varepsilon_{\mathrm{HIn}}\right)} \tag{11.3.8}$$

Proceeding in the same fashion, we derive a similar equation for the concentration of HIn

$$[\mathrm{HIn}] = \frac{A_{\mathrm{In}} - A}{b\left(\varepsilon_{\mathrm{ln}} - \varepsilon_{\mathrm{Hln}}\right)} \tag{11.3.9}$$

where A_{In}, which is equal to $\varepsilon_{In}bC$, is the absorbance when the pH is basic enough that only In^- contributes to the absorbance. Substituting Equation 11.3.8 and Equation 11.3.9 into the equilibrium constant expression for HIn gives

$$K_a = \frac{[\mathrm{H_3O^+}][\mathrm{In^-}]}{[\mathrm{HIn}]} = [\mathrm{H_3O^+}] \times \frac{A - A_{\mathrm{HIn}}}{A_{\mathrm{In}} - A} \tag{11.3.10}$$

We can use Equation 11.3.10 to determine K_a in one of two ways. The simplest approach is to prepare three solutions, each of which contains the same amount, *C*, of indicator. The pH of one solution is made sufficiently acidic such that [HIn] >> [In^-]. The absorbance of this solution gives A_{HIn}. The value of A_{In} is determined by adjusting the pH of the second solution such that [In^-] >> [HIn]. Finally, the pH of the third solution is adjusted to an intermediate value, and the pH and absorbance, *A*, recorded. The value of K_a is calculated using Equation 11.3.10.

✔ EXAMPLE 10.3.5

The acidity constant for an acid–base indicator is determined by preparing three solutions, each of which has a total concentration of indicator equal to 5.00×10^{-5} M. The first solution is made strongly acidic with HCl and has an absorbance of 0.250. The second solution is made strongly basic and has an absorbance of 1.40. The pH of the third solution is 2.91 and has an absorbance of 0.662. What is the value of K_a for the indicator?

Solution

The value of K_a is determined by making appropriate substitutions into 10.20 where $[H_3O^+]$ is 1.23×10^{-3}; thus

$$K_a = \left(1.23 \times 10^{-3}\right) \times \frac{0.662 - 0.250}{1.40 - 0.662} = 6.87 \times 10^{-4}$$

EXERCISE 10.3.5

To determine the K_a of a merocyanine dye, the absorbance of a solution of 3.5×10^{-4} M dye was measured at a pH of 2.00, a pH of 6.00, and a pH of 12.00, yielding absorbances of 0.000, 0.225, and 0.680, respectively. What is the value of K_a for this dye? The data for this problem is adapted from Lu, H.; Rutan, S. C. *Anal. Chem.*, **1996**, *68*, 1381–1386.

Answer

The value of K_a is

$$K_a = \left(1.00 \times 10^{-6}\right) \times \frac{0.225 - 0.000}{0.680 - 0.225} = 4.95 \times 10^{-7}$$

A second approach for determining K_a is to prepare a series of solutions, each of which contains the same amount of indicator. Two solutions are used to determine values for A_{HIn} and A_{In}. Taking the log of both sides of Equation 11.3.10 and rearranging leave us with the following equation.

$$\log \frac{A - A_{HIn}}{A_{In^-} - A} = \text{pH} - \text{p}K_a \tag{11.3.11}$$

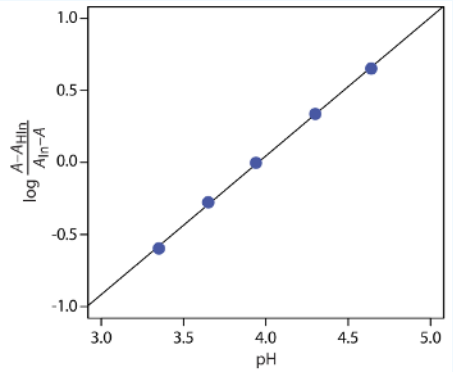
A plot of $\log[(A - A_{HIn})/(A_{In} - A)]$ versus pH is a straight-line with a slope of +1 and a *y*-intercept of $-\text{p}K_a$.

EXERCISE 10.3.6

To determine the K_a for the indicator bromothymol blue, the absorbance of each a series of solutions that contain the same concentration of bromothymol blue is measured at pH levels of 3.35, 3.65, 3.94, 4.30, and 4.64, yielding absorbance values of 0.170, 0.287, 0.411, 0.562, and 0.670, respectively. Acidifying the first solution to a pH of 2 changes its absorbance to 0.006, and adjusting the pH of the last solution to 12 changes its absorbance to 0.818. What is the value of K_a for bromothymol blue? The data for this problem is from Patterson, G. S. *J. Chem. Educ.*, **1999**, *76*, 395–398.

Answer

To determine K_a we use Equation 11.3.11, plotting $\log[(A - A_{HIn})/(A_{In} - A)]$ versus pH, as shown below.



Fitting a straight-line to the data gives a regression model of

$$\log \frac{A - A_{HIn}}{A_{In} - A} = -3.80 + 0.962\text{pH}$$

The *y*-intercept is $-\text{p}K_a$; thus, the $\text{p}K_a$ is 3.80 and the K_a is 1.58×10^{-4}.

In developing these approaches for determining K_a we considered a relatively simple system in which the absorbance of HIn and In^- are easy to measure and for which it is easy to determine the concentration of H_3O^+. In addition to acid–base reactions, we can adapt these approaches to any reaction of the general form

$$X(aq) + Y(aq) \rightleftharpoons Z(aq)$$

including metal–ligand complexation reactions and redox reactions, provided we can determine spectrophotometrically the concentration of the product, *Z*, and one of the reactants, either *X* or *Y*, and that we can determine the concentration of the other reactant by some other method. With appropriate modifications, a more complicated system in which we cannot determine the concentration of one or more of the reactants or products also is possible [Ramette, R. W. *Chemical Equilibrium and Analysis*, Addison-Wesley: Reading, MA, 1981, Chapter 13].

EVALUATION OF UV/VIS AND IR SPECTROSCOPY

SCALE OF OPERATIONS

Molecular UV/Vis absorption routinely is used for the analysis of trace analytes in macro and meso samples. Major and minor analytes are determined by diluting the sample before analysis, and concentrating a sample may allow for the analysis of ultratrace analytes. The scale of operations for infrared absorption is generally poorer than that for UV/Vis absorption.

ACCURACY

Under normal conditions a relative error of 1–5% is easy to obtained with UV/Vis absorption. Accuracy usually is limited by the quality of the blank. Examples of the type of problems that are encountered include the pres- ence of particulates in the sample that scatter radiation, and the presence of interferents that react with analytical reagents. In the latter case the interferent may react to form an absorbing species, which leads to a positive determinate error. Interferents also may prevent the analyte from reacting, which leads to a negative determinate error. With care, it is possible to improve the accuracy of an analysis by as much as an order of magnitude.

PRECISION

In absorption spectroscopy, precision is limited by indeterminate errors—primarily instrumental noise—which are introduced when we measure absorbance. Precision generally is worse for low absorbances where $P_0 \approx P_T$, and for high absorbances where P_T approaches 0. We might expect, therefore, that precision will vary with transmittance.

We can derive an expression between precision and transmittance by applying the propagation of uncertainty as described in Chapter 4. To do so we rewrite Beer's law as

$$C = -\frac{1}{\varepsilon b}\log T \tag{11.3.12}$$

Table 4.3.1 in Chapter 4 helps us complete the propagation of uncertainty for Equation 11.3.12; thus, the absolute uncertainty in the concentration, s_C, is

$$s_c = -\frac{0.4343}{\varepsilon b} \times \frac{s_T}{T} \tag{11.3.13}$$

where s_T is the absolute uncertainty in the transmittance. Dividing Equation 11.3.13 by Equation 11.3.12 gives the relative uncertainty in concentration, s_C/C, as

$$\frac{s_c}{C} = \frac{0.4343 s_T}{T \log T}$$

If we know the transmittance's absolute uncertainty, then we can determine the relative uncertainty in concentration for any measured transmittance.

Determining the relative uncertainty in concentration is complicated because s_T is a function of the transmittance. As shown in Table 10.3.3 , three categories of indeterminate instrumental error are observed [Rothman, L. D.; Crouch, S. R.; Ingle, J. D. Jr. *Anal. Chem.* **1975**, *47*, 1226–1233]. A constant s_T is observed for the uncertainty associated with reading %*T* on a meter's analog or digital scale. Typical values are ±0.2–0.3% (a k_1 of ±0.002–0.003) for an analog scale and ±0.001% a (k_1 of ±0.00001) for a digital scale.

Table 10.3.3 . Effect of Indeterminate Errors on Relative Uncertainty in Concentration

category	sources of indeterminate error	relative uncertainty in concentration
$s_T = k_1$	%T readout resolution noise in thermal detectors	$\frac{s_C}{C} = \frac{0.4343 k_1}{T \log T}$
$s_T = k_2\sqrt{T^2 + T}$	noise in photon detectors	$\frac{s_C}{C} = \frac{0.4343 k_2}{\log T}\sqrt{1 + \frac{1}{T}}$
$s_T = k_3 T$	positioning of sample cell fluctuations in source intensity	$\frac{s_C}{C} = \frac{0.4343 k_3}{\log T}$

A constant s_T also is observed for the thermal transducers used in infrared spectrophotometers. The effect of a constant s_T on the relative uncertainty in concentration is shown by curve A in Figure 10.3.16 . Note that the relative uncertainty is very large for both high absorbances and low absorbances, reaching a minimum when the absorbance is 0.4343. This source of indeterminate error is important for infrared spectrophotometers and for inexpensive UV/Vis spectrophotometers. To obtain a relative uncertainty in concentration of ±1–2%, the absorbance is kept within the range 0.1–1.

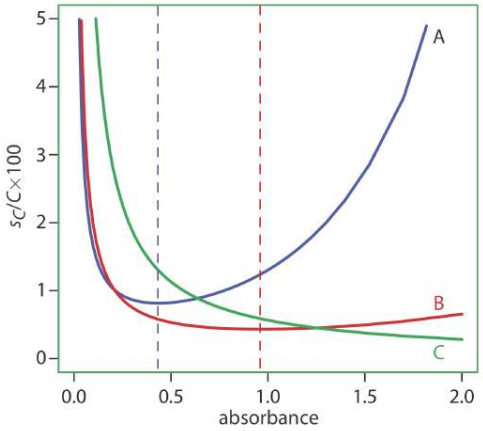


Figure 10.3.16 . Percent relative uncertainty in concentration as a function of absorbance for the categories of indeterminate errors in Table 11.3.10.3. A: k_1 = ±0.0030; B: k_2 = ±0.0030; and C: k_3= ±0.0130. The dashed lines correspond to the minimum uncertainty for curve A (absorbance of 0.4343) and for curve B (absorbance of 0.963).

Values of s_T are a complex function of transmittance when indeterminate errors are dominated by the noise associated with photon detectors. Curve B in Figure 10.3.16 shows that the relative uncertainty in concentration is very large for low absorbances, but is smaller at higher absorbances. Although the relative uncertainty reaches a minimum when the absorbance is 0.963, there is little change in the relative uncertainty for absorbances between 0.5 and 2. This source of indeterminate error generally limits the precision of high quality UV/Vis spectrophotometers for mid-to-high absorbances.

Finally, the value of s_T is directly proportional to transmittance for indeterminate errors that result from fluctuations in the source's intensity and from uncertainty in positioning the sample within the spectrometer. The latter is particularly important because the optical properties of a sample cell are not uniform. As a result, repositioning the sample cell may lead to a change in the intensity of transmitted radiation. As shown by curve C in Figure 10.3.16 , the effect is important only at low absorbances. This source of indeterminate errors usually is the limiting factor for high quality UV/Vis spectrophotometers when the absorbance is relatively small.

When the relative uncertainty in concentration is limited by the %T readout resolution, it is possible to improve the precision of the analysis by redefining 100% T and 0% T. Normally 100% T is established using a blank and 0% T is established while preventing the source's radiation from reaching the detector. If the absorbance is too high, precision is improved by resetting 100% T using a standard solution of analyte whose concentration is less than that of the sample (Figure 10.3.17 a). For a sample whose absorbance is too low, precision is improved by redefining 0% T using a standard solution of the analyte whose concentration is greater than that of the analyte (Figure 10.3.17 b). In this case a calibration curve is required because a linear relationship between absorbance and concentration no longer exists. Precision is further increased by combining these two methods (Figure 10.3.17 c). Again, a calibration curve is necessary since the relation- ship between absorbance and concentration is no longer linear.

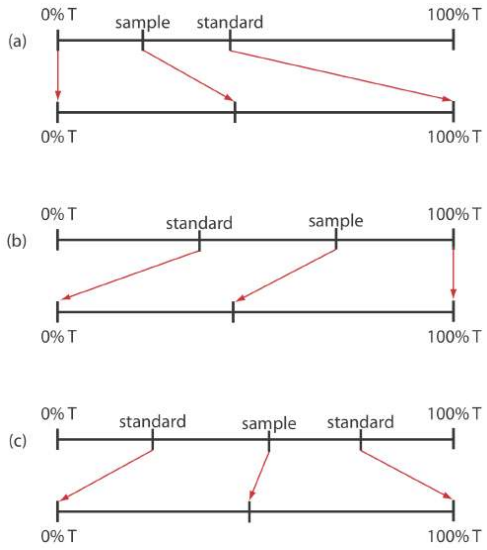


Figure 10.3.17 . Methods for improving the precision of absorption methods: (a) high-absorbance method; (b) low-absorbance method; (c) maximum precision method.

SENSITIVITY

The sensitivity of a molecular absorption method, which is the slope of a Beer's law calibration curve, is the product of the analyte's absorptivity and the pathlength of the sample cell (εb). You can improve a method's sensitivity by selecting a wavelength where absorbance is at a maximum or by increasing pathlength.

> See Figure 10.2.10 for an example of how the choice of wavelength affects a calibration curve's sensitivity.

SELECTIVITY

Selectivity rarely is a problem in molecular absorption spectrophotometry. In many cases it is possible to find a wavelength where only the analyte absorbs. When two or more species do contribute to the measured absorbance, a multicomponent analysis is still possible, as shown in Example 10.3.2 and Example 10.3.3 .

TIME, COST, AND EQUIPMENT

The analysis of a sample by molecular absorption spectroscopy is relatively rapid, although additional time is required if we need to convert a nonabsorbing analyte into an absorbing form. The cost of UV/Vis instrumentation ranges from several hundred dollars for a simple filter photometer, to more than $50,000 for a computer-controlled, high-resolution double-beam instrument equipped with variable slit widths, and operating over an extended range of wavelengths. Fourier transform infrared spectrometers can be obtained for as little as $15,000–$20,000, although more expensive models are available.

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11.4: ATOMIC ABSORPTION SPECTROSCOPY

Guystav Kirchoff and Robert Bunsen first used atomic absorption—along with atomic emission—in 1859 and 1860 as a means for identify atoms in flames and hot gases. Although atomic emission continued to develop as an analytical technique, progress in atomic absorption languished for almost a century. Modern atomic absorption spectroscopy has its beginnings in 1955 as a result of the independent work of A. C. Walsh and C. T. J. Alkemade [(a) Walsh, A. *Anal. Chem.* **1991**, *63*, 933A–941A; (b) Koirtyohann, S. R. *Anal. Chem.* **1991**, *63*, 1024A–1031A; (c) Slavin, W. *Anal. Chem.* **1991**, *63*, 1033A–1038A]. Commercial instruments were in place by the early 1960s, and the importance of atomic absorption as an analytical technique soon was evident.

INSTRUMENTATION

Atomic absorption spectrophotometers use the same single-beam or double-beam optics described earlier for molecular absorption spectrophotometers (see Figure 10.3.2 and Figure 10.3.3). There is, however, an important additional need in atomic absorption spectroscopy: we first must covert the analyte into free atoms. In most cases the analyte is in solution form. If the sample is a solid, then we must bring the analyte into solution before the analysis. When analyzing a lake sediment for Cu, Zn, and Fe, for example, we bring the analytes into solution as Cu^{2+}, Zn^{2+}, and Fe^{3+} by extracting them with a suitable reagent. For this reason, only the introduction of solution samples is considered in this chapter.

> What reagent we choose to use to bring an analyte into solution depends on our research goals. If we need to know the total amount of metal in the sediment, then we might try a microwave digestion using a mixture of concentrated acids, such as HNO_3, HCl, and HF. This destroys the sediment's matrix and brings everything into solution. On the other hand, if our interest is biologically available metals, we might extract the sample under milder conditions using, for example, a dilute solution of HCl or CH_3COOH at room temperature.

ATOMIZATION

The process of converting an analyte to a free gaseous atom is called ***atomization***. Converting an aqueous analyte into a free atom requires that we strip away the solvent, volatilize the analyte, and, if necessary, dissociate the analyte into free atoms. Desolvating an aqueous solution of $CuCl_2$, for example, leaves us with solid particulates of $CuCl_2$. Converting the particulate $CuCl_2$ to gas phases atoms of Cu and Cl requires thermal energy.

$$\mathrm{CuCl_2}(aq) \rightarrow \mathrm{CuCl_2}(s) \rightarrow \mathrm{Cu}(g) + 2\mathrm{Cl}(g)$$

There are two common atomization methods: flame atomization and electrothermal atomization, although a few elements are atomized using other methods.

FLAME ATOMIZER

Figure 10.4.1 shows a typical flame atomization assembly with close-up views of several key components. In the unit shown here, the aqueous sample is drawn into the assembly by passing a high-pressure stream of compressed air past the end of a capillary tube immersed in the sample. When the sample exits the nebulizer it strikes a glass impact bead, which converts it into a fine aerosol mist within the spray chamber. The aerosol mist is swept through the spray chamber by the combustion gases—compressed air and acetylene in this case—to the burner head where the flame's thermal energy desolvates the aerosol mist to a dry aerosol of small, solid particulates. The flame's thermal energy then volatilizes the particles, producing a vapor that consists of molecular species, ionic species, and free atoms.

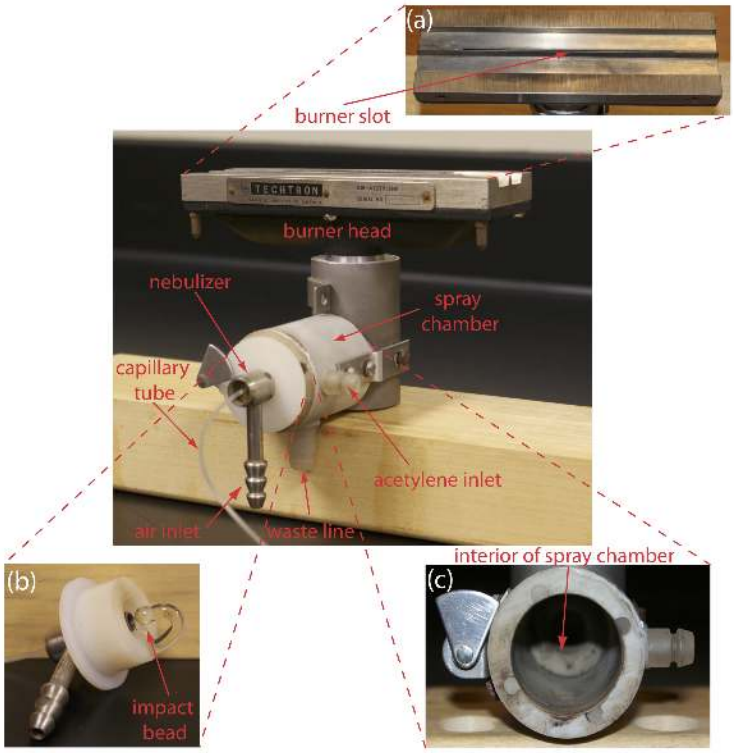


Figure 10.4.1 . Flame atomization assembly with expanded views of (a) the burner head showing the burner slot where the flame is located; (b) the nebulizer's impact bead; and (c) the interior of the spray chamber. Although the unit shown here is from an instrument dating to the 1970s, the basic components of a modern flame AA spectrometer are the same.

Burner. The slot burner in Figure 10.4.1 a provides a long optical pathlength and a stable flame. Because absorbance is directly proportional to pathlength, a long pathlength provides greater sensitivity. A stable flame minimizes uncertainty due to fluctuations in the flame.

The burner is mounted on an adjustable stage that allows the entire assembly to move horizontally and vertically. Horizontal adjustments ensure the flame is aligned with the instrument's optical path. Vertical adjustments change the height within the flame from which absorbance is monitored. This is important because two competing processes affect the concentration of free atoms in the flame. The more time an analyte spends in the flame the greater the atomization efficiency; thus, the production of free atoms increases with height. On the other hand, a longer residence time allows more opportunity for the free atoms to combine with oxygen to form a molecular oxide. As seen in Figure 10.4.2 , for a metal this is easy to oxidize, such as Cr, the concentration of free atoms is greatest just above the burner head. For a metal, such as Ag, which is difficult to oxidize, the concentration of free atoms increases steadily with height.

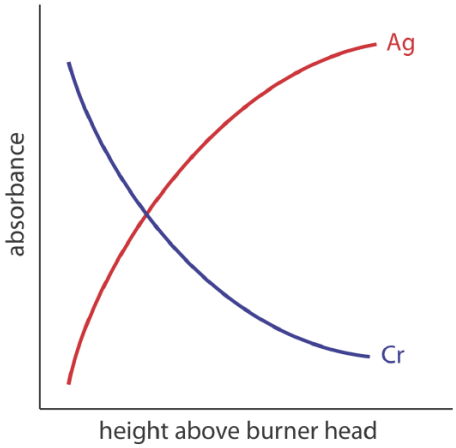


Figure 10.4.2 . Absorbance versus height profiles for Ag and Cr in flame atomic absorption spectroscopy.

Flame. The flame's temperature, which affects the efficiency of atomization, depends on the fuel–oxidant mixture, several examples of which are listed in Table 10.4.1 . Of these, the air–acetylene and the nitrous oxide–acetylene flames are the most popular. Normally the fuel and oxidant are mixed in an approximately stoichiometric ratio; however, a fuel-rich mixture may be necessary for easily oxidized analytes.

Table 10.4.1 . Fuels and Oxidants Used for Flame Combustion

fuel	oxidant	temperature range (°C)
natural gas	air	1700–1900
hydrogen	air	2000–2100
acetylene	air	2100–2400
acetylene	nitrous oxide	2600–2800
acetylene	oxygen	3050–3150

Figure 10.4.3 shows a cross-section through the flame, looking down the source radiation's optical path. The primary combustion zone usually is rich in gas combustion products that emit radiation, limiting is useful- ness for atomic absorption. The interzonal region generally is rich in free atoms and provides the best location for measuring atomic absorption. The hottest part of the flame typically is 2–3 cm above the primary combustion zone. As atoms approach the flame's secondary combustion zone, the decrease in temperature allows for formation of stable molecular species.

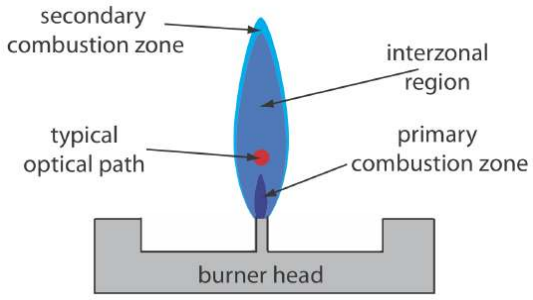


Figure 10.4.3 . Profile of typical flame using a slot burner. The relative size of each zone depends on many factors, including the choice of fuel and oxidant, and their relative proportions.

Sample Introduction. The most common means for introducing a sample into a flame atomizer is a continuous aspiration in which the sample flows through the burner while we monitor absorbance. Continuous aspiration is sample intensive, typically requiring from 2–5 mL of sample.

Flame microsampling allows us to introduce a discrete sample of fixed volume, and is useful if we have a limited amount of sample or when the sample's matrix is incompatible with the flame atomizer. For example, continuously aspirating a sample that has a high concentration of dissolved solids—sea water, for example, comes to mind—may build-up a solid de- posit on the burner head that obstructs the flame and that lowers the absorbance. Flame microsampling is accomplished using a micropipet to place 50–250 μL of sample in a Teflon funnel connected to the nebulizer, or by dipping the nebulizer tubing into the sample for a short time. Dip sampling usually is accomplished with an automatic sampler. The signal for flame microsampling is a transitory peak whose height or area is proportional to the amount of analyte that is injected.

Advantages and Disadvantages of Flame Atomization. The principal advantage of flame atomization is the reproducibility with which the sample is introduced into the spectrophotometer; a significant disadvantage is that the efficiency of atomization is quite poor. There are two reasons for poor atomization efficiency. First, the majority of the aerosol droplets produced during nebulization are too large to be carried to the flame by the combustion gases. Consequently, as much as 95% of the sample never reaches the flame, which is the reason for the waste line shown at the bottom of the spray chamber in Figure 10.4.1 . A second reason for poor atomization efficiency is that the large volume of combustion gases significantly dilutes the sample. Together, these contributions to the efficiency of atomization reduce sensitivity because the analyte's concentration in the flame may be a factor of 2.5×10^{-6} less than that in solution [Ingle, J. D.; Crouch, S. R. *Spectrochemical Analysis*, Prentice-Hall: Englewood Cliffs, NJ, 1988; p. 275].

ELECTROTHERMAL ATOMIZERS

A significant improvement in sensitivity is achieved by using the resistive heating of a graphite tube in place of a flame. A typical electrothermal atomizer, also known as a ***graphite furnace***, consists of a cylindrical graphite tube approximately 1–3 cm in length and 3–8 mm in diameter. As shown in Figure 10.4.4 , the graphite tube is housed in an sealed assembly that has an optically transparent window at each end. A continuous stream of inert gas is passed through the furnace, which protects the graphite tube from oxidation and removes the gaseous products produced during atomization. A power supply is used to pass a current through the graphite tube, resulting in resistive heating.

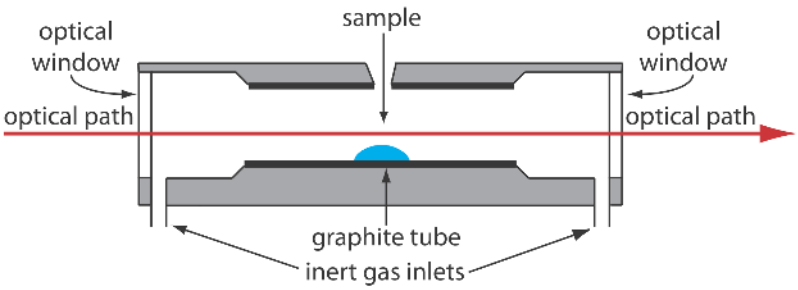


Figure 10.4.4 . Diagram showing a cross-section of an electrothermal analyzer.

Samples of between 5–50 μL are injected into the graphite tube through a small hole at the top of the tube. Atomization is achieved in three stages. In the first stage the sample is dried to a solid residue using a current that raises the temperature of the graphite tube to about 110°C. In the second stage, which is called ashing, the temperature is increased to between 350–1200°C. At these temperatures organic material in the sample is converted to CO_2 and H_2O, and volatile inorganic materials are vaporized. These gases are removed by the inert gas flow. In the final stage the sample is atomized by rapidly increasing the temperature to between 2000–3000°C. The result is a transient absorbance peak whose height or area is proportional to the absolute amount of analyte injected into the graphite tube. Together, the three stages take approximately 45–90 s, with most of this time used for drying and ashing the sample.

Electrothermal atomization provides a significant improvement in sensitivity by trapping the gaseous analyte in the small volume within the graphite tube. The analyte's concentration in the resulting vapor phase is as much as 1000× greater than in a flame atomization [Parsons, M. L.; Major, S.; Forster, A. R. *Appl. Spectrosc.* **1983**, *37*, 411–418]. This improvement in sensitivity—and the resulting improvement in detection limits—is offset by a significant decrease in precision. Atomization efficiency is influenced strongly by the sample's contact with the graphite tube, which is difficult to control reproducibly.

MISCELLANEOUS ATOMIZATION METHODS

A few elements are atomized by using a chemical reaction to produce a volatile product. Elements such as As, Se, Sb, Bi, Ge, Sn, Te, and Pb, for example, form volatile hydrides when they react with $NaBH_4$ in the presence of acid. An inert gas carries the volatile hydride to either a flame or to a heated quartz observation tube situated in the optical path. Mercury is determined by the cold-vapor method in which it is reduced to elemental mercury with $SnCl_2$. The volatile Hg is carried by an inert gas to an unheated observation tube situated in the instrument's optical path.

QUANTITATIVE APPLICATIONS

Atomic absorption is used widely for the analysis of trace metals in a variety of sample matrices. Using Zn as an example, there are standard atomic absorption methods for its determination in samples as diverse as water and wastewater, air, blood, urine, muscle tissue, hair, milk, breakfast cereals, shampoos, alloys, industrial plating baths, gasoline, oil, sediments, and rocks.

Developing a quantitative atomic absorption method requires several considerations, including choosing a method of atomization, selecting the wavelength and slit width, preparing the sample for analysis, minimizing spectral and chemical interferences, and selecting a method of standardization. Each of these topics is considered in this section.

DEVELOPING A QUANTITATIVE METHOD

Flame or Electrothermal Atomization? The most important factor in choosing a method of atomization is the analyte's concentration. Because of its greater sensitivity, it takes less analyte to achieve a given absorbance when using electrothermal atomization. Table 10.4.2 , which compares the amount of analyte needed to achieve an absorbance of 0.20 when using flame atomization and electrothermal atomization, is useful when selecting an atomization method. For example, flame atomization is the method of choice if our samples contain 1–10 mg Zn^{2+}/L, but electrothermal atomization is the best choice for samples that contain 1–10 μg Zn^{2+}/L.

Table 10.4.2 . Concentration of Analyte (in mg/L) That Yields an Absorbance of 0.20

element	flame atomization	electrothermal atomization
Ag	1.5	0.0035
Al	40	0.015
As	40	0.050
Ca	0.8	0.003
Cd	0.6	0.001
Co	2.5	0.021
Cr	2.5	0.0075
Cu	1.5	0.012
Fe	2.5	0.006
Hg	70	0.52
Mg	0.15	0.00075
Mn	1	0.003
Na	0.3	0.00023
Ni	2	0.024
Pb	5	0.080
Pt	70	0.29
Sn	50	0.023
Zn	0.3	0.00071

Source: Varian Cookbook, SpectraAA Software Version 4.00 Pro.
As: 10 mg/L by hydride vaporization; Hg: 11.5 mg/L by cold-vapor; and Sn:18 mg/L by hydride vaporization

Selecting the Wavelength and Slit Width. The source for atomic absorption is a hollow cathode lamp that consists of a cathode and anode enclosed within a glass tube filled with a low pressure of an inert gas, such as Ne or Ar (Figure 10.4.5). Applying a potential across the electrodes ionizes the filler gas. The positively charged gas ions collide with the negatively charged cathode, sputtering atoms from the cathode's surface. Some of the sputtered atoms are in the excited state and emit radiation characteristic of the metal(s) from which the cathode is manufactured. By fashioning the cathode from the metallic analyte, a hollow cathode lamp provides emission lines that correspond to the analyte's absorption spectrum.

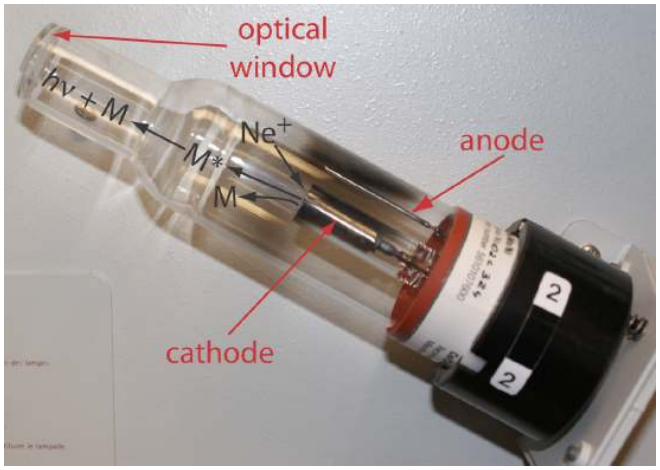


Figure 10.4.5 . Photo of a typical multielemental hollow cathode lamp. The cathode in this lamp is fashioned from an alloy of Co, Cr, Cu, Fe, Mn, and Ni, and is surrounded by a glass shield that isolates it from the anode. The lamp is filled with Ne gas. Also shown is the process that leads to atomic emission. Note the black deposit of sputtered metal on the outer wall of the hollow cathode lamp. See the text for additional details.

Because atomic absorption lines are narrow, we need to use a line source instead of a continuum source (compare, for example, Figure 10.2.4 with Figure 10.2.6). The effective bandwidth when using a continuum source is roughly 1000× larger than an atomic absorption line; thus, $P_T \approx P_0$, $\%T \approx 100$, and $A \approx 0$. Because a hollow cathode lamp is a line source, P_T and P_0 have different values giving a $\%T < 100$ and $A > 0$.

Each element in a hollow cathode lamp provides several atomic emission lines that we can use for atomic absorption. Usually the wavelength that provides the best sensitivity is the one we choose to use, although a less sensitive wavelength may be more appropriate for a sample that has higher concentration of analyte. For the Cr hollow cathode lamp in Table 10.4.3 , the best sensitivity is obtained using a wavelength of 357.9 nm.

Table 10.4.3 . Atomic Emission Lines for a Cr Hollow Cathode Lamp

wavelength (nm)	slit width (nm)	mg Cr/L giving $A = 0.20$	P_0 (relative)
357.9	0.2	2.5	40
425.4	0.2	12	85
429.0	0.5	20	100
520.5	0.2	1500	15
520.8	0.2	500	20

Another consideration is the emission line's intensity. If several emission lines meet our requirements for sensitivity, we may wish to use the emission line with the largest relative P_0 because there is less uncertainty in measuring P_0 and P_T. When analyzing a sample that is ≈10 mg Cr/L, for example, the first three wavelengths in Table 10.4.3 provide an appropriate sensitivity; the wavelengths of 425.4 nm and 429.0 nm, however, have a greater P_0 and will provide less uncertainty in the measured absorbance.

The emission spectrum for a hollow cathode lamp includes, in addition to the analyte's emission lines, additional emission lines from impurities present in the metallic cathode and from the filler gas. These additional lines are a potential source of stray radiation that could result in an instrumental deviation from Beer's law. The monochromator's slit width is set as wide as possible to improve the throughput of radiation and narrow enough to eliminate these sources of stray radiation.

Preparing the Sample. Flame and electrothermal atomization require that the analyte is in solution. Solid samples are brought into solution by dissolving in an appropriate solvent. If the sample is not soluble it is digested, either on a hot-plate or by microwave, using HNO_3, H_2SO_4, or $HClO_4$. Alternatively, we can extract the analyte using a Soxhlet extractor. Liquid samples are analyzed directly or the analytes extracted if the matrix is in- compatible with the method of atomization. A serum sample, for instance, is difficult to aspirate when using flame atomization and may produce an unacceptably high background absorbance when using electrothermal atomization. A liquid–liquid extraction using an organic solvent and a chelating agent frequently is used to concentrate analytes. Dilute solutions of Cd^{2+}, Co^{2+}, Cu^{2+}, Fe^{3+}, Pb^{2+}, Ni^{2+}, and Zn^{2+}, for example, are concentrated by extracting with a solution of ammonium pyrrolidine dithiocarbamate in methyl isobutyl ketone.

Minimizing Spectral Interference. A spectral interference occurs when an analyte's absorption line overlaps with an interferent's absorption line or band. Because they are so narrow, the overlap of two atomic absorption lines seldom is a problem. On the other hand, a molecule's broad absorption band or the scattering of source radiation is a potentially serious spectral interference.

An important consideration when using a flame as an atomization source is its effect on the measured absorbance. Among the products of combustion are molecular species that exhibit broad absorption bands and particulates that scatter radiation from the source. If we fail to compensate for these spectral interferences, then the intensity of transmitted radiation is smaller than expected. The result is an apparent increase in the sample's absorbance. Fortunately, absorption and scattering of radiation by the flame are corrected by analyzing a blank.

Spectral interferences also occur when components of the sample's matrix other than the analyte react to form molecular species, such as oxides and hydroxides. The resulting absorption and scattering constitutes the sample's background and may present a significant problem, particularly at wavelengths below 300 nm where the scattering of radiation becomes more important. If we know the composition of the sample's matrix, then we can prepare our samples using an identical matrix. In this case the background absorption is the same for both the samples and the standards. Alternatively, if the background is due to a known matrix component, then we can add that component in excess to all samples and standards so that the contribution of the naturally occurring interferent is insignificant. Finally, many interferences due to the sample's matrix are eliminated by increasing the atomization temperature. For example, switching to a higher temperature flame helps prevents the formation of interfering oxides and hydroxides.

If the identity of the matrix interference is unknown, or if it is not possible to adjust the flame or furnace conditions to eliminate the interference, then we must find another method to compensate for the background interference. Several methods have been developed to compensate for matrix interferences, and most atomic absorption spectrophotometers include one or more of these methods.

One of the most common methods for ***background correction*** is to use a continuum source, such as a D_2 lamp. Because a D_2 lamp is a continuum source, absorbance of its radiation by the analyte's narrow absorption line is negligible. Only the background, therefore, absorbs radiation from the D_2 lamp. Both the analyte and the background, on the other hand, absorb the hollow cathode's radiation. Subtracting the absorbance for the D_2 lamp from that for the hollow cathode lamp gives a corrected absorbance that compensates for the background interference. Although this method of background correction is effective, it does assume that the background absorbance is constant over the range of wavelengths passed by the monochromator. If this is not true, then subtracting the two absorbances underestimates or overestimates the background.

> Other methods of background correction have been developed, including Zeeman effect background correction and Smith–Hieftje background correction, both of which are included in some commercially available atomic absorption spectrophotometers. Consult the chapter's additional resources for additional information.

Minimizing Chemical Interferences. The quantitative analysis of some elements is complicated by chemical interferences that occur during atomization. The most common chemical interferences are the formation of nonvolatile compounds that contain the analyte and ionization of the analyte.

One example of the formation of a nonvolatile compound is the effect of PO_4^{3-} or Al^{3+} on the flame atomic absorption analysis of Ca^{2+}. In one study, for example, adding 100 ppm Al^{3+} to a solution of 5 ppm Ca^{2+} decreased calcium ion's absorbance from 0.50 to 0.14, while adding 500 ppm PO_4^{3-} to a similar solution of Ca^{2+} decreased the absorbance from 0.50 to 0.38. These interferences are attributed to the formation of nonvolatile particles of $Ca_3(PO_4)_2$ and an Al–Ca–O oxide [Hosking, J. W.; Snell, N. B.; Sturman, B. T. *J. Chem. Educ.* **1977**, *54*, 128–130].

When using flame atomization, we can minimize the formation of non-volatile compounds by increasing the flame's temperature by changing the fuel-to-oxidant ratio or by switching to a different combination of fuel and oxidant. Another approach is to add a releasing agent or a protecting agent to the sample. A ***releasing agent*** is a species that reacts preferentially with the interferent, releasing the analyte during atomization. For example, Sr^{2+} and La^{3+} serve as releasing agents for the analysis of Ca^{2+} in the presence of PO_4^{3-} or Al^{3+}. Adding 2000 ppm $SrCl_2$ to the Ca^{2+}/ PO_4^{3-} and to the Ca^{2+}/Al^{3+} mixtures described in the previous paragraph increased the absorbance to 0.48. A ***protecting agent*** reacts with the analyte to form a stable volatile complex. Adding 1% w/w EDTA to the Ca^{2+}/ PO_4^{3-} solution described in the previous paragraph increased the absorbance to 0.52.

An ionization interference occurs when thermal energy from the flame or the electrothermal atomizer is sufficient to ionize the analyte

$$M(s) \rightleftharpoons M^+(aq) + e^- \tag{11.4.1}$$

where M is the analyte. Because the absorption spectra for M and M^+ are different, the position of the equilibrium in reaction 11.4.1 affects the absorbance at wavelengths where M absorbs. To limit ionization we add a high concentration of an ***ionization suppressor***, which is a species that ionizes more easily than the analyte. If the ionization suppressor's concentration is sufficient, then the increased concentration of electrons in the flame pushes reaction 11.4.1 to the left, preventing the analyte's ionization. Potassium and cesium frequently are used as an ionization suppressor because of their low ionization energy.

Standardizing the Method. Because Beer's law also applies to atomic absorption, we might expect atomic absorption calibration curves to be linear. In practice, however, most atomic absorption calibration curves are nonlinear or linear over a limited range of concentrations. Nonlinearity in atomic absorption is a consequence of instrumental limitations, including stray radiation from the hollow cathode lamp and the variation in molar absorptivity across the absorption line. Accurate quantitative work, therefore, requires a suitable means for computing the calibration curve from a set of standards.

When possible, a quantitative analysis is best conducted using external standards. Unfortunately, matrix interferences are a frequent problem, particularly when using electrothermal atomization. For this reason the method of standard additions often is used. One limitation to this method of standardization, however, is the requirement of a linear relationship between absorbance and concentration.

> Most instruments include several different algorithms for computing the calibration curve. The instrument in my lab, for example, includes five algorithms. Three of the algorithms fit absorbance data using linear, quadratic, or cubic polynomial functions of the analyte's concentration. It also includes two algorithms that fit the concentrations of the standards to quadratic functions of the absorbance.

REPRESENTATIVE METHOD 10.4.1: DETERMINATION OF CU AND ZN IN TISSUE SAMPLES

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of Cu and Zn in biological tissues provides an instructive example of a typical procedure. The description here is based on Bhattacharya, S. K.; Goodwin, T. G.; Crawford, A. J. *Anal. Lett.* **1984**, *17*, 1567–1593, and Crawford, A. J.; Bhattacharya, S. K. Varian Instruments at Work, Number AA–46, April 1985.

Description of Method.

Copper and zinc are isolated from tissue samples by digesting the sample with HNO_3 after first removing any fatty tissue. The concentration of copper and zinc in the supernatant are determined by atomic absorption using an air-acetylene flame.

Procedure.

Tissue samples are obtained by a muscle needle biopsy and dried for 24–30 h at 105ºC to remove all traces of moisture. The fatty tissue in a dried sample is removed by extracting overnight with anhydrous ether. After removing the ether, the sample is dried to obtain the fat-free dry tissue weight (FFDT). The sample is digested at 68ºC for 20–24 h using 3 mL of 0.75 M HNO_3. After centrifuging at 2500 rpm for 10 minutes, the supernatant is transferred to a 5-mL volumetric flask. The digestion is repeated two more times, for 2–4 hours each, using 0.9-mL aliquots of 0.75 M HNO_3. These supernatants are added to the 5-mL volumetric flask, which is diluted to volume with 0.75 M HNO_3. The concentrations of Cu and Zn in the diluted supernatant are determined by flame atomic absorption spectroscopy using an air-acetylene flame and external standards. Copper is analyzed at a wavelength of 324.8 nm with a slit width of 0.5 nm, and zinc is analyzed at 213.9 nm

with a slit width of 1.0 nm. Background correction using a D_2 lamp is necessary for zinc. Results are reported as µg of Cu or Zn per gram of FFDT.

Questions.

1. Describe the appropriate matrix for the external standards and for the blank?

The matrix for the standards and the blank should match the matrix of the samples; thus, an appropriate matrix is 0.75 M HNO_3. Any interferences from other components of the sample matrix are minimized by background correction.

2. Why is a background correction necessary for the analysis of Zn, but not for the analysis of Cu?

Background correction compensates for background absorption and scattering due to interferents in the sample. Such interferences are most severe when using a wavelength less than 300 nm. This is the case for Zn, but not for Cu.

3. A Cu hollow cathode lamp has several emission lines, the properties of which are shown in the following table. Explain why this method uses the line at 324.8 nm.

wavelength (nm)	slit width (nm)	mg Cu/L for A = 0.20	P_0 (relative)
217.9	0.2	15	3
218.2	0.2	15	3
222.6	0.2	60	5
244.2	0.2	400	15
249.2	0.5	200	24
324.8	0.5	1.5	100
327.4	0.5	3	87

With 1.5 mg Cu/L giving an absorbance of 0.20, the emission line at 324.8 nm has the best sensitivity. In addition, it is the most intense emission line, which decreases the uncertainty in the measured absorbance.

EXAMPLE 10.4.1

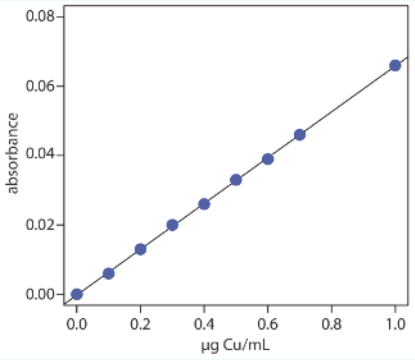
To evaluate the method described in Representative Method 10.4.1, a series of external standard is prepared and analyzed, providing the results shown here [Crawford, A. J.; Bhattacharya, S. K. “Microanalysis of Copper and Zinc in Biopsy-Sized Tissue Specimens by Atomic Absorption Spectroscopy Using a Stoichiometric Air-Acetylene Flame,” Varian Instruments at Work, Number AA–46, April 1985].

µg Cu/mL	absorbance	µg Cu/mL	absorbance
0.000	0.000	0.500	0.033
0.100	0.006	0.600	0.039
0.200	0.013	0.700	0.046
0.300	0.020	1.00	0.066
0.400	0.026		

A bovine liver standard reference material is used to evaluate the method’s accuracy. After drying and extracting the sample, a 11.23-mg FFDT tissue sample gives an absorbance of 0.023. Report the amount of copper in the sample as µg Cu/g FFDT.

Solution

Linear regression of absorbance versus the concentration of Cu in the standards gives the calibration curve shown below and the following calibration equation.



https://chem.libretexts.org/@go/page/540067

$$A = -0.0002 + 0.0661 \times \frac{\mu\text{g Cu}}{\text{mL}}$$

Substituting the sample's absorbance into the calibration equation gives the concentration of copper as 0.351 μg/mL. The concentration of copper in the tissue sample, therefore, is

$$\frac{\frac{0.351 \mu\text{g Cu}}{\text{mL}} \times 5.000 \text{ mL}}{0.01123 \text{ g sample}} = 156 \ \mu\text{g Cu/g FDT}$$

EVALUATION OF ATOMIC ABSORPTION SPECTROSCOPY

SCALE OF OPERATION

Atomic absorption spectroscopy is ideally suited for the analysis of trace and ultratrace analytes, particularly when using electrothermal atomization. For minor and major analytes, sample are diluted before the analysis. Most analyses use a macro or a meso sample. The small volume requirement for electrothermal atomization or for flame microsampling, however, makes practical the analysis of micro and ultramicro samples.

ACCURACY

If spectral and chemical interferences are minimized, an accuracy of 0.5–5% is routinely attainable. When the calibration curve is nonlinear, accuracy is improved by using a pair of standards whose absorbances closely bracket the sample's absorbance and assuming that the change in absorbance is linear over this limited concentration range. Determinate errors for electrothermal atomization often are greater than those obtained with flame atomization due to more serious matrix interferences.

PRECISION

For an absorbance greater than 0.1–0.2, the relative standard deviation for atomic absorption is 0.3–1% for flame atomization and 1–5% for electrothermal atomization. The principle limitation is the uncertainty in the concentration of free analyte atoms that result from variations in the rate of aspiration, nebulization, and atomization for a flame atomizer, and the consistency of injecting samples for electrothermal atomization.

SENSITIVITY

The sensitivity of a flame atomic absorption analysis is influenced by the flame's composition and by the position in the flame from which we monitor the absorbance. Normally the sensitivity of an analysis is optimized by aspirating a standard solution of analyte and adjusting the fuel-to-oxidant ratio, the nebulizer flow rate, and the height of the burner, to give the greatest absorbance. With electrothermal atomization, sensitivity is influenced by the drying and ashing stages that precede atomization. The temperature and time at each stage is optimized for each type of sample.

Sensitivity also is influenced by the sample's matrix. We already noted, for example, that sensitivity is decreased by a chemical interference. An increase in sensitivity may be realized by adding a low molecular weight alcohol, ester, or ketone to the solution, or by using an organic solvent.

SELECTIVITY

Due to the narrow width of absorption lines, atomic absorption provides excellent selectivity. Atomic absorption is used for the analysis of over 60 elements at concentrations at or below the level of μg/L.

TIME, COST, AND EQUIPMENT

The analysis time when using flame atomization is short, with sample throughputs of 250–350 determinations per hour when using a fully automated system. Electrothermal atomization requires substantially more time per analysis, with maximum sample throughputs of 20–30 determinations per hour. The cost of a new instrument ranges from between $10,000– $50,000 for flame atomization, and from $18,000–$70,000 for electrothermal atomization. The more expensive instruments in each price range include double-beam optics, automatic samplers, and can be programmed for multielemental analysis by allowing the wavelength and hollow cathode lamp to be changed automatically.

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11.5: EMISSION SPECTROSCOPY

An analyte in an excited state possesses an energy, E_2, that is greater than its energy when it is in a lower energy state, E_1. When the analyte returns to its lower energy state—a process we call relaxation—the excess energy, ΔE

$$\Delta E = E_2 - E_1$$

is released. Figure 10.1.4 shows a simplified picture of this process.

The amount of time an analyte, *A*, spends in its excited state—what we call the excited state's ***lifetime***—is short, typically 10^{-5}–10^{-9} s for an electronic excited state and 10–15 s for a vibrational excited state. Relaxation of the analyte's excited state, *A**, occurs through several mechanisms, including collisions with other species in the sample, photochemical reactions, and the emission of photons. In the first process, which we call vibrational relaxation or nonradiative relaxation, the excess energy is released as heat.

$$A^* \longrightarrow A + \text{ heat}$$

Relaxation by a photochemical reaction may involve simple decomposition

$$A^* \longrightarrow X + Y$$

or a reaction between *A** and another species

$$A^* + Z \longrightarrow X + Y$$

In both cases the excess energy is used up in the chemical reaction or released as heat.

In the third mechanism, the excess energy is released as a photon of electromagnetic radiation.

$$A^* \longrightarrow A + h\nu$$

The release of a photon following thermal excitation is called emission and that following the absorption of a photon is called photoluminescence. In chemiluminescence and bioluminescence, excitation results from a chemical or a biochemical reaction, respectively. Spectroscopic methods based on photoluminescence are the subject of the next section and atomic emission is covered in Chapter 10.7.

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11.6: PHOTOLUMINESCENT SPECTROSCOPY

Photoluminescence is divided into two categories: fluorescence and phosphorescence. A pair of electrons that occupy the same electronic ground state have opposite spins and are in a singlet spin state (Figure 10.6.1 a).

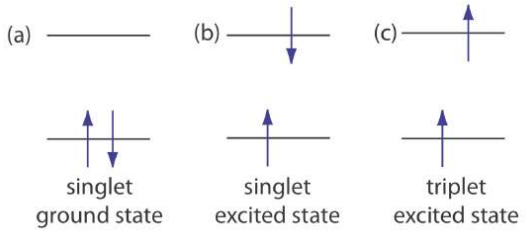


Figure 10.6.1 . Electron configurations for (a) a singlet ground state; (b) a singlet excited state; and (c) a triplet excited state.

When an analyte absorbs an ultraviolet or a visible photon, one of its valence electrons moves from the ground state to an excited state with a conservation of the electron's spin (Figure 10.6.1 b). Emission of a photon from a ***singlet excited state*** to the singlet ground state—or between any two energy levels with the same spin—is called ***fluorescence***. The probability of fluorescence is very high and the average lifetime of an electron in the excited state is only 10^{-5}–10^{-8} s. Fluorescence, therefore, rapidly decays once the source of excitation is removed.

In some cases an electron in a singlet excited state is transformed to a ***triplet excited state*** (Figure 10.6.1 c) in which its spin no is longer paired with the ground state. Emission between a triplet excited state and a singlet ground state—or between any two energy levels that differ in their respective spin states–is called ***phosphorescence***. Because the average lifetime for phosphorescence ranges from 10^{-4}–10^{4} s, phosphorescence may continue for some time after we remove the excitation source.

The use of molecular fluorescence for qualitative analysis and for semi-quantitative analysis dates to the early to mid 1800s, with more accurate quantitative methods appearing in the 1920s. Instrumentation for fluorescence spectroscopy using a filter or a monochromator for wavelength selection appeared in, respectively, the 1930s and 1950s. Although the discovery of phosphorescence preceded that of fluorescence by almost 200 years, qualitative and quantitative applications of molecular phosphorescence did not receive much attention until after the development of fluorescence instrumentation.

> As you might expect, the persistence of long-lived phosphorescence made it more noticeable.

FLUORESCENCE AND PHOSPHORESCENCE SPECTRA

To appreciate the origin of fluorescence and phosphorescence we must consider what happens to a molecule following the absorption of a photon. Let's assume the molecule initially occupies the lowest vibrational energy level of its electronic ground state, which is the singlet state labeled S_0 in Figure 10.6.2 . Absorption of a photon excites the molecule to one of several vibrational energy levels in the first excited electronic state, S_1, or the second electronic excited state, S_2, both of which are singlet states. Relaxation to the ground state occurs by a number of mechanisms, some of which result in the emission of a photon and others that occur without the emission of a photon. These relaxation mechanisms are shown in Figure 10.6.2 . The most likely relaxation pathway from any excited state is the one with the shortest lifetime.

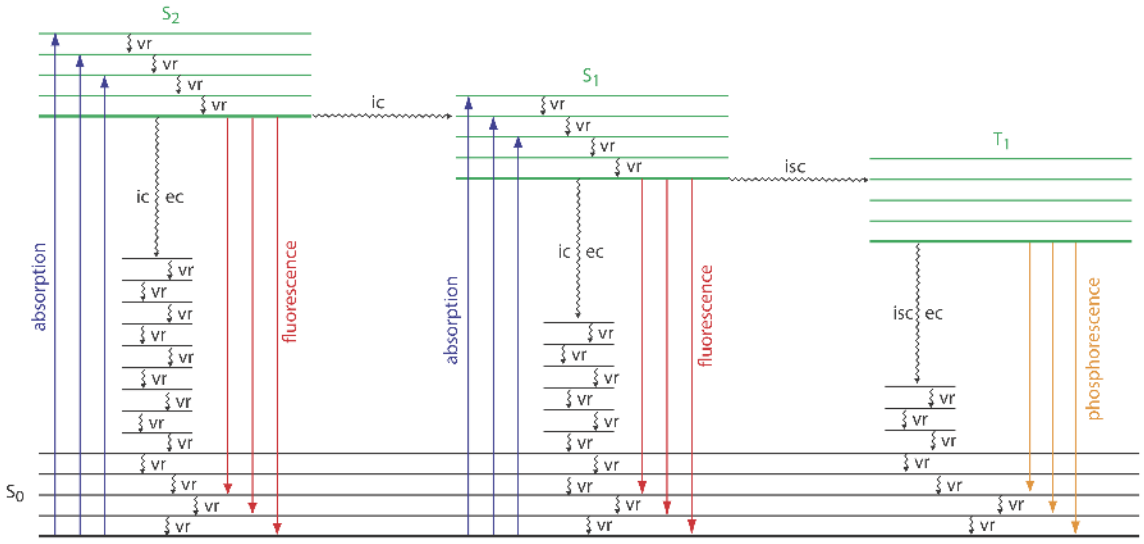


Figure 10.6.2 . Energy level diagram for a molecule that shows pathways for the deactivation of an excited state: ***vr*** is vibrational relaxation; ***ic*** is internal conversion; ***ec*** is external conversion; and ***isc*** is an intersystem crossing. The lowest vibrational energy for each electronic state is indicated by the thicker line. The electronic ground state is shown in black and the three electronic excited states are shown in green. The absorption, fluorescence, and phosphorescence of photons also are shown.

RADIATIONLESS DEACTIVATION

When a molecule relaxes without emitting a photon we call the process ***radiationless deactivation***. One example of radiationless deactivation is ***vibrational relaxation***, in which a molecule in an excited vibrational energy level loses energy by moving to a lower vibrational energy level in the same electronic state. Vibrational relaxation is very rapid, with an average lifetime of $<10^{-12}$ s. Because vibrational relaxation is so efficient, a molecule in one of its excited state's higher vibrational energy levels quickly returns to the excited state's lowest vibrational energy level.

Another form of radiationless deactivation is an ***internal conversion*** in which a molecule in the ground vibrational level of an excited state passes directly into a higher vibrational energy level of a lower energy electronic state of the same spin state. By a combination of internal conversions and vibrational relaxations, a molecule in an excited electronic state may return to the ground electronic state without emitting a photon. A related form of radiationless deactivation is an ***external conversion*** in which excess energy is transferred to the solvent or to another component of the sample's matrix.

> Let's use Figure 10.6.2 to illustrate how a molecule can relax back to its ground state without emitting a photon. Suppose our molecule is in the highest vibrational energy level of the second electronic excited state. After a series of vibrational relaxations brings the molecule to the lowest vibrational energy level of S_2, it undergoes an internal conversion into a higher vibrational energy level of the first excited electronic state. Vibrational relaxations bring the molecule to the lowest vibrational energy level of S_1. Following an internal conversion into a higher vibrational energy level of the ground state, the molecule continues to undergo vibrational relaxation until it reaches the lowest vibrational energy level of S_0.

A final form of radiationless deactivation is an ***intersystem crossing*** in which a molecule in the ground vibrational energy level of an excited electronic state passes into one of the higher vibrational energy levels of a lower energy electronic state with a different spin state. For example, an intersystem crossing is shown in Figure 10.6.2 between the singlet excited state S_1 and the triplet excited state T_1.

RELAXATION BY FLUORESCENCE

Fluorescence occurs when a molecule in an excited state's lowest vibrational energy level returns to a lower energy electronic state by emitting a photon. Because molecules return to their ground state by the fastest mechanism, fluorescence is observed only if it is a more efficient means of relaxation than a combination of internal conversions and vibrational relaxations.

A quantitative expression of fluorescence efficiency is the fluorescent ***quantum yield***, Φ_f, which is the fraction of excited state molecules that return to the ground state by fluorescence. The fluorescent quantum yields range from 1 when every molecule in an excited state undergoes fluorescence, to 0 when fluorescence does not occur.

The intensity of fluorescence, I_f, is proportional to the amount of radiation absorbed by the sample, $P_0 - P_T$, and the fluorescent quantum yield

$$I_f = k\Phi_f (P_0 - P_T) \tag{11.6.1}$$

where k is a constant that accounts for the efficiency of collecting and detecting the fluorescent emission. From Beer's law we know that

$$\frac{P_T}{P_0} = 10^{-\varepsilon bC} \tag{11.6.2}$$

where C is the concentration of the fluorescing species. Solving Equation 11.6.2 for P_T and substituting into Equation 11.6.1 gives, after simplifying

$$I_f = k\Phi_f P_0 \left(1 - 10^{-\varepsilon bC}\right) \tag{11.6.3}$$

When $\varepsilon bC < 0.01$, which often is the case when the analyte's concentration is small, Equation 11.6.3 simplifies to

$$I_f = 2.303k\Phi_f \varepsilon bCP_0 = k'P_0 \tag{11.6.4}$$

where k' is a collection of constants. The intensity of fluorescence, therefore, increases with an increase in the quantum efficiency, the source's incident power, and the molar absorptivity and the concentration of the fluorescing species.

Fluorescence generally is observed when the molecule's lowest energy absorption is a $\pi \rightarrow \pi^*$ transition, although some $n \rightarrow \pi^*$ transitions show weak fluorescence. Many unsubstituted, nonheterocyclic aromatic compounds have a favorable fluorescence quantum yield, although substitutions on the aromatic ring can effect Φ_f significantly. For example, the presence of an electron-withdrawing group, such as –NO_2, decreases Φ_f, while adding an electron-donating group, such as –OH, increases Φ_f. Fluorrescence also increases for aromatic ring systems and for aromatic molecules with rigid planar structures. Figure 10.6.3 shows the fluorescence of quinine under a UV lamp.



Figure 10.6.3 . Tonic water, which contains quinine, is fluorescent when placed under a UV lamp. Source: Splarka (commons.Wikipedia.org).

A molecule's fluorescent quantum yield also is influenced by external variables, such as temperature and solvent. Increasing the temperature generally decreases Φ_f because more frequent collisions between the molecule and the solvent increases external conversion. A decrease in the solvent's viscosity decreases Φ_f for similar reasons. For an analyte with acidic or basic functional groups, a change in pH may change the analyte's structure and its fluorescent properties.

As shown in Figure 10.6.2 , fluorescence may return the molecule to any of several vibrational energy levels in the ground electronic state. Fluorescence, therefore, occurs over a range of wavelengths. Because the change in energy for fluorescent emission generally is less than that for absorption, a molecule's fluorescence spectrum is shifted to higher wavelengths than its absorption spectrum.

RELAXATION BY PHOSPHORESCENCE

A molecule in a triplet electronic excited state's lowest vibrational energy level normally relaxes to the ground state by an intersystem crossing to a singlet state or by an external conversion. Phosphorescence occurs when the molecule relaxes by emitting a photon. As shown in Figure 10.6.2 , phosphorescence occurs over a range of wavelengths, all of which are at lower energies than the molecule's absorption band. The intensity of phosphorescence, I_p, is given by an equation similar to Equation 11.6.4 for fluorescence

$$I_P = 2.303k\Phi_P \varepsilon bCP_0 \tag{11.6.5}$$

$$= k'P_0 \tag{11.6.6}$$

where Φ_p is the ***phosphorescent quantum yield***.

Phosphorescence is most favorable for molecules with $n \rightarrow \pi^*$ transitions, which have a higher probability for an intersystem crossing than $\pi \rightarrow \pi^*$ transitions. For example, phosphorescence is observed with aromatic molecules that contain carbonyl groups or heteroatoms. Aromatic compounds that contain halide atoms also have a higher efficiency for phosphorescence. In general, an increase in phosphorescence corresponds to a decrease in fluorescence.

Because the average lifetime for phosphorescence can be quite long, ranging from 10^{-4}–10^{4} s, the phosphorescent quantum yield usually is quite small. An improvement in Φ_p is realized by decreasing the efficiency of external conversion. This is accomplished in several ways, including lowering the temperature, using a more viscous solvent, depositing the sample on a solid substrate, or trapping the molecule in solution. Figure 10.6.4 shows an example of phosphorescence.

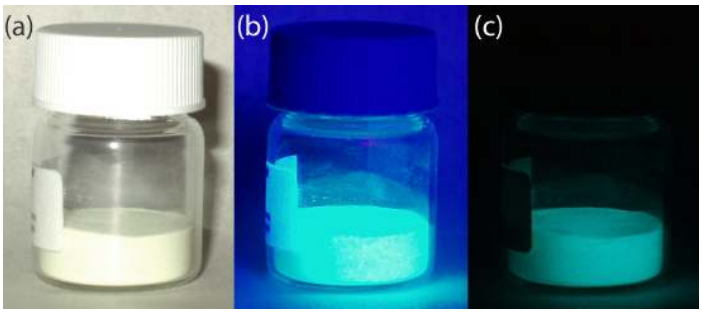


Figure 10.6.4 . An europium doped strontium silicate-aluminum oxide powder under (a) natural light, (b) a long-wave UV lamp, and (c) in total darkness. The photo taken in total darkness shows the phosphorescent emission. Source: modified from Splarka (commons.Wikipedia.org).

EXCITATION VERSUS EMISSION SPECTRA

Photoluminescence spectra are recorded by measuring the intensity of emitted radiation as a function of either the excitation wavelength or the emission wavelength. An ***excitation spectrum*** is obtained by monitoring emission at a fixed wavelength while varying the excitation wavelength. When corrected for variations in the source's intensity and the detector's response, a sample's excitation spectrum is nearly identical to its absorbance spectrum. The excitation spectrum provides a convenient means for selecting the best excitation wavelength for a quantitative or qualitative analysis.

In an ***emission spectrum*** a fixed wavelength is used to excite the sample and the intensity of emitted radiation is monitored as function of wavelength. Although a molecule has a single excitation spectrum, it has two emission spectra, one for fluorescence and one for phosphorescence. Figure 10.6.5 shows the UV absorption spectrum and the UV fluorescence emission spectrum for quinine.

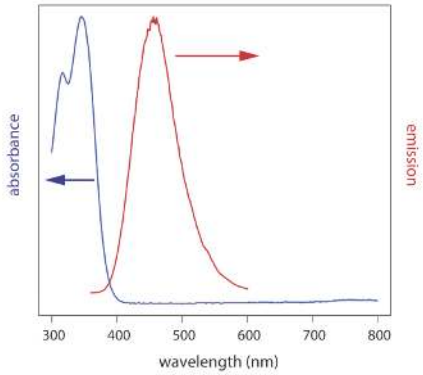


Figure 10.6.5 . Absorbance spectrum and fluorescence emission spectrum for quinine in 0.05 M H_2SO_4. The emission spectrum uses an excitation wavelength of 350 nm with a bandwidth of 20 nm. Both spectra are normalized so that the maximum absorbance is 1.00 and the maximum emission is 1.00. The actual maximum absorbance is 0.444 and the actual maximum emission is 126747. Source: data from Daniel Scott, Department of Chemistry & Biochemistry, DePauw University.

INSTRUMENTATION

The basic instrumentation for monitoring fluorescence and phosphorescence—a source of radiation, a means of selecting a narrow band of radiation, and a detector—are the same as those for absorption spectroscopy. The unique demands of fluorescence and phosphorescence, however, require some modifications to the instrument designs seen earlier in Figure 10.3.1 (filter photometer), Figure 10.3.2 (single-beam spectrophotometer), Figure 10.3.3 (double-beam spectrophotometer), and Figure 10.3.4 (diode array spectrometer). The most important difference is that the detector cannot be placed directly across from the source. Figure 10.6.6 shows why this is the case. If we place the detector along the source's axis it receives both the transmitted source radiation, P_T, and the fluorescent, I_f, or phosphorescent, I_p, radiation. Instead, we rotate the director and place it at 90º to the source.

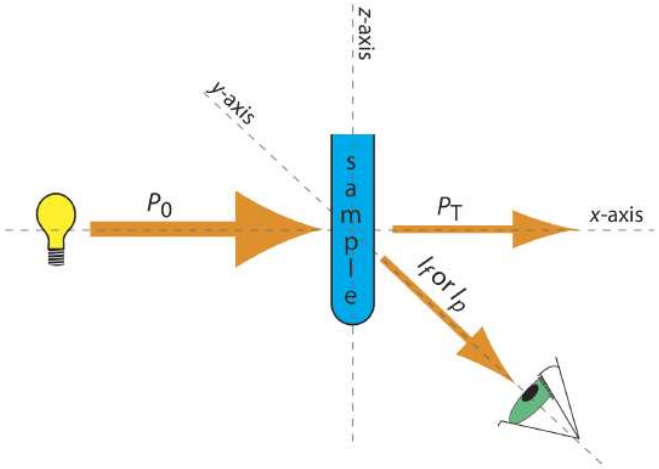


Figure 10.6.6 . Schematic diagram showing the orientation of the source and the detector when measuring fluorescence and phosphorescence. Contrast this to Figure 10.2.7, which shows the orientation for absorption spectroscopy.

INSTRUMENTS FOR MEASURING FLUORESCENCE

Figure 10.6.7 shows the basic design of an instrument for measuring fluorescence, which includes two wavelength selectors, one for selecting the source's excitation wavelength and one for selecting the analyte's emission wavelength. In a ***fluorimeter*** the excitation and emission wavelengths are selected using absorption or interference filters. The excitation source for a fluorimeter usually is a low-pressure Hg vapor lamp that provides intense emission lines distributed throughout the ultraviolet and visible region. When a monochromator is used to select the excitation and the emission wavelengths, the instrument is called a ***spectrofluorometer***. With a monochromator the excitation source usually is a high-pressure Xe arc lamp, which has a continuous emission spectrum. Either instrumental design is appropriate for quantitative work, although only a spectrofluorometer can record an excitation or emission spectrum.

> A Hg vapor lamp has emission lines at 254, 312, 365, 405, 436, 546, 577, 691, and 773 nm.

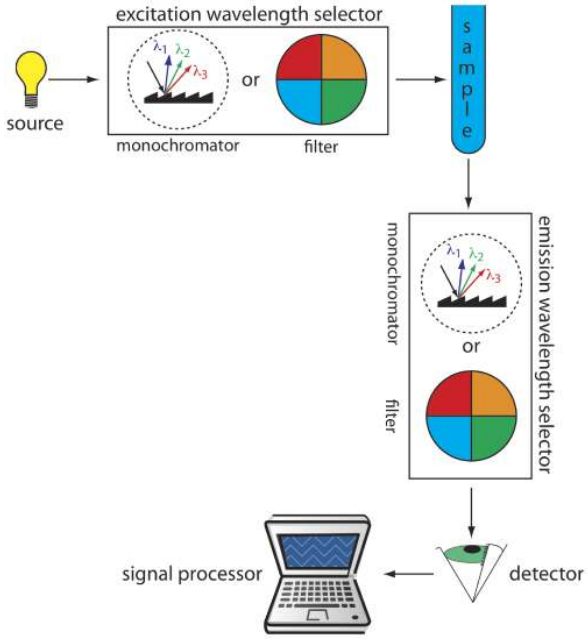


Figure 10.6.7 . Schematic diagram for measuring fluorescence showing the placement of the wavelength selectors for excitation and emission. When a filter is used the instrument is called a fluorimeter and when a monochromator is used the instrument is called a spectrofluorimeter.

The sample cells for molecular fluorescence are similar to those for molecular absorption (see Figure 10.3.6). Remote sensing using a fiber optic probe (see Figure 10.3.7) is possible using with either a fluorimeter or spectrofluorometer. An analyte that is fluorescent is monitored directly. For an analyte that is not fluorescent, a suitable fluorescent probe molecule is incorporated into the tip of the fiber optic probe. The analyte's reaction with the probe molecule leads to an increase or decrease in fluorescence.

INSTRUMENTS FOR MEASURING PHOSPHORESCENCE

An instrument for molecular phosphorescence must discriminate between phosphorescence and fluorescence. Because the lifetime for fluorescence is shorter than that for phosphorescence, discrimination is achieved by incorporating a delay between exciting the sample and measuring the phosphorescent emission. Figure 10.6.8 shows how two out-of-phase choppers allow us to block fluorescent emission from reaching the detector when the sample is being excited and to prevent the source radiation from causing fluorescence when we are measuring the phosphorescent emission.

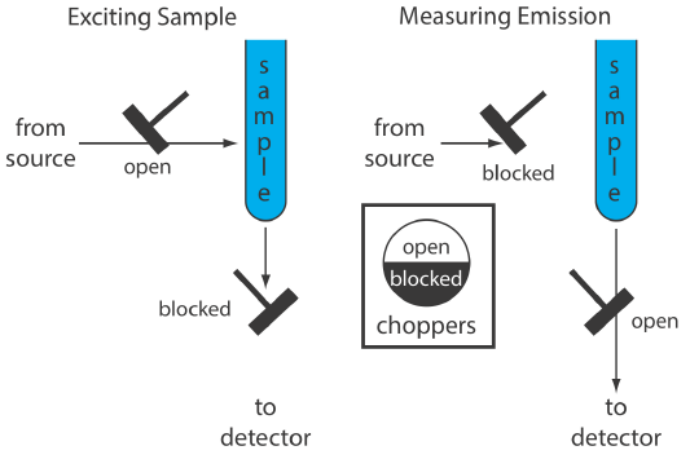


Figure 10.6.8 . Schematic diagram showing how choppers are used to prevent fluorescent emission from interfering with the measurement of phosphorescent emission.

Because phosphorescence is such a slow process, we must prevent the excited state from relaxing by external conversion. One way this is accomplished is by dissolving the sample in a suitable organic solvent, usually a mixture of ethanol, isopentane, and diethylether. The resulting solution is frozen at liquid-N_2 temperatures to form an optically clear solid. The solid matrix minimizes external conversion due to collisions between the analyte and the solvent. External conversion also is minimized by immobilizing the sample on a solid substrate, making possible room temperature measurements. One approach is to place a drop of a solution that contains the analyte on a small disc of filter paper. After drying the sample under a heat lamp, the sample is placed in the spectrofluorometer for analysis. Other solid substrates include silica gel, alumina, sodium acetate, and sucrose. This approach is particularly useful for the analysis of thin layer chromatography plates.

QUANTITATIVE APPLICATIONS

Molecular fluorescence and, to a lesser extent, phosphorescence are used for the direct or indirect quantitative analysis of analytes in a variety of matrices. A direct quantitative analysis is possible when the analyte's fluorescent or phosphorescent quantum yield is favorable. If the analyte is not fluorescent or phosphorescent, or if the quantum yield is unfavorable, then an indirect analysis may be feasible. One approach is to react the analyte with a reagent to form a product that is fluorescent or phosphorescent. Another approach is to measure a decrease in fluorescence or phosphores- cence when the analyte is added to a solution that contains a fluorescent or phosphorescent probe molecule. A decrease in emission is observed when the reaction between the analyte and the probe molecule enhances radiationless deactivation or results in a nonemitting product. The application of fluorescence and phosphorescence to inorganic and organic analytes are considered in this section.

INORGANIC ANALYTES

Except for a few metal ions, most notably UO_2^+, most inorganic ions are not sufficiently fluorescent for a direct analysis. Many metal ions are determined indirectly by reacting with an organic ligand to form a fluorescent or, less commonly, a phosphorescent metal–ligand complex. One example is the reaction of Al^{3+} with the sodium salt of 2, 4, 3′-trihydroxyazobenzene-5′-sulfonic acid—also known as alizarin garnet R—which forms a fluorescent metal–ligand complex (Figure 10.6.9). The analysis is carried out using an excitation wavelength of 470 nm, with fluorescence monitored at 500 nm. Table 10.6.1 provides additional examples of chelating reagents that form fluorescent metal–ligand complexes with metal ions. A few inorganic nonmetals are determined by their ability to decrease, or quench, the fluorescence of another species. One example is the analysis for F^- based on its ability to quench the fluorescence of the Al^{3+}–alizarin garnet R complex.

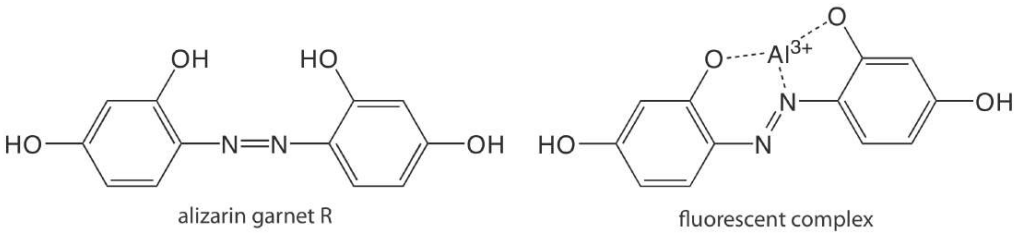


Figure 10.6.9 . Structure of alizarin garnet R and its metal–ligand complex with Al^{3+}.

Table 10.6.1 . Chelating Agents for the Fluorescent Analysis of Metal Ions

chelating agent	metal ions
8-hydroxyquinoline	Al^{3+}, Be^{2+}, Zn^{2+}, Li^{+}, Mg^{2+} (and others)
flavonal	Zr^{2+}, Sn^{4+}
benzoin	$B_4O_6^{2-}$, Zn^{2+}
$2',3',4',5,7-$ pentahydroxylflavone	Be^{2+}
2-(*o*-hydroxyphenyl) benzoxazole	Cd^{2+}

ORGANIC ANALYTES

As noted earlier, organic compounds that contain aromatic rings generally are fluorescent and aromatic heterocycles often are phosphorescent. Table 10.6.2 provides examples of several important biochemical, pharmaceutical, and environmental compounds that are analyzed quantitatively by fluorimetry or phosphorimetry. If an organic analyte is not naturally fluorescent or phosphorescent, it may be possible to incorporate it into a chemical reaction that produces a fluorescent or phosphorescent product. For example, the enzyme creatine phosphokinase is determined by using it to catalyze the formation of creatine from phosphocreatine. Reacting the creatine with ninhydrin produces a fluorescent product of unknown structure.

Table 10.6.2 . Examples of Naturally Photoluminescent Organic Analytes

class	compounds (F = fluorescence, P = phosphorescence)
aromatic amino acids	phenylalanine (F) tyrosine (F) tryptophan (F, P)
vitamins	vitamin A (F) vitamin B2 (F) vitamin B6 (F) vitamin B12 (F) vitamin E (F) folic acid (F)
catecholamines	dopamine (F) norepinephrine (F)
pharmaceuticals and drugs	quinine (F) salicylic acid (F, P) morphine (F) barbiturates (F) LSD (F) codeine (P) caffeine (P) sulfanilamide (P)
environmental pollutants	pyrene (F) benzo[a]pyrene (F) organothiophosphorous pesticides (F) carbamate insecticides (F) DDT (P)

STANDARDIZING THE METHOD

From Equation 11.6.4 and Equation 11.6.6 we know that the intensity of fluorescence or phosphorescence is a linear function of the analyte's concentration provided that the sample's absorbance of source radiation ($A = \varepsilon bC$) is less than approximately 0.01. Calibration curves often are linear over four to six orders of magnitude for fluorescence and over two to four orders of magnitude for phosphorescence. For higher concentrations of analyte the calibration curve becomes nonlinear because the assumptions that led to Equation 11.6.4 and Equation 11.6.6 no longer apply. Nonlinearity may be observed for smaller concentrations of analyte fluorescent or phosphorescent contaminants are present. As discussed earlier, quantum efficiency is sensitive to temperature and sample matrix, both of which must be con- trolled when using external standards. In addition, emission intensity depends on the molar absorptivity of the photoluminescent species, which is sensitive to the sample matrix.

REPRESENTATIVE METHOD 10.6.1: DETERMINATION OF QUININE IN URINE

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of quinine in urine provides an instructive example of a typical procedure. The description here is based on Mule, S. J.; Hushin, P. L. *Anal. Chem.* **1971**, *43*, 708–711, and O'Reilly, J. E.; *J. Chem. Educ.* **1975**, *52*, 610–612. Figure 10.6.3 shows the fluorescence of the quinine in tonic water.

Description of the Method

Quinine is an alkaloid used to treat malaria. It is a strongly fluorescent compound in dilute solutions of H_2SO_4 ($\Phi_f = 0.55$). Quinine's excitation spectrum has absorption bands at 250 nm and 350 nm and its emission spectrum has a single emission band at 450 nm. Quinine is excreted rapidly from the body in urine and is determined by measuring its fluorescence following its extraction from the urine sample.

Procedure

Transfer a 2.00-mL sample of urine to a 15-mL test tube and use 3.7 M NaOH to adjust its pH to between 9 and 10. Add 4 mL of a 3:1 (v/v) mixture of chloroform and isopropanol and shake the contents of the test tube for one minute. Allow the organic and the aqueous (urine) layers to separate and transfer the organic phase to a clean test tube. Add 2.00 mL of 0.05 M H_2SO_4 to the organic phase and shake the contents for one minute. Allow the organic and the aqueous layers to separate and transfer the aqueous phase to the sample cell. Measure the fluorescent emission at 450 nm using an excitation wavelength of 350 nm. Determine the concentration of quinine in the urine sample using a set of external standards in 0.05 M H_2SO_4, prepared from a 100.0 ppm solution of quinine in 0.05 M H_2SO_4. Use distilled water as a blank.

Questions

1. Chloride ion quenches the intensity of quinine's fluorescent emission. For example, in the presence of 100 ppm NaCl (61 ppm Cl^-) quinine's emission intensity is only 83% of its emission intensity in the absence of chloride. The presence of 1000 ppm NaCl (610 ppm Cl^-) further reduces quinine's fluorescent emission to less than 30% of its emission intensity in the absence of chloride. The concentration of chloride in urine typically ranges from 4600–6700 ppm Cl^-. Explain how this procedure prevents an interference from chloride.

The procedure uses two extractions. In the first of these extractions, quinine is separated from urine by extracting it into a mixture of chloroform and isopropanol, leaving the chloride ion behind in the original sample.

2. Samples of urine may contain small amounts of other fluorescent compounds, which will interfere with the analysis if they are carried through the two extractions. Explain how you can modify the procedure to take this into account?

One approach is to prepare a blank that uses a sample of urine known to be free of quinine. Subtracting the blank's fluorescent signal from the measured fluorescence from urine samples corrects for the interfering compounds.

The fluorescent emission for quinine at 450 nm can be induced using an excitation frequency of either 250 nm or 350 nm. The fluorescent quantum efficiency is the same for either excitation wavelength. Quinine's absorption spectrum shows that ε_{250} is greater than ε_{350}. Given that quinine has a stronger absorbance at 250 nm, explain why its fluorescent emission intensity is greater when using 350 nm as the excitation wavelength.

From Equation 11.6.4 we know that I_f is a function of the following terms: k, Φ_f, P_0, ε, b, and C. We know that Φ_f, b, and C are the same for both excitation wavelengths and that ε is larger for a wavelength of 250 nm; we can, therefore, ignore these terms. The greater emission intensity when using an excitation wavelength of 350 nm must be due to a larger value for P_0 or k . In fact, P_0 at 350 nm for a high-pressure Xe arc lamp is about 170% of that at 250 nm. In addition, the sensitivity of a typical photomultiplier detector (which contributes to the value of k) at 350 nm is about 140% of that at 250 nm.

EXAMPLE 10.6.1

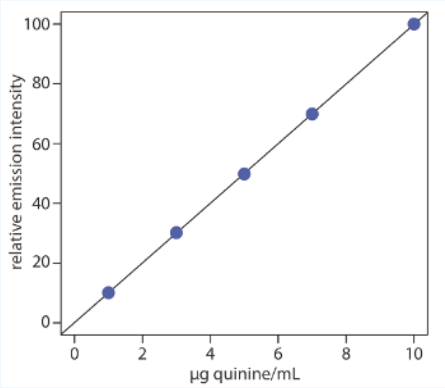
To evaluate the method described in Representative Method 10.6.1, a series of external standard are prepared and analyzed, providing the results shown in the following table. All fluorescent intensities are corrected using a blank prepared from a quinine-free sample of urine. The fluorescent intensities are normalized by setting I_f for the highest concentration standard to 100.

[quinine] (μg/mL)	I_f
1.00	10.11
3.00	30.20
5.00	49.84
7.00	69.89
10.00	100.0

After ingesting 10.0 mg of quinine, a volunteer provides a urine sample 24-h later. Analysis of the urine sample gives a relative emission intensity of 28.16. Report the concentration of quinine in the sample in mg/L and the percent recovery for the ingested quinine.

Solution

Linear regression of the relative emission intensity versus the concentration of quinine in the standards gives the calibration curve shown below and the following calibration equation.



$$I_f = 0.122 + 9.978 \times \frac{\text{g quinine}}{\text{mL}}$$

Substituting the sample's relative emission intensity into the calibration equation gives the concentration of quinine as 2.81 µg/mL. Because the volume of urine taken, 2.00 mL, is the same as the volume of 0.05 M H_2SO_4 used to extract the quinine, the concentration of quinine in the urine also is 2.81 µg/mL. The recovery of the ingested quinine is

$$\frac{\frac{2.81\ \mu\text{g quinine}}{\text{mL urine}} \times 2.00\ \text{mL urine} \times \frac{1\text{mg}}{1000\ \mu\text{g}}}{10.0\ \text{mg quinine ingested}} \times 100 = 0.0562\%$$

It can take 10–11 days for the body to completely excrete quinine so it is not surprising that such a small amount of quinine is recovered from this sample of urine.

EVALUATION OF PHOTOLUMINESCENCE SPECTROSCOPY

SCALE OF OPERATION

Photoluminescence spectroscopy is used for the routine analysis of trace and ultratrace analytes in macro and meso samples. Detection limits for fluorescence spectroscopy are influenced by the analyte's quantum yield. For an analyte with $\Phi_f > 0.5$, a picomolar detection limit is possible when using a high quality spectrofluorometer. For example, the detection limit for quinine sulfate, for which Φ is 0.55, generally is between 1 part per billion and 1 part per trillion. Detection limits for phosphorescence are somewhat higher, with typical values in the nanomolar range for low-temperature phosphorimetry and in the micromolar range for room-temperature phosphorimetry using a solid substrate.

ACCURACY

The accuracy of a fluorescence method generally is between 1–5% when spectral and chemical interferences are insignificant. Accuracy is limited by the same types of problems that affect other optical spectroscopic methods. In addition, accuracy is affected by interferences that affect the fluorescent quantum yield. The accuracy of phosphorescence is somewhat greater than that for fluorescence.

PRECISION

The relative standard deviation for fluorescence usually is between 0.5–2% when the analyte's concentration is well above its detection limit. Precision usually is limited by the stability of the excitation source. The precision for phosphorescence often is limited by reproducibility in preparing samples for analysis, with relative standard deviations of 5–10% being common.

SENSITIVITY

From Equation 11.6.4 and Equation 11.6.6 we know that the sensitivity of a fluorescent or a phosphorescent method is affected by a number of parameters. We already have considered the importance of quantum yield and the effect of temperature and solution composition on Φ_f and Φ_p. Besides quantum yield, sensitivity is improved by using an excitation source that has a greater emission intensity, P_0, at the desired wavelength, and by selecting an excitation wavelength for which the analyte has a greater molar absorptivity, ε. Another approach for improving sensitivity is to increase the volume from which emission is monitored. Figure 10.6.10 shows how rotating a monochromator's slits from their usual vertical orientation to a horizontal orientation increases the sampling volume. The result can increase the emission from the sample by $5 - 30\times$.

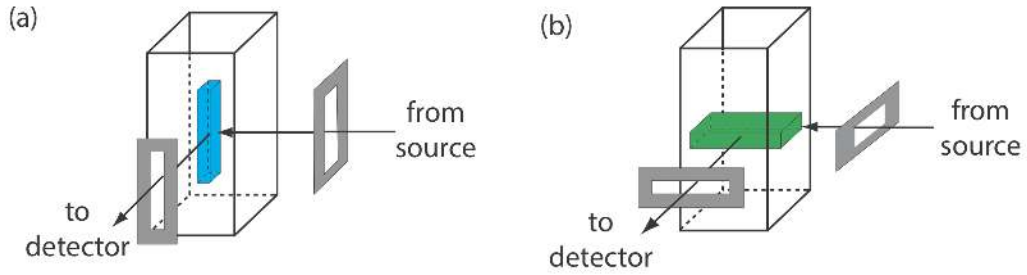


Figure 10.6.10 . Use of slit orientation to change the volume from which fluorescence is measured: (a) vertical slit orientation; (b) horizontal slit orientation. Suppose the slit's dimensions are 0.1 mm × 3 mm. In (a) the dimensions of the sampling volume are 0.1 mm × 0.1 mm × 3 mm, or 0.03 mm^3. For (b) the dimensions of the sampling volume are 0.1 mm × 3 mm × 3 mm, or 0.9 mm^3, a 30-fold increase in the sampling volume.

SELECTIVITY

The selectivity of fluorescence and phosphorescence is superior to that of absorption spectrophotometry for two reasons: first, not every compound that absorbs radiation is fluorescent or phosphorescent; and, second, selectivity between an analyte and an interferent is possible if there is a difference in either their excitation or their emission spectra. The total emission intensity is a linear sum of that from each fluorescent or phosphorescent species. The analysis of a sample that contains *n* analytes, therefore, is accomplished by measuring the total emission intensity at *n* wavelengths.

TIME, COST, AND EQUIPMENT

As with other optical spectroscopic methods, fluorescent and phosphorescent methods provide a rapid means for analyzing samples and are capable of automation. Fluorimeters are relatively inexpensive, ranging from several hundred to several thousand dollars, and often are satisfactory for quantitative work. Spectrofluorometers are more expensive, with models often exceeding $50,000.

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11.7: ATOMIC EMISSION SPECTROSCOPY

The focus of this section is on the emission of ultraviolet and visible radiation following the thermal excitation of atoms. Atomic emission spectroscopy has a long history. Qualitative applications based on the color of flames were used in the smelting of ores as early as 1550 and were more fully developed around 1830 with the observation of atomic spectra generated by flame emission and spark emission [Dawson, J. B. *J. Anal. At. Spectrosc.* **1991**, *6*, 93–98]. Quantitative applications based on the atomic emission from electric sparks were developed by Lockyer in the early 1870 and quantitative applications based on flame emission were pioneered by Lundegardh in 1930. Atomic emission based on emission from a plasma was introduced in 1964.

> For an on-line introduction to much of the material in this section, see Atomic Emission Spectroscopy (AES) by Tomas Spudich and Alexander Scheeline, a resource that is part of the Analytical Sciences Digital Library.

ATOMIC EMISSION SPECTRA

Atomic emission occurs when a valence electron in a higher energy atomic orbital returns to a lower energy atomic orbital. Figure 10.7.1 shows a portion of the energy level diagram for sodium, which consists of a series of discrete lines at wavelengths that correspond to the difference in energy between two atomic orbitals.

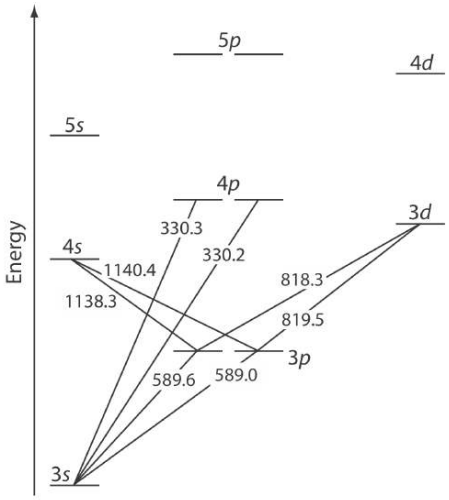


Figure 10.7.1 . Valence shell energy level diagram for sodium. The wavelengths corresponding to several transitions are shown. Note that this is the same energy level diagram as Figure 10.2.5.

The intensity of an atomic emission line, I_e, is proportional to the number of atoms, N^*, that populate the excited state,

$$I_e = kN^* \tag{11.7.1}$$

where k is a constant that accounts for the efficiency of the transition. If a system of atoms is in thermal equilibrium, the population of excited state i is related to the total concentration of atoms, N, by the Boltzmann distribution. For many elements at temperatures of less than 5000 K the Boltzmann distribution is approximated as

$$N^* = N\left(\frac{g_i}{g_0}\right)e^{-E_i/kT} \tag{11.7.2}$$

where g_i and g_0 are statistical factors that account for the number of equivalent energy levels for the excited state and the ground state, E_i is the energy of the excited state relative to a ground state energy, E_0, k is Boltzmann's constant (1.3807×10^{-23} J/K), and T is the temperature in Kelvin. From Equation 11.7.2 we expect that excited states with lower energies have larger populations and more intense emission lines. We also expect emission intensity to increase with temperature.

EQUIPMENT

An atomic emission spectrometer is similar in design to the instrumentation for atomic absorption. In fact, it is easy to adapt most flame atomic absorption spectrometers for atomic emission by turning off the hollow cathode lamp and monitoring the difference between the emission intensity when aspirating the sample and when aspirating a blank. Many atomic emission spectrometers, however, are dedicated instruments designed to take advantage of features unique to atomic emission, including the use of plasmas, arcs, sparks, and lasers as atomization and excitation sources, and an enhanced capability for multielemental analysis.

ATOMIZATION AND EXCITATION

Atomic emission requires a means for converting into a free gaseous atom an analyte that is present in a solid, liquid, or solution sample. The same source of thermal energy used for atomization usually serves as the excitation source. The most common methods are flames and plasmas, both of which are useful for liquid or solution samples. Solid samples are analyzed by dissolving in a solvent and using a flame or plasma atomizer.

FLAME SOURCES

Atomization and excitation in flame atomic emission is accomplished with the same nebulization and spray chamber assembly used in atomic absorption (Figure 10.4.1). The burner head consists of a single or multiple slots, or a Meker-style burner. Older atomic emission instruments often used a total consumption burner in which the sample is drawn through a capillary tube and injected directly into the flame.

> A Meker burner is similar to the more common Bunsen burner found in most laboratories; it is designed to allow for higher temperatures and for a larger diameter flame.

PLASMA SOURCES

A ***plasma*** is a hot, partially ionized gas that contains an abundant concentration of cations and electrons. The plasma used in atomic emission is formed by ionizing a flowing stream of argon gas, producing argon ions and electrons. A plasma's high temperature results from resistive heating as the electrons and argon ions move through the gas. Because a plasma operates at a much higher temperature than a flame, it provides for a better atomization efficiency and a higher population of excited states.

A schematic diagram of the inductively coupled plasma source (ICP) is shown in Figure 10.7.2 . The ICP torch consists of three concentric quartz tubes, surrounded at the top by a radio-frequency induction coil. The sample is mixed with a stream of Ar using a nebulizer, and is carried to the plasma through the torch's central capillary tube. Plasma formation is initiated by a spark from a Tesla coil. An alternating radio-frequency current in the induction coil creates a fluctuating magnetic field that induces the argon ions and the electrons to move in a circular path. The resulting collisions with the abundant unionized gas give rise to resistive heating, providing temperatures as high as 10000 K at the base of the plasma, and between 6000 and 8000 K at a height of 15–20 mm above the coil, where emission usually is measured. At these high temperatures the outer quartz tube must be thermally isolated from the plasma. This is accomplished by the tangential flow of argon shown in the schematic diagram.

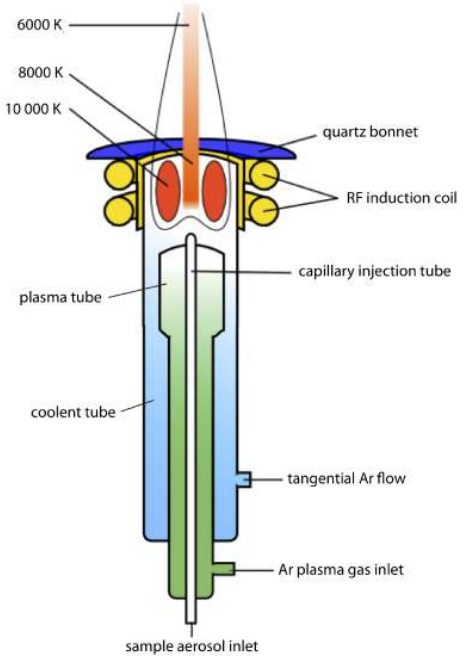


Figure 10.7.2 . Schematic diagram of an inductively coupled plasma torch.

MULTIELEMENTAL ANALYSIS

Atomic emission spectroscopy is ideally suited for a multielemental analysis because all analytes in a sample are excited simultaneously. If the instrument includes a scanning monochromator, we can program it to move rapidly to an analyte's desired wavelength, pause to record its emission intensity, and then move to the next analyte's wavelength. This sequential analysis allows for a sampling rate of 3–4 analytes per minute.

Another approach to a multielemental analysis is to use a multichannel instrument that allows us to monitor simultaneously many analytes. A simple design for a multichannel spectrometer, shown in Figure 10.7.3 , couples a monochromator with multiple detectors that are positioned in a semicircular array around the monochromator at positions that correspond to the wavelengths for the analytes.

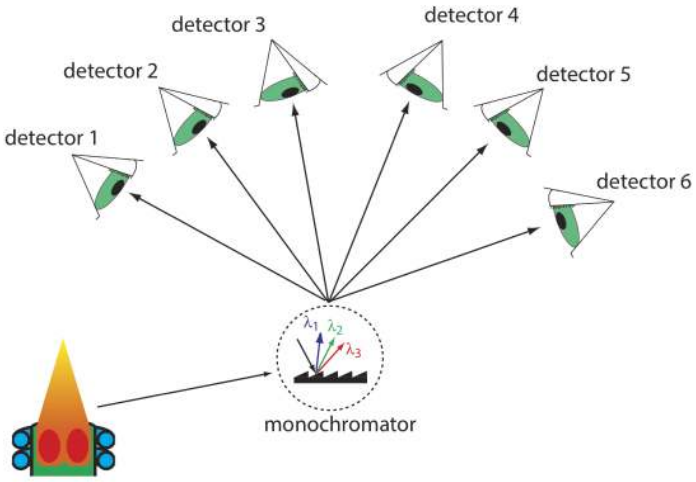


Figure 10.7.3 . Schematic diagram of a multichannel atomic emission spectrometer for the simultaneous analysis of several elements. Instruments may contain as many as 48–60 detectors.

QUANTITATIVE APPLICATIONS

Atomic emission is used widely for the analysis of trace metals in a variety of sample matrices. The development of a quantitative atomic emission method requires several considerations, including choosing a source for atomization and excitation, selecting a wavelength and slit width, preparing the sample for analysis, minimizing spectral and chemical interferences, and selecting a method of standardization.

CHOICE OF ATOMIZATION AND EXCITATION SOURCE

Except for the alkali metals, detection limits when using an ICP are significantly better than those obtained with flame emission (Table 10.7.1). Plasmas also are subject to fewer spectral and chemical interferences. For these reasons a plasma emission source is usually the better choice.

Table \(\PageIndex{1}\). Detection Limits for Atomic Emission

element	detection limit (µg/mL): flame emission	detection limit (µg/mL): ICP
Ag	2	0.2
Al	3	0.2
As	2000	2
Ca	0.1	0.0001
Cd	300	0.07
Co	5	0.1
Cr	1	0.08
Fe	10	0.09
Hg	150	1
K	0.01	30
Li	0.001	0.02
Mg	1	0.02
Mn	1	0.01
Na	0.01	0.1
Ni	10	0.2
Pb	0.2	1
Pt	2000	0.9
Sn	100	3
Zn	1000	0.1
Source: Parsons, M. L.; Major, S.; Forster, A. R.; App. Spectrosc. 1983, 37, 411–418.		

SELECTING THE WAVELENGTH AND SLIT WIDTH

The choice of wavelength is dictated by the need for sensitivity and the need to avoid interferences from the emission lines of other constituents in the sample. Because an analyte's atomic emission spectrum has an abundance of emission lines—particularly when using a

high temperature plasma source—it is inevitable that there will be some overlap between emission lines. For example, an analysis for Ni using the atomic emission line at 349.30 nm is complicated by the atomic emission line for Fe at 349.06 nm.

A narrower slit width provides better resolution, but at the cost of less radiation reaching the detector. The easiest approach to selecting a wavelength is to record the sample's emission spectrum and look for an emission line that provides an intense signal and is resolved from other emission lines.

PREPARING THE SAMPLE

Flame and plasma sources are best suited for samples in solution and in liquid form. Although a solid sample can be analyzed by directly inserting it into the flame or plasma, they usually are first brought into solution by digestion or extraction.

MINIMIZING SPECTRAL INTERFERENCES

The most important spectral interference is broad, background emission from the flame or plasma and emission bands from molecular species. This background emission is particularly severe for flames because the temperature is insufficient to break down refractory compounds, such as oxides and hydroxides. Background corrections for flame emission are made by scanning over the emission line and drawing a baseline (Figure 10.7.4). Because a plasma's temperature is much higher, a background interference due to molecular emission is less of a problem. Although emission from the plasma's core is strong, it is insignificant at a height of 10–30 mm above the core where measurements normally are made.

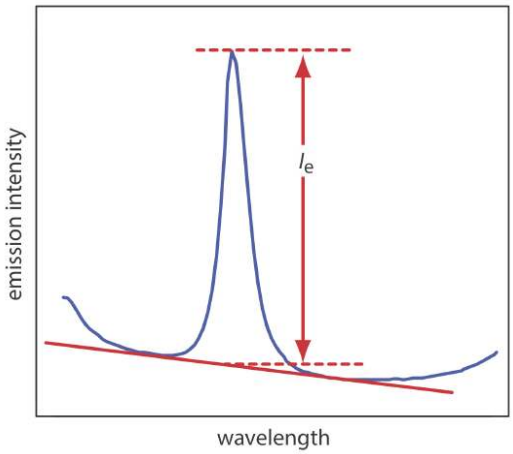


Figure 10.7.4 . Method for correcting an analyte's emission for the flame's background emission.

MINIMIZING CHEMICAL INTERFERENCES

Flame emission is subject to the same types of chemical interferences as atomic absorption; they are minimized using the same methods: by adjusting the flame's composition and by adding protecting agents, releasing agents, or ionization suppressors. An additional chemical interference results from ***self-absorption***. Because the flame's temperature is greatest at its center, the concentration of analyte atoms in an excited state is greater at the flame's center than at its outer edges. If an excited state atom in the flame's center emits a photon, then a ground state atom in the cooler, outer regions of the flame may absorb the photon, which decreases the emission intensity. For higher concentrations of analyte self-absorption may invert the center of the emission band (Figure 10.7.5).

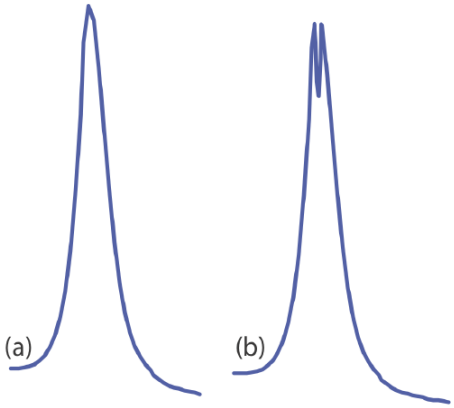


Figure 10.7.5 . Atomic emission lines for (a) a low concentration of analyte, and (b) a high concentration of analyte showing the effect of self-absorption.

Chemical interferences when using a plasma source generally are not significant because the plasma's higher temperature limits the formation of nonvolatile species. For example, PO_4^{3-} is a significant interferent when analyzing samples for Ca^{2+} by flame emission, but has a negligible effect when using a plasma source. In addition, the high concentration of electrons from the ionization of argon minimizes ionization interferences.

STANDARDIZING THE METHOD

From Equation 11.7.1 we know that emission intensity is proportional to the population of the analyte's excited state, N^*. If the flame or plasma is in thermal equilibrium, then the excited state population is proportional to the analyte's total population, N, through the Boltzmann distribution (Equation 11.7.2).

A calibration curve for flame emission usually is linear over two to three orders of magnitude, with ionization limiting linearity when the analyte's concentrations is small and self-absorption limiting linearity at higher concentrations of analyte. When using a plasma, which suffers from fewer chemical interferences, the calibration curve often is linear over four to five orders of magnitude and is not affected significantly by changes in the matrix of the standards.

Emission intensity is affected significantly by many parameters, including the temperature of the excitation source and the efficiency of atomization. An increase in temperature of 10 K, for example, produces a 4% increase in the fraction of Na atoms in the 3*p* excited state, an uncertainty in the signal that may limit the use of external standards. The method of internal standards is used when the variations in source parameters are difficult to control. To compensate for changes in the temperature of the excitation source, the internal standard is selected so that its emission line is close to the analyte's emission line. In addition, the internal standard should be subject to the same chemical interferences to compensate for changes in atomization efficiency. To accurately correct for these errors the analyte and internal standard emission lines are monitored simultaneously.

REPRESENTATIVE METHOD 10.7.1: DETERMINATION OF SODIUM IN A SALT SUBSTITUTE

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of sodium in salt substitutes provides an instructive example of a typical procedure. The description here is based on Goodney, D. E. *J. Chem. Educ.* **1982**, *59*, 875–876.

Description of Method

Salt substitutes, which are used in place of table salt for individuals on low-sodium diets, replaces NaCl with KCl. Depending on the brand, fumaric acid, calcium hydrogen phosphate, or potassium tartrate also are present. Although intended to be sodium-free, salt substitutes contain small amounts of NaCl as an impurity. Typically, the concentration of sodium in a salt substitute is about 100 µg/g The exact concentration of sodium is determined by flame atomic emission. Because it is difficult to match the matrix of the standards to that of the sample, the analysis is accomplished by the method of standard additions.

Procedure

A sample is prepared by placing an approximately 10-g portion of the salt substitute in 10 mL of 3 M HCl and 100 mL of distilled water. After the sample has dissolved, it is transferred to a 250-mL volumetric flask and diluted to volume with distilled water. A series of standard additions is prepared by placing 25-mL portions of the diluted sample into separate 50-mL volumetric flasks, spiking each with a known amount of an approximately 10 mg/L standard solution of Na^+, and diluting to volume. After zeroing the instrument with an appropriate blank, the instrument is optimized at a wavelength of 589.0 nm while aspirating a standard solution of Na^+. The emission intensity is measured for each of the standard addition samples and the concentration of sodium in the salt substitute is reported in µg/g.

Questions

1. Potassium ionizes more easily than sodium. What problem might this present if you use external standards prepared from a stock solution of 10 mg Na/L instead of using a set of standard additions?

Because potassium is present at a much higher concentration than is sodium, its ionization suppresses the ionization of sodium. Normally suppressing ionization is a good thing because it increases emission intensity. In this case, however, the difference between the standard's matrix and the sample's matrix means that the sodium in a standard experiences more ionization than an equivalent amount of sodium in a sample. The result is a determinate error.

2. One way to avoid a determinate error when using external standards is to match the matrix of the standards to that of the sample. We could, for example, prepare external standards using reagent grade KCl to match the matrix to that of the sample. Why is this not a good idea for this analysis?

Sodium is a common contaminant in many chemicals. Reagent grade KCl, for example, may contain 40–50 µg Na/g. This is a significant source of sodium, given that the salt substitute contains approximately 100 µg Na/g.

3. Suppose you decide to use an external standardization. Given the previous questions, is the result of your analysis likely to underestimate or to overestimate the amount of sodium in the salt substitute?

The solid black line in Figure 10.7.6 shows the ideal calibration curve, assuming we match the standard's matrix to the sample's matrix, and that we do so without adding any additional sodium. If we prepare the external standards without adding KCl, the emission for each standard decreases due to increased ionization. This is shown by the lower of the two dashed red lines. Preparing the standards by adding reagent grade KCl increases the concentration of sodium due to its contamination. Because we underestimate the actual concentration of sodium in the standards, the resulting calibration curve is shown by the other dashed red line. In both cases, the sample's emission results in our overestimating the concentration of sodium in the sample.

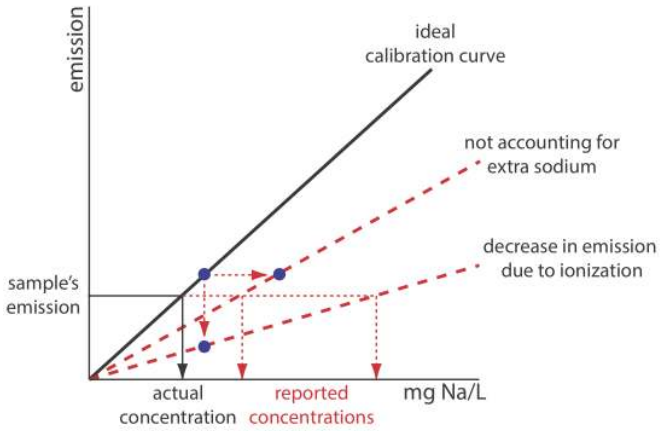


Figure 10.7.6 . External standards calibration curves for the flame atomic emission analysis of Na in a salt substitute. The solid black line shows the ideal calibration curve assuming we match the matrix of the samples and the standards using pure KCl. The lower of the two dashed red lines shows the effect of failing to add KCl to the external standards, which decreases emission. The other dashed red line shows the effect of using KCl that is contaminated with NaCl, which causes us to underestimate the concentration of Na in the standards. In both cases, the result is a positive determinate error in the analysis of samples.

4. One problem with analyzing salt samples is their tendency to clog the aspirator and burner assembly. What effect does this have on the analysis?

Clogging the aspirator and burner assembly decreases the rate of aspiration, which decreases the analyte's concentration in the flame. The result is a decrease in the emission intensity and a negative determinate error.

EXAMPLE 10.7.1

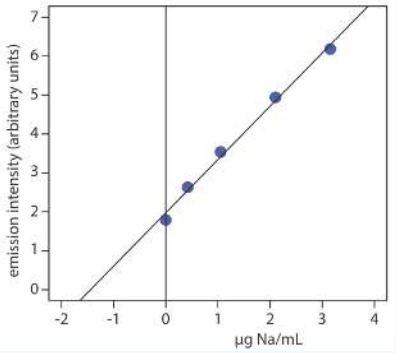
To evaluate the method described in Representative Method 10.7.1, a series of standard additions is prepared using a 10.0077-g sample of a salt substitute. The results of a flame atomic emission analysis of the standards is shown here [Goodney, D. E. *J. Chem. Educ.* **1982**, *59*, 875–876].

added Na (µg/mL)	I_e (arb. units)
0.000	1.79
0.420	2.63
1.051	3.54
2.102	4.94
3.153	6.18

What is the concentration of sodium, in µg/g, in the salt substitute.

Solution

Linear regression of emission intensity versus the concentration of added Na gives the standard additions calibration curve shown below, which has the following calibration equation.



$$I_e = 1.97 + 1.37 \times \frac{\mu g\ Na}{mL}$$

The concentration of sodium in the sample is the absolute value of the calibration curve's *x*-intercept. Substituting zero for the emission intensity and solving for sodium's concentration gives a result of 1.44 μgNa/mL. The concentration of sodium in the salt substitute is

$$\frac{\frac{1.44\ \mu g\ Na}{mL} \times \frac{50.00\ mL}{25.00\ mL} \times 250.0\ mL}{10.0077\ g\ sample} = 71.9\ \mu g\ Na/g$$

EVALUATION OF ATOMIC EMISSION SPECTROSCOPY

SCALE OF OPERATION

The scale of operations for atomic emission is ideal for the direct analysis of trace and ultratrace analytes in macro and meso samples. With appropriate dilutions, atomic emission can be applied to major and minor analytes.

ACCURACY

When spectral and chemical interferences are insignificant, atomic emission can achieve quantitative results with accuracies of 1–5%. For flame emission, accuracy frequently is limited by chemical interferences. Because the higher temperature of a plasma source gives rise to more emission lines, accuracy when using plasma emission often is limited by stray radiation from overlapping emission lines.

PRECISION

For samples and standards in which the analyte's concentration exceeds the detection limit by at least a factor of 50, the relative standard deviation for both flame and plasma emission is about 1–5%. Perhaps the most important factor that affect precision is the stability of the flame's or the plasma's temperature. For example, in a 2500 K flame a temperature fluctuation of ± 2.5 K gives a relative standard deviation of 1% in emission intensity. Significant improvements in precision are realized when using internal standards.

SENSITIVITY

Sensitivity is influenced by the temperature of the excitation source and the composition of the sample matrix. Sensitivity is optimized by aspirating a standard solution of analyte and maximizing the emission by adjusting the flame's composition and the height from which we monitor the emission. Chemical interferences, when present, decrease the sensitivity of the analysis. Because the sensitivity of plasma emission is less affected by the sample matrix, a calibration curve prepared using standards in a matrix of distilled water is possible even for samples that have more complex matrices.

SELECTIVITY

The selectivity of atomic emission is similar to that of atomic absorption. Atomic emission has the further advantage of rapid sequential or simultaneous analysis of multiple analytes.

TIME, COST, AND EQUIPMENT

Sample throughput with atomic emission is rapid when using an automated system that can analyze multiple analytes. For example, sampling rates of 3000 determinations per hour are possible using a multichannel ICP, and sampling rates of 300 determinations per hour when using a sequential ICP. Flame emission often is accomplished using an atomic absorption spectrometer, which typically costs between $10,000–$50,000. Sequential ICP's range in price from $55,000–$150,000, while an ICP capable of simultaneous multielemental analysis costs between $80,000–$200,000. Combination ICP's that are capable of both sequential and simultaneous analysis range in price from $150,000–$300,000. The cost of Ar, which is consumed in significant quantities, can not be overlooked when considering the expense of operating an ICP.

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11.8: SPECTROSCOPY BASED ON SCATTERING

The blue color of the sky during the day and the red color of the sun at sunset are the result of light scattered by small particles of dust, molecules of water, and other gases in the atmosphere. The efficiency of a photon's scattering depends on its wavelength. We see the sky as blue during the day because violet and blue light scatter to a greater extent than other, longer wavelengths of light. For the same reason, the sun appears red at sunset because red light is less efficiently scattered and is more likely to pass through the atmosphere than other wavelengths of light. The scattering of radiation has been studied since the late 1800s, with applications beginning soon thereafter. The earliest quantitative applications of scattering, which date from the early 1900s, used the elastic scattering of light by colloidal suspensions to determine the concentration of colloidal particles.

ORIGIN OF SCATTERING

If we send a focused, monochromatic beam of radiation with a wavelength λ through a medium of particles with dimensions $< 1.5\lambda$, the radiation scatters in all directions. For example, visible radiation of 500 nm is scattered by particles as large as 750 nm in the longest dimension. Two general categories of scattering are recognized. In elastic scattering, radiation is first absorbed by the particles and then emitted without undergoing a change in the radiation's energy. When the radiation emerges with a change in energy, the scattering is inelastic. Only elastic scattering is considered in this text.

Elastic scattering is divided into two types: Rayleigh, or small-particle scattering, and large-particle scattering. Rayleigh scattering occurs when the scattering particle's largest dimension is less than 5% of the radiation's wavelength. The intensity of the scattered radiation is proportional to its frequency to the fourth power, ν^4—which accounts for the greater scattering of blue light than red light—and is distributed symmetrically (Figure 10.8.1 a). For larger particles, scattering increases in the forward direction and decreases in the backward direction as the result of constructive and destructive interferences (Figure 10.8.1 b).

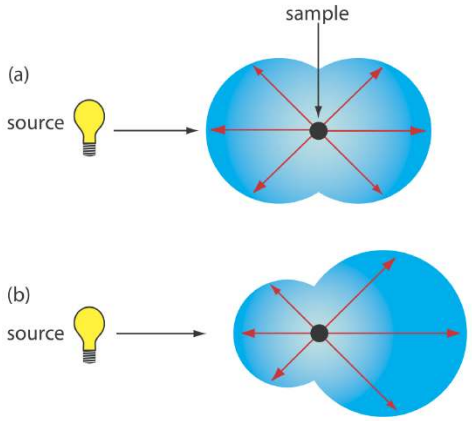


Figure 10.8.1 . Distribution of radiation for (a) Rayleigh, or small-particle scattering, and (b) large-particle scattering.

TURBIDIMETRY AND NEPHELOMETRY

Turbidimetry and nephelometry are two techniques that rely on the elastic scattering of radiation by a suspension of colloidal particles. In ***turbidimetry*** the detector is placed in line with the source and the decrease in the radiation's transmitted power is measured. In ***nephelometry*** the scattered radiation is measured at an angle of 90° to the source. The similarity of turbidimetry to absorbance spectroscopy and of nephelometry to fluorescence spectroscopy is evident in the instrumental designs shown in Figure 10.8.2 . In fact, we can use a UV/Vis spectrophotometer for turbidimetry and we can use a spectrofluorometer for nephelometry.

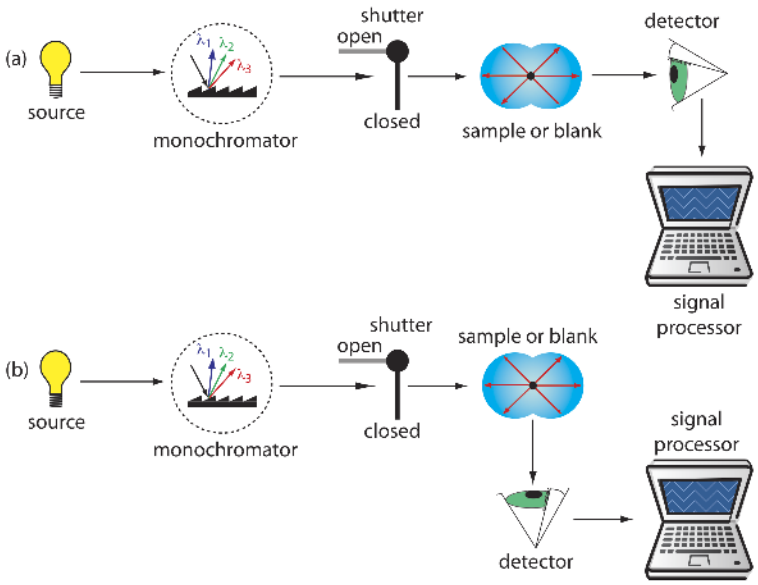


Figure 10.8.2 . Schematic diagrams for (a) a turbimeter, and (b) a nephelometer.

TURBIDIMETRY OR NEPHELOMETRY?

When developing a scattering method the choice between using turbidimetry or using nephelometry is determined by two factors. The most important consideration is the intensity of the scattered radiation relative to the intensity of the source's radiation. If the solution contains a small concentration of scattering particles, then the intensity of the transmitted radiation, I_T, is approximately the same as the intensity of the source's radiation, I_0. As we learned earlier in the section on molecular absorption, there is substantial uncertainty in determining a small difference between two intense signals. For this reason, nephelometry is a more appropriate choice for a sample that contains few scattering particles. Turbidimetry is a better choice when the sample contains a high concentration of scattering particles.

A second consideration in choosing between turbidimetry and nephelometry is the size of the scattering particles. For nephelometry, the intensity of scattered radiation at 90º increases when the particles are small and Rayleigh scattering is in effect. For larger particles, as shown in Figure 10.8.1 , the intensity of scattering decreases at 90º. When using an ultraviolet or a visible source of radiation, the optimum particle size is 0.1–1 μm. The size of the scattering particles is less important for turbidimetry where the signal is the relative decrease in transmitted radiation. In fact, turbidimetric measurements are feasible even when the size of the scattering particles results in an increase in reflection and refraction, although a linear relationship between the signal and the concentration of scattering particles may no longer hold.

DETERMINING CONCENTRATION BY TURBIDIMETRY

For turbidimetry the measured transmittance, T, is the ratio of the intensity of source radiation transmitted by the sample, I_T, to the intensity of source radiation transmitted by a blank, I_0.

$$T = \frac{I_T}{I_0}$$

The relationship between transmittance and the concentration of the scattering particles is similar to that given by Beer's law

$$-\log T = kbC \tag{11.8.1}$$

where C is the concentration of the scattering particles in mass per unit volume (w/v), b is the pathlength, and k is a constant that depends on several factors, including the size and shape of the scattering particles and the wavelength of the source radiation. The exact relationship is established by a calibration curve prepared using a series of standards that contain known concentrations of analyte. As with Beer's law, Equation 11.8.1 may show appreciable deviations from linearity.

DETERMINING CONCENTRATION BY NEPHELOMETRY

For nephelometry the relationship between the intensity of scattered radiation, I_S, and the concentration of scattering particles is

$$I_s = kI_0C \tag{11.8.2}$$

where k is an empirical constant for the system and I_0 is the intensity of the source radiation. The value of k is determined from a calibration curve prepared using a series of standards that contain known concentrations of analyte.

SELECTING A WAVELENGTH FOR THE INCIDENT RADIATION

The choice of wavelength is based primarily on the need to minimize potential interferences. For turbidimetry, where the incident radiation is transmitted through the sample, a monochromator or filter allow us to avoid wavelengths that are absorbed instead of scattered by the sample. For nephelometry, the absorption of incident radiation is not a problem unless it induces fluorescence from the sample. With a nonfluorescent sample there is no need for wavelength selection and a source of white light may be used as the incident radiation. For both techniques, other considerations in choosing a wavelength including the intensity of scattering, the trans- ducer's sensitivity (many common photon transducers are more sensitive to radiation at 400 nm than at 600 nm), and the source's intensity.

PREPARING THE SAMPLE FOR ANALYSIS

Although Equation 11.8.1 and Equation 11.8.2 relate scattering to the concentration of the scattering particles, the intensity of scattered radiation also is influenced by the size and the shape of the scattering particles. Samples that contain the same number of scattering particles may show significantly different values for $-\log T$ or I_S depending on the average diameter of the particles. For a quantitative analysis, therefore, it is necessary to maintain a uniform distribution of particle sizes throughout the sample and between samples and standards.

Most turbidimetric and nephelometric methods rely on precipitation reaction to form the scattering particles. As we learned in Chapter 8, a precipitate's properties, including particle size, are determined by the conditions under which it forms. To maintain a reproducible distribution of particle sizes between samples and standards, it is necessary to control parameters such as the concentration of reagents, the order of adding reagents, the pH and temperature, the agitation or stirring rate, the ionic strength, and the time between the precipitate's initial formation and the measurement of transmittance or scattering. In many cases a surface-active agent—such as glycerol, gelatin, or dextrin—is added to stabilize the precipitate in a colloidal state and to prevent the coagulation of the particles.

APPLICATIONS

Turbidimetry and nephelometry are used to determine the clarity of water. The primary standard for measuring clarity is formazin, an easily prepared, stable polymer suspension (Figure 10.8.3) [Hach, C. C.; Bryant, M. "Turbidity Standards," Technical Information Series, Booklet No. 12, Hach Company: Loveland, CO, 1995]. A stock standard of formazin is prepared by combining a 1g/100mL solution of hydrazine sulfate, $N_2H_4 \cdot H_2SO_4$, with a 10 g/100 mL solution of hexamethylenetetramine to produce a suspension of particles that is defined as 4000 nephelometric turbidity units (NTU). A set of external standards with NTUs between 0 and 40 is prepared by diluting the stock standard. This method is readily adapted to the analysis of the clarity of orange juice, beer, and maple syrup.

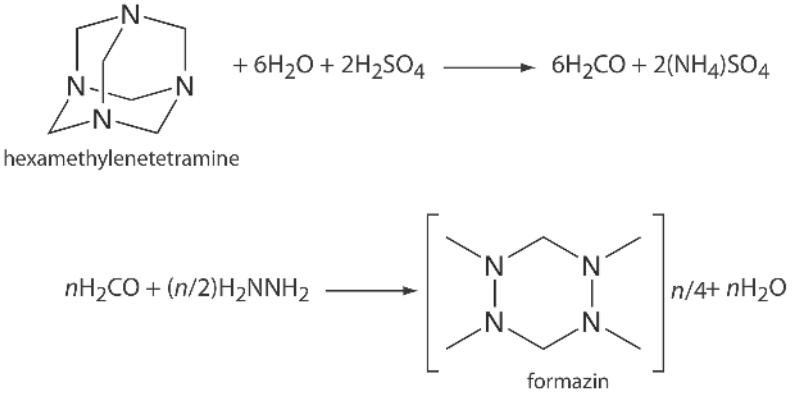


Figure 10.8.3 . Scheme for preparing formazin for use as a turbidity standard.

A number of inorganic cations and anions are determined by precipitating them under well-defined conditions. The transmittance or scattering of light, as defined by Equation 11.8.1 or Equation 11.8.2, is proportional to the concentration of the scattering particles, which, in turn, is related by the stoichiometry of the precipitation reaction to the analyte's concentration. Several examples of analytes determined in this way are listed in Table 10.8.1 .

Table 10.8.1 . Examples of Analytes Determined by Turbidimetry or Nephelometry

analyte	precipitant	precipitate
Ag^+	NaCl	AgCl
Ca^{2+}	$Na_2C_2O_4$	CaC_2O_4
Cl^-	$AgNO_3$	AgCl
CN^-	$AgNO_3$	AgCN
CO_3^{2-}	$BaCl_2$	$BaCO_3$
F^-	$CaCl_2$	CaF_2
SO_4^{2-}	$BaCl_2$	$BaSO_4$

REPRESENTATIVE METHOD 10.8.1: TURBIDIMETRIC DETERMINATION OF SULFATE IN WATER

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of sulfate in water provides an instructive example of a typical procedure. The description here is based on Method 4500–SO42—C in *Standard Methods for the Analysis of Water and Wastewater*, American Public Health Association: Washington, D. C. 20th Ed., 1998.

Description of Method

Adding $BaCl_2$ to an acidified sample precipitates SO_4^{2-} as $BaSO_4$. The concentration of SO_4^{2-} is determined either by turbidimetry or by nephelometry using an incident source of radiation of 420 nm. External standards that contain know concentrations of SO_4^{2-} are used to standardize the method.

Procedure

Transfer a 100-mL sample to a 250-mL Erlenmeyer flask along with 20.00 mL of an appropriate buffer. For a sample that contains more than 10 mg SO_4^{2-}/L, the buffer's composition is 30 g of $MgCl_2$•$6H_2O$, 5 g of CH_3COONa•$3H_2O$, 1.0 g of KNO_3, and 20 mL of glacial CH_3COOH per liter. The buffer for a sample that contain less than 10 mg SO_4^{2-}/L is the same except for the addition of 0.111 g of Na_2SO_4 per L.

Place the sample and the buffer on a magnetic stirrer operated at the same speed for all samples and standards. Add a spoonful of 20–30 mesh $BaCl_2$, using a measuring spoon with a capacity of 0.2–0.3 mL, to precipitate the SO_4^{2-} as BaSO4. Begin timing when the $BaCl_2$ is added and stir the suspension for 60 ± 2 s. When the stirring is complete, allow the solution to sit without stirring for 5.0± 0.5 min before measuring its transmittance or its scattering.

Prepare a calibration curve over the range 0–40 mg SO_4^{2-}/L by diluting a stock standard that is 100-mg SO_4^{2-}/L. Treat each standard using the procedure described above for the sample. Prepare a calibration curve and use it to determine the amount of sulfate in the sample.

Questions

1. What is the purpose of the buffer?

If the precipitate's particles are too small, I_T is too small to measure reliably. Because rapid precipitation favors the formation of microcrystalline particles of $BaSO_4$, we use conditions that favor the precipitate's growth over the nucleation of new particles. The buffer's high ionic strength and its acidity favor the precipitate's growth and prevent the formation of microcrystalline $BaSO_4$.

2. Why is it important to use the same stirring rate and time for the samples and standards?

How fast and how long we stir the sample after we add $BaCl_2$ influences the size of the precipitate's particles.

3. Many natural waters have a slight color due to the presence of humic and fulvic acids, and may contain suspended matter (Figure 10.8.4). Explain why these might interfere with the analysis for sulfate. For each interferent, suggest a way to minimize its effect on the analysis.



Figure 10.8.4 . Waterfall on the River Swale in Richmond, England. The river, which flows out of the moors in the Yorkshire Dales, is brown in color as the result of organic matter that leaches from the peat found in the moors.

Suspended matter in a sample contributes to scattering and, therefore, results in a positive determinate error. We can eliminate this interference by filtering the sample prior to its analysis. A sample that is colored may absorb some of the source's radiation, leading to a positive determinate error. We can compensate for this interference by taking a sample through the analysis without adding $BaCl_2$. Because no precipitate forms, we use the transmittance of this sample blank to correct for the interference.

4. Why is Na_2SO_4 added to the buffer for samples that contain less than 10 mg SO_4^{2-}/L?

The uncertainty in a calibration curve is smallest near its center. If a sample has a high concentration of SO_4^{2-}, we can dilute it so that its concentration falls near the middle of the calibration curve. For a sample with a small concentration of SO_4^{2-}, the buffer increases the concentration of sulfate by

$$\frac{0.111\ \text{g}\ Na_2SO_4}{\text{L}} \times \frac{96.06\ \text{g}\ SO_4^{2-}}{142.04\ \text{g}\ Na_2SO_4} \times \frac{1000\ \text{mg}}{\text{g}} \times \frac{20.00\ \text{mL}}{250.0\ \text{mL}} = 6.00\ \text{mg}\ SO_4^{2-}/\text{L}$$

After using the calibration curve to determine the amount of sulfate in the sample as analyzed, we subtract 6.00 mg SO_4^{2-}/L to determine the amount of sulfate in the original sample.

EXAMPLE 10.8.1

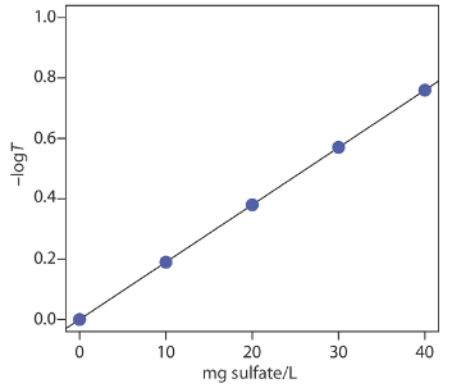
To evaluate the method described in Representative Method 10.8.1, a series of external standard was prepared and analyzed, providing the results shown in the following table.

mg SO_4^{2-}/L	transmittance
0.00	1.00
10.00	0.646
20.00	0.417
30.00	0.269
40.00	0.174

Analysis of a 100.0-mL sample of a surface water gives a transmittance of 0.538. What is the concentration of sulfate in the sample?

Solution

Linear regression of –log*T* versus concentration of SO_4^{2-} gives the calibration curve shown below, which has the following calibration equation.



$$-\log T = -1.04 \times 10^{-5} + 0.0190 \times \frac{\text{mg}\ SO_4^{2-}}{\text{L}}$$

Substituting the sample's transmittance into the calibration curve's equation gives the concentration of sulfate in sample as 14.2 mg SO_4^{2-}/L.

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11.9: PROBLEMS

1. Provide the missing information in the following table.

wavelength (m)	frequency (s^{-1})	wavenumber (cm^{-1})	energy (J)
4.50×10^{-9}			
	1.33×10^{15}		
		3215	
			7.20×10^{-19}

2. Provide the missing information in the following table.

[analyte] (M)	absorbance	%T	molar absorptivity (M^{-1} cm^{-1})	pathlength (cm)
1.40×10^{-4}			1120	1.00
	0.563		750	1.00
2.56×10^{-4}	0.225		456540	
1.55×10^{-3}	0.167		1550	5.00
		33.3		1.00
4.35×10^{-3}		21.2		
1.20×10^{-4}		81.3		10.00

3. A solution's transmittance is 35.0%. What is the transmittance if you dilute 25.0 mL of the solution to 50.0 mL?

4. A solution's transmittance is 85.0% when measured in a cell with a pathlength of 1.00 cm. What is the %T if you increase the pathlength to 10.00 cm?

5. The accuracy of a spectrophotometer is evaluated by preparing a solution of 60.06 ppm $K_2Cr_2O_7$ in 0.0050 M H_2SO_4, and measuring its absorbance at a wavelength of 350 nm in a cell with a pathlength of 1.00 cm. The expected absorbance is 0.640. What is the expected molar absorptivity of $K_2Cr_2O_7$ at this wavelength?

6. A chemical deviation to Beer's law may occur if the concentration of an absorbing species is affected by the position of an equilibrium reaction. Consider a weak acid, HA, for which K_a is 2×10^{-5}. Construct Beer's law calibration curves of absorbance versus the total concentration of weak acid (C_{total} = [HA] + [A^-]), using values for C_{total} of 1.0×10^{-5}, 3.0×10^{-5}, 5.0×10^{-5}, 7.0×10^{-5}, 9.0×10^{-5}, 11×10^{-5}, and 13×10^{-5} M for the following sets of conditions and comment on your results:

(a) $\varepsilon_{HA} = \varepsilon_{A^-} = 2000$ M^{-1} cm^{-1}; unbuffered solution.

(b) $\varepsilon_{HA} = 2000$ M^{-1} cm^{-1}; $\varepsilon_{A^-} = 500$ M^{-1} cm^{-1}; unbuffered solution.

(c) $\epsilon_{HA} = 2000$ M^{-1} cm^{-1}; $\epsilon_{A^-} = 500$ M^{-1} cm^{-1}; solution buffered to a pH of 4.5.

Assume a constant pathlength of 1.00 cm for all samples.

7. One instrumental limitation to Beer's law is the effect of polychromatic radiation. Consider a line source that emits radiation at two wavelengths, λ' and λ''. When treated separately, the absorbances at these wavelengths, A' and A'', are

$$A' = -\log \frac{P'_T}{P'_0} = \varepsilon' bC \qquad A'' = -\log \frac{P''_T}{P''_0} = \varepsilon'' bC$$

If both wavelengths are measured simultaneously the absorbance is

$$A = -\log \frac{\left(P'_T + P''_T\right)}{\left(P'_0 + P''_0\right)}$$

(a) Show that if the molar absorptivities at λ' and λ'' are the same ($\varepsilon' = \varepsilon'' = \varepsilon$), then the absorbance is equivalent to

$$A = \varepsilon bC$$

(b) Construct Beer's law calibration curves over the concentration range of zero to 1×10^{-4} M using $\varepsilon' = 1000$ M^{-1} cm^{-1} and $\varepsilon'' = 1000$ M^{-1} cm^{-1}, and $\varepsilon' = 1000$ M^{-1} cm^{-1} and $\varepsilon'' = 100$ M^{-1} cm^{-1}. Assume a value of 1.00 cm for the pathlength and that $P'_0 = P''_0 = 1$. Explain the difference between the two curves.

8. A second instrumental limitation to Beer's law is stray radiation. The following data were obtained using a cell with a pathlength of 1.00 cm when stray light is insignificant (P_{stray} = 0).

[analyte] (mM)	absorbance
0.00	0.00
2.00	0.40
4.00	0.80
6.00	1.20
8.00	1.60
10.00	3.00

Calculate the absorbance of each solution when P_{stray} is 5% of P_0, and plot Beer's law calibration curves for both sets of data. Explain any differences between the two curves. (*Hint*: Assume P_0 is 100).

9. In the process of performing a spectrophotometric determination of iron, an analyst prepares a calibration curve using a single-beam spectrophotometer similar to that shown in Figure 10.3.2. After preparing the calibration curve, the analyst drops and breaks the cuvette. The analyst acquires a new cuvette, measures the absorbance of the sample, and determines the %w/w Fe in the sample. Does the change in cuvette lead to a determinate error in the analysis? Explain.

10. The spectrophotometric methods for determining Mn in steel and for determining glucose use a chemical reaction to produce a colored spe- cies whose absorbance we can monitor. In the analysis of Mn in steel, colorless Mn^{2+} is oxidized to give the purple MnO_4^- ion. To analyze for glucose, which is also colorless, we react it with a yellow colored solution of the $Fe(CN)_6^{3-}$, forming the colorless $Fe(CN)_6^{4-}$ ion. The directions for the analysis of Mn do not specify precise reaction conditions, and samples and standards are treated separately. The conditions for the analysis of glucose, however, require that the samples and standards are treated simultaneously at exactly the same temperature and for exactly the same length of time. Explain why these two experimental procedures are so different.

11. One method for the analysis of Fe^{3+}, which is used with a variety of sample matrices, is to form the highly colored Fe^{3+}–thioglycolic acid complex. The complex absorbs strongly at 535 nm. Standardizing the method is accomplished using external standards. A 10.00-ppm Fe^{3+} working standard is prepared by transferring a 10-mL aliquot of a 100.0 ppm stock solution of Fe^{3+} to a 100-mL volumetric flask and diluting to volume. Calibration standards of 1.00, 2.00, 3.00, 4.00, and 5.00 ppm are prepared by transferring appropriate amounts of the 10.0 ppm working solution into separate 50-mL volumetric flasks, each of which contains 5 mL of thioglycolic acid, 2 mL of 20% w/v ammonium citrate, and 5 mL of 0.22 M NH_3. After diluting to volume and mixing, the absorbances of the external standards are measured against an appropriate blank. Samples are prepared for analysis by taking a portion known to contain approximately 0.1 g of Fe^{3+}, dissolving it in a minimum amount of HNO_3, and diluting to volume in a 1-L volumetric flask. A 1.00-mL aliquot of this solution is transferred to a 50-mL volumetric flask, along with 5 mL of thioglycolic acid, 2 mL of 20% w/v ammonium citrate, and 5 mL of 0.22 M NH_3 and diluted to volume. The absorbance of this solution is used to determine the concentration of $Fe3^+$ in the sample.

(a) What is an appropriate blank for this procedure?

(b) Ammonium citrate is added to prevent the precipitation of Al^{3+}. What is the effect on the reported concentration of iron in the sample if there is a trace impurity of Fe^{3+} in the ammonium citrate?

(c) Why does the procedure specify that the sample contain approximately 0.1 g of Fe^{3+}?

(d) Unbeknownst to the analyst, the 100-mL volumetric flask used to prepare the 10.00 ppm working standard of Fe^{3+} has a volume that is significantly smaller than 100.0 mL. What effect will this have on the reported concentration of iron in the sample?

12. A spectrophotometric method for the analysis of iron has a linear calibration curve for standards of 0.00, 5.00, 10.00, 15.00, and 20.00 mg Fe/L. An iron ore sample that is 40–60% w/w is analyzed by this method. An approximately 0.5-g sample is taken, dissolved in a minimum of concentrated HCl, and diluted to 1 L in a volumetric flask using distilled water. A 5.00 mL aliquot is removed with a pipet. To what volume—10, 25, 50, 100, 250, 500, or 1000 mL—should it be diluted to minimize the uncertainty in the analysis? Explain.

13. Lozano-Calero and colleagues developed a method for the quantitative analysis of phosphorous in cola beverages based on the formation of the blue-colored phosphomolybdate complex, $(NH_4)_3[PO_4(MoO_3)_{12}]$ [Lozano-Calero, D.; Martín-Palomeque, P.; Madueño-Loriguillo, S. *J. Chem. Educ.* **1996**, *73*, 1173–1174]. The complex is formed by adding $(NH_4)_6Mo_7O_{24}$ to the sample in the presence of a reducing agent, such as ascorbic acid. The concentration of the complex is determined spectrophotometrically at a wavelength of 830 nm, using an external standards calibration curve.

In a typical analysis, a set of standard solutions that contain known amounts of phosphorous is prepared by placing appropriate volumes of a 4.00 ppm solution of P_2O_5 in a 5-mL volumetric flask, adding 2 mL of an ascorbic acid reducing solution, and diluting to volume with distilled water. Cola beverages are prepared for analysis by pouring a sample into a beaker and allowing it to stand for 24 h to expel the dissolved CO_2. A 2.50-mL sample of the degassed sample is transferred to a 50-mL volumetric flask and diluted to volume. A 250-µL aliquot of the diluted sample is then transferred to a 5-mL volumetric flask, treated with 2 mL of the ascorbic acid reducing solution, and diluted to volume with distilled water.

(a) The authors note that this method can be applied only to noncol- ored cola beverages. Explain why this is true.

(b) How might you modify this method so that you can apply it to any cola beverage?

(c) Why is it necessary to remove the dissolved gases?

(d) Suggest an appropriate blank for this method?

(e) The author's report a calibration curve of

$$A = -0.02 + \left(0.72\ \text{ppm}^{-1}\right) \times C_{\text{P}_2\text{O}_5}$$

A sample of Crystal Pepsi, analyzed as described above, yields an absorbance of 0.565. What is the concentration of phosphorous, reported as ppm P, in the original sample of Crystal Pepsi?

> Crystal Pepsi was a colorless, caffeine-free soda produced by PepsiCo. It was available in the United States from 1992 to 1993.

14. EDTA forms colored complexes with a variety of metal ions that may serve as the basis for a quantitative spectrophotometric method of analysis. The molar absorptivities of the EDTA complexes of Cu^{2+}, Co^{2+}, and Ni^{2+} at three wavelengths are summarized in the following table (all values of ε are in M^{-1} cm^{-1}).

metal ion	$\varepsilon_{462.9}$	$\varepsilon_{732.0}$	$\varepsilon_{378.7}$
Co^{2+}	15.8	2.11	3.11
Cu^{2+}	2.32	95.2	7.73
Ni^{2+}	1.79	3.03	13.5

Using this information determine the following, assuming a pathlength, *b*, of 1.00 cm for all measurements:

(a) The concentration of Cu^{2+} in a solution that has an absorbance of 0.338 at a wavelength of 732.0 nm.

(b) The concentrations of Cu^{2+} and Co^{2+} in a solution that has an absorbance of 0.453 at a wavelength of 732.0 nm and 0.107 at a wavelength of 462.9 nm.

(c) The concentrations of Cu^{2+}, Co^{2+}, and Ni^{2+} in a sample that has an absorbance of 0.423 at a wavelength of 732.0 nm, 0.184 at a wavelength of 462.9 nm, and 0.291 at a wavelength of 378.7 nm.

15. The concentration of phenol in a water sample is determined by using steam distillation to separate the phenol from non-volatile impurities, followed by reacting the phenol in the distillate with 4-aminoantipyrine and $K_3Fe(CN)_6$ at pH 7.9 to form a colored antipyrine dye. A phenol standard with a concentration of 4.00 ppm has an absorbance of 0.424 at a wavelength of 460 nm using a 1.00 cm cell. A water sample is steam distilled and a 50.00-mL aliquot of the distillate is placed in a 100-mL volumetric flask and diluted to volume with distilled water. The absorbance of this solution is 0.394. What is the concentration of phenol (in parts per million) in the water sample?

16. Saito describes a quantitative spectrophotometric procedure for iron based on a solid-phase extraction using bathophenanthroline in a poly(vinyl chloride) membrane [Saito, T. *Anal. Chim. Acta* **1992**, *268*, 351–355]. In the absence of Fe^{2+} the membrane is colorless, but when immersed in a solution of Fe^{2+} and I^-, the membrane develops a red color as a result of the formation of an Fe^{2+}–bathophenanthroline complex. A calibration curve determined using a set of external standards with known concentrations of Fe^{2+} gave a standardization relationship of

$$A = \left(8.60 \times 10^3\ \text{M}^{-1}\right) \times \left[\text{Fe}^{2+}\right]$$

What is the concentration of iron, in mg Fe/L, for a sample with an absorbance of 0.100?

17. In the DPD colorimetric method for the free chlorine residual, which is reported as mg Cl_2/L, the oxidizing power of free chlorine converts the colorless amine N,N-diethyl-*p*-phenylenediamine to a colored dye that absorbs strongly over the wavelength range of 440–580 nm. Analysis of a set of calibration standards gave the following results.

mg Cl_2/L	absorbance
0.00	0.000
0.50	0.270
1.00	0.543
1.50	0.813
2.00	1.084

A sample from a public water supply is analyzed to determine the free chlorine residual, giving an absorbance of 0.113. What is the free chlorine residual for the sample in mg Cl_2/L?

18. Lin and Brown described a quantitative method for methanol based on its effect on the visible spectrum of methylene blue [Lin, J.; Brown, C. W. *Spectroscopy* **1995**, *10(5)*, 48–51]. In the absence of methanol, methylene blue has two prominent absorption bands at 610 nm and 663 nm, which correspond to the monomer and the dimer, respectively. In the presence of methanol, the intensity of the dimer's absorption band decreases, while that for the monomer increases. For concentrations of methanol between 0 and 30% v/v, the ratio of the

two absorbance, A_{663}/A_{610}, is a linear function of the amount of methanol. Use the following standardization data to determine the %v/v methanol in a sample if A_{610} is 0.75 and A_{663} is 1.07.

%v/v methanol	A_{663}/A_{610}	%v/v methanol	A_{663}/A_{610}
0.0	1.21	20.0	1.62
5.0	1.29	25.0	1.74
10.0	1.42	30.0	1.84
15.0	1.52		

19. The concentration of the barbiturate barbital in a blood sample is determined by extracting 3.00 mL of blood with 15 mL of $CHCl_3$. The chloroform, which now contains the barbital, is extracted with 10.0 mL of 0.45 M NaOH (pH ≈ 13). A 3.00-mL sample of the aqueous extract is placed in a 1.00-cm cell and an absorbance of 0.115 is measured. The pH of the sample in the absorption cell is then adjusted to approximately 10 by adding 0.50 mL of 16% w/v NH_4Cl, giving an absorbance of 0.023. When 3.00 mL of a standard barbital solution with a concentration of 3 mg/100 mL is taken through the same procedure, the absorbance at pH 13 is 0.295 and the absorbance at a pH of 10 is 0.002. Report the mg barbital/100 mL in the sample.

20. Jones and Thatcher developed a spectrophotometric method for analyzing analgesic tablets that contain aspirin, phenacetin, and caffeine [Jones, M.; Thatcher, R. L. *Anal. Chem.* **1951**, *23*, 957–960]. The sample is dissolved in $CHCl_3$ and extracted with an aqueous solution of $NaHCO_3$ to remove the aspirin. After the extraction is complete, the chloroform is transferred to a 250-mL volumetric flask and diluted to volume with $CHCl_3$. A 2.00-mL portion of this solution is then diluted to volume in a 200-mL volumetric flask with $CHCl_3$. The absorbance of the final solution is measured at wavelengths of 250 nm and 275 nm, at which the absorptivities, in $ppm^{-1}\ cm^{-1}$, for caffeine and phenacetin are

analyte	ε_{250}	ε_{275}
caffeine	0.0131	0.0485
phenacetin	0.0702	0.0159

Aspirin is determined by neutralizing the $NaHCO_3$ in the aqueous solution and extracting the aspirin into $CHCl_3$. The combined extracts are diluted to 500 mL in a volumetric flask. A 20.00-mL portion of the solution is placed in a 100-mL volumetric flask and diluted to volume with $CHCl_3$. The absorbance of this solution is measured at 277 nm, where the absorptivity of aspirin is 0.00682 $ppm^{-1}\ cm^{-1}$. An analgesic tablet treated by this procedure is found to have absorbances of 0.466 at 250 nm, 0.164 at 275 nm, and 0.600 at 277 nm when using a cell with a 1.00 cm pathlength. Report the milligrams of aspirin, caffeine, and phenacetin in the analgesic tablet.

21. The concentration of SO_2 in a sample of air is determined by the *p*-rosaniline method. The SO_2 is collected in a 10.00-mL solution of $HgCl_4^{2-}$, where it reacts to form $Hg(SO_3)_2$, by pulling air through the solution for 75 min at a rate of 1.6 L/min. After adding *p*-rosaniline and formaldehyde, the colored solution is diluted to 25 mL in a volumetric flask. The absorbance is measured at 569 nm in a 1-cm cell, yielding a value of 0.485. A standard sample is prepared by substituting a 1.00-mL sample of a standard solution that contains the equivalent of 15.00 ppm SO_2 for the air sample. The absorbance of the standard is found to be 0.181. Report the concentration of SO_2 in the air in mg SO_2/L. The density of air is 1.18 g/liter.

22. Seaholtz and colleagues described a method for the quantitative analysis of CO in automobile exhaust based on the measurement of infrared radiation at 2170 cm^{-1} [Seaholtz, M. B.; Pence, L. E.; Moe, O. A. Jr. *J. Chem. Educ.* **1988**, *65*, 820–823]. A calibration curve is prepared by filling a 10-cm IR gas cell with a known pressure of CO and measuring the absorbance using an FT-IR, giving a calibration equation of

$$A = -1.1 \times 10^{-4} + \left(9.9 \times 10^{-4}\right) \times P_{CO}$$

Samples are prepared by using a vacuum manifold to fill the gas cell. After measuring the total pressure, the absorbance at 2170 cm^{-1} is measured. Results are reported as %CO (P_{CO}/P_{total}). The analysis of five exhaust samples from a 1973 coupe gives the following results.

P_{total} (torr)	absorbance
595	0.1146
354	0.0642
332	0.0591
233	0.0412
143	0.0254

Determine the %CO for each sample, and report the mean and the 95% confidence interval.

23. Figure 10.3.8 shows an example of a disposable IR sample card made using a thin sheet of polyethylene. To prepare an analyte for analysis, it is dissolved in a suitable solvent and a portion of the sample placed on the IR card. After the solvent evaporates, leaving the analyte behind as a thin film, the sample's IR spectrum is obtained. Because the thickness of the polyethylene film is not uniform, the

primary application of IR cards is for a qualitative analysis. Zhao and Malinowski reported how an internal standardization with KSCN can be used for a quantitative IR analysis of polystyrene [Zhao, Z.; Malinowski, E. R. *Spectroscopy* **1996**, *11(7)*, 44–49]. Polystyrene is monitored at 1494 cm^{-1} and KSCN at 2064 cm^{-1}. Standard solutions are prepared by placing weighed portions of polystyrene in a 10-mL volumetric flask and diluting to volume with a solution of 10 g/L KSCN in methyl isobutyl ketone. A typical set of results is shown here.

g polystyrene	0.1609	0.3290	0.4842	0.6402	0.8006
A_{1494}	0.0452	0.1138	0.1820	0.3275	0.3195
A_{2064}	0.1948	0.2274	0.2525	0.3580	0.2703

When a 0.8006-g sample of a poly(styrene/maleic anhydride) copolymer is analyzed, the following results are obtained.

replicate	A_{1494}	A_{2064}
1	0.2729	0.3582
2	0.2074	0.2820
3	0.2785	0.3642

What is the %w/w polystyrene in the copolymer? Given that the reported %w/w polystyrene is 67%, is there any evidence for a determinate error at $\alpha = 0.05$?

24. The following table lists molar absorptivities for the Arsenazo complexes of copper and barium [Grossman, O.; Turanov, A. N. *Anal. Chim. Acta* **1992**, *257*, 195–202]. Suggest appropriate wavelengths for analyzing mixtures of copper and barium using their Arsenzao complexes.

wavelength (nm)	ε_{Cu} (M^{-1} cm^{-1})	ε_{Ba} (M^{-1} cm^{-1})
595	11900	7100
600	15500	7200
607	18300	7400
611	19300	6900
614	19300	7000
620	17800	7100
626	16300	8400
635	10900	9900
641	7500	10500
645	5300	10000
650	3500	8600
655	2200	6600
658	1900	6500
665	1500	3900
670	1500	2800
680	1800	1500

25. Blanco and colleagues report several applications of multiwavelength linear regression analysis for the simultaneous determination of two-component mixtures [Blanco, M.; Iturriaga, H.; Maspoch, S.; Tarin, P. *J. Chem. Educ.* **1989**, *66*, 178–180]. For each of the following, determine the molar concentration of each analyte in the mixture.

(a) Titanium and vanadium are determined by forming complexes with H_2O_2. Results for a mixture of Ti(IV) and V(V) and for stan-dards of 63.1 ppm Ti(IV) and 96.4 ppm V(V) are listed in the following table.

wavelength (nm)	$A_{Ti(V)\ Std}$	$A_{V(V)\ Std}$	A_{mix}
390	0.895	0.326	0.651
430	0.884	0.497	0.743
450	0.694	0.528	0.665
470	0.481	0.512	0.547
510	0.173	0.374	0.314

(b) Copper and zinc are determined by forming colored complexes with 2-pyridyl-azo-resorcinol (PAR). The absorbances for PAR, a mixture of Cu^{2+} and Zn^{2+}, and standards of 1.00 ppm Cu^{2+} and 1.00 ppm Zn^{2+} are listed in the following table. Note that you must correct the absorbances for the each metal for the contribution from PAR.

wavelength (nm)	A_{PAR}	$A_{Cu\ Std}$	$A_{Zn\ Std}$	A_{mix}
480	0.211	0.698	0.971	0.656
496	0.137	0.732	1.018	0.668
510	0.100	0.732	0.891	0.627
526	0.072	0.602	0.672	0.498
540	0.056	0.387	0.306	0.290

26. The stoichiometry of a metal–ligand complex, ML_n, is determined by the method of continuous variations. A series of solutions is prepared in which the combined concentrations of M and L are held constant at 5.15×10^{-4} M. The absorbances of these solutions are measured at a wavelength where only the metal–ligand complex absorbs. Using the following data, determine the formula of the metal–ligand complex.

mole fraction of M	mole fraction of L	absorbance
1.0	0.0	0.001
0.9	0.1	0.126
0.8	0.2	0.260
0.7	0.3	0.389
0.6	0.4	0.515
0.5	0.5	0.642
0.4	0.6	0.775
0.3	0.7	0.771
0.2	0.8	0.513
0.1	0.9	0.253
0.0	1.0	0.000

27. The stoichiometry of a metal–ligand complex, ML_n, is determined by the mole-ratio method. A series of solutions are prepared in which the metal's concentration is held constant at 3.65×10^{-4} M and the ligand's concentration is varied from 1×10^{-4} M to 1×10^{-3} M. Using the following data, determine the stoichiometry of the metal-ligand complex.

[ligand] (M)	absorbance	[ligand] (M)	absorbance
1.0×10^{-4}	0.122	6.0×10^{-4}	0.752
2.0×10^{-4}	0.251	7.0×10^{-4}	0.873
3.0×10^{-4}	0.376	8.0×10^{-4}	0.937
4.0×10^{-4}	0.496	9.0×10^{-4}	0.962
5.0×10^{-4}	0.625	1.0×10^{-3}	1.002

28. The stoichiometry of a metal–ligand complex, ML_n, is determined by the slope-ratio method. Two sets of solutions are prepared. For the first set of solutions the metal's concentration is held constant at 0.010 M and the ligand's concentration is varied. The following data are obtained at a wavelength where only the metal–ligand complex absorbs.

[ligand] (M)	absorbance
1.0×10^{-5}	0.012
2.0×10^{-5}	0.029
3.0×10^{-5}	0.042
4.0×10^{-5}	0.055
5.0×10^{-5}	0.069

For the second set of solutions the concentration of the ligand is held constant at 0.010 M, and the concentration of the metal is varied, yielding the following absorbances.

[metal] (M)	absorbance
1.0×10^{-5}	0.040
2.0×10^{-5}	0.085
3.0×10^{-5}	0.125
4.0×10^{-5}	0.162
5.0×10^{-5}	0.206

Using this data, determine the stoichiometry of the metal-ligand complex.

29. Kawakami and Igarashi developed a spectrophotometric method for nitrite based on its reaction with 5, 10, 15, 20-tetrakis(4-aminophenyl) porphrine (TAPP). As part of their study they investigated the stoichiometry of the reaction between TAPP and NO_2^-. The

following data are derived from a figure in their paper [Kawakami, T.; Igarashi, S. *Anal. Chim. Acta* **1996**, *333*, 175–180].

[TAPP] (M)	$[NO_2^-]$ (M)	absorbance
8.0×10^{-7}	0	0.227
8.0×10^{-7}	4.0×10^{-8}	0.223
8.0×10^{-7}	8.0×10^{-8}	0.211
8.0×10^{-7}	1.6×10^{-7}	0.191
8.0×10^{-7}	3.2×10^{-7}	0.152
8.0×10^{-7}	4.8×10^{-7}	0.127
8.0×10^{-7}	6.4×10^{-7}	0.107
8.0×10^{-7}	8.0×10^{-7}	0.092
8.0×10^{-7}	1.6×10^{-6}	0.058
8.0×10^{-7}	2.4×10^{-6}	0.045
8.0×10^{-7}	3.2×10^{-6}	0.037
8.0×10^{-7}	4.0×10^{-6}	0.034

What is the stoichiometry of the reaction?

30. The equilibrium constant for an acid–base indicator is determined by preparing three solutions, each of which has a total indicator concentration of 1.35×10^{-5} M. The pH of the first solution is adjusted until it is acidic enough to ensure that only the acid form of the indicator is present, yielding an absorbance of 0.673. The absorbance of the second solution, whose pH is adjusted to give only the base form of the indicator, is 0.118. The pH of the third solution is adjusted to 4.17 and has an absorbance of 0.439. What is the acidity constant for the acid–base indicator?

31. The acidity constant for an organic weak acid is determined by measuring its absorbance as a function of pH while maintaining a constant total concentration of the acid. Using the data in the following table, determine the acidity constant for the organic weak acid.

pH	absorbance	pH	absorbance
1.53	0.010	4.88	0.193
2.20	0.010	5.09	0.227
3.66	0.035	5.69	0.288
4.11	0.072	7.20	0.317
4.35	0.103	7.78	0.317
4.75	0.169		

32. Suppose you need to prepare a set of calibration standards for the spectrophotometric analysis of an analyte that has a molar absorptivity of 1138 M^{-1} cm^{-1} at a wavelength of 625 nm. To maintain an acceptable precision for the analysis, the %T for the standards should be between 15% and 85%.

(a) What is the concentration for the most concentrated and for the least concentrated standard you should prepare, assuming a 1.00-cm sample cell.

(b) Explain how you will analyze samples with concentrations that are 10 μM, 0.1 mM, and 1.0 mM in the analyte.

33. When using a spectrophotometer whose precision is limited by the uncertainty of reading %T, the analysis of highly absorbing solutions can lead to an unacceptable level of indeterminate errors. Consider the analysis of a sample for which the molar absorptivity is 1.0×10^4 M^{-1} cm^{-1} and for which the pathlength is 1.00 cm.

(a) What is the relative uncertainty in concentration for an analyte whose concentration is 2.0×10^{-4} M if s_T is ±0.002?

(b) What is the relative uncertainty in the concentration if the spectrophotometer is calibrated using a blank that consists of a 1.0×10^{-4} M solution of the analyte?

34. Hobbins reported the following calibration data for the flame atomic absorption analysis for phosphorous [Hobbins, W. B. “Direct Determination of Phosphorous in Aqueous Matricies by Atomic Absorption,” Varian Instruments at Work, Number AA-19, February 1982].

mg P/L	absorbance
2130	0.048
4260	0.110
6400	0.173
8530	0.230

To determine the purity of a sample of Na_2HPO_4, a 2.469-g sample is dissolved and diluted to volume in a 100-mL volumetric flask. Analysis of the resulting solution gives an absorbance of 0.135. What is the purity of the Na_2HPO_4?

35. Bonert and Pohl reported results for the atomic absorption analysis of several metals in the caustic suspensions produced during the manufacture of soda by the ammonia-soda process [Bonert, K.; Pohl, B. "The Determination of Cd, Cr, Cu, Ni, and Pb in Concentrated $CaCl_2$/NaCl solutions by AAS," AA Instruments at Work (Varian) Number 98, November, 1990].

(a) The concentration of Cu is determined by acidifying a 200.0-mL sample of the caustic solution with 20 mL of concentrated HNO_3, adding 1 mL of 27% w/v H_2O_2, and boiling for 30 min. The resulting solution is diluted to 500 mL in a volumetric flask, filtered, and analyzed by flame atomic absorption using matrix matched standards. The results for a typical analysis are shown in the following table.

solution	mg Cu/L	absorbance
blank	0.000	0.007
standard 1	0.200	0.014
standard 2	0.500	0.036
standard 3	1.000	0.072
standard 4	2.000	0.146
sample		0.027

Determine the concentration of Cu in the caustic suspension.

(b) The determination of Cr is accomplished by acidifying a 200.0-mL sample of the caustic solution with 20 mL of concentrated HNO_3, adding 0.2 g of Na_2SO_3 and boiling for 30 min. The Cr is isolated from the sample by adding 20 mL of NH_3, producing a precipitate that includes the chromium as well as other oxides. The precipitate is isolated by filtration, washed, and transferred to a beaker. After acidifying with 10 mL of HNO_3, the solution is evaporated to dryness. The residue is redissolved in a combination of HNO_3 and HCl and evaporated to dryness. Finally, the residue is dissolved in 5 mL of HCl, filtered, diluted to volume in a 50-mL volumetric flask, and analyzed by atomic absorption using the method of standard additions. The atomic absorption results are summarized in the following table.

sample	mg Cr_{added}/L	absorbance
blank		0.001
sample		0.045
standard addition 1	0.200	0.083
standard addition 2	0.500	0.118
standard addition 3	1.000	0.192

Report the concentration of Cr in the caustic suspension.

36. Quigley and Vernon report results for the determination of trace metals in seawater using a graphite furnace atomic absorption spectrophotometer and the method of standard additions [Quigley, M. N.; Vernon, F. *J. Chem. Educ.* **1996**, *73*, 671–673]. The trace metals are first separated from their complex, high-salt matrix by coprecipitating with Fe^{3+}. In a typical analysis a 5.00-mL portion of 2000 ppm Fe^{3+} is added to 1.00 L of seawater. The pH is adjusted to 9 using NH_4OH, and the precipitate of $Fe(OH)_3$ allowed to stand overnight. After isolating and rinsing the precipitate, the $Fe(OH)_3$ and coprecipitated metals are dissolved in 2 mL of concentrated HNO_3 and diluted to volume in a 50-mL volumetric flask. To analyze for Mn^{2+}, a 1.00-mL sample of this solution is diluted to 100 mL in a volumetric flask. The following samples are injected into the graphite furnace and analyzed.

sample	absorbance
2.5-µL sample + 2.5 µL of 0 ppb Mn^{2+}	0.223
2.5-µL sample + 2.5 µL of 2.5 ppb Mn^{2+}	0.294
2.5-µL sample + 2.5 µL of 5.0 ppb Mn^{2+}	0.361

Report the ppb Mn^{2+} in the sample of seawater.

37. The concentration of Na in plant materials are determined by flame atomic emission. The material to be analyzed is prepared by grinding, homogenizing, and drying at 103ºC. A sample of approximately 4 g is transferred to a quartz crucible and heated on a hot plate to char the organic material. The sample is heated in a muffle furnace at 550ºC for several hours. After cooling to room temperature the residue is dissolved by adding 2 mL of 1:1 HNO_3 and evaporated to dryness. The residue is redissolved in 10 mL of 1:9 HNO_3, filtered and diluted to 50 mL in a volumetric flask. The following data are obtained during a typical analysis for the concentration of Na in a 4.0264-g sample of oat bran.

sample	mg Na/L	emission (arbitrary units)
blank	0.00	0.0
standard 1	2.00	90.3
standard 2	4.00	181
standard 3	6.00	272
standard 4	8.00	363
standard 5	10.00	448
sample		238

Report the concentration of μg Na/g sample.

38. Yan and colleagues developed a method for the analysis of iron based its formation of a fluorescent metal–ligand complex with the ligand 5-(4-methylphenylazo)-8-aminoquinoline [Yan, G.; Shi, G.; Liu, Y. *Anal. Chim. Acta* **1992**, *264*, 121–124]. In the presence of the surfactant cetyltrimethyl ammonium bromide the analysis is carried out using an excitation wavelength of 316 nm with emission monitored at 528 nm. Standardization with external standards gives the following calibration curve.

$$I_f = -0.03 + \left(1.594\ \text{mg}^{-1}\ \text{L}\right) \times \frac{\text{mg Fe}^{3+}}{\text{L}}$$

A 0.5113-g sample of dry dog food is ashed to remove organic materials, and the residue dissolved in a small amount of HCl and diluted to volume in a 50-mL volumetric flask. Analysis of the resulting solution gives a fluorescent emission intensity of 5.72. Determine the mg Fe/L in the sample of dog food.

39. A solution of 5.00×10^{-5} M 1,3-dihydroxynaphthelene in 2 M NaOH has a fluorescence intensity of 4.85 at a wavelength of 459 nm. What is the concentration of 1,3-dihydroxynaphthelene in a solution that has a fluorescence intensity of 3.74 under identical conditions?

40. The following data is recorded for the phosphorescent intensity of several standard solutions of benzo[a]pyrene.

[benzo[a]pyrene] (M)	emission intensity
0	0.00
1.00×10^{-5}	0.98
3.00×10^{-5}	3.22
6.00×10^{-5}	6.25
1.00×10^{-4}	10.21

What is the concentration of benzo[a]pyrene in a sample that yields a phosphorescent emission intensity of 4.97?

41. The concentration of acetylsalicylic acid, $C_9H_8O_4$, in aspirin tablets is determined by hydrolyzing it to the salicylate ion, $C_7H_5O_2^-$, and determining its concentration spectrofluorometrically. A stock standard solution is prepared by weighing 0.0774 g of salicylic acid, $C_7H_6O_2$, into a 1-L volumetric flask and diluting to volume. A set of calibration standards is prepared by pipeting 0, 2.00, 4.00, 6.00, 8.00, and 10.00 mL of the stock solution into separate 100-mL volumetric flasks that contain 2.00 mL of 4 M NaOH and diluting to volume. Fluorescence is measured at an emission wavelength of 400 nm using an excitation wavelength of 310 nm with results shown in the following table.

mL of stock solution	emission intensity
0.00	0.00
2.00	3.02
4.00	5.98
6.00	9.18
8.00	12.13
10.00	14.96

Several aspirin tablets are ground to a fine powder in a mortar and pestle. A 0.1013-g portion of the powder is placed in a 1-L volumetric flask and diluted to volume with distilled water. A portion of this solution is filtered to remove insoluble binders and a 10.00-mL aliquot transferred to a 100-mL volumetric flask that contains 2.00 mL of 4 M NaOH. After diluting to volume the fluorescence of the resulting solution is 8.69. What is the %w/w acetylsalicylic acid in the aspirin tablets?

42. Selenium (IV) in natural waters is determined by complexing with ammonium pyrrolidine dithiocarbamate and extracting into $CHCl_3$. This step serves to concentrate the Se(IV) and to separate it from Se(VI). The Se(IV) is then extracted back into an aqueous matrix using HNO_3. After complexing with 2,3-diaminonaphthalene, the complex is extracted into cyclohexane. Fluorescence is measured at 520 nm following its excitation at 380 nm. Calibration is achieved by adding known amounts of Se(IV) to the water sample before beginning the analysis. Given the following results what is the concentration of Se(IV) in the sample.

[Se(IV)] added (nM)	emission intensity
0.00	323
2.00	597
4.00	862
6.00	1123

43. Fibrinogen is a protein that is produced by the liver and found in human plasma. Its concentration in plasma is clinically important. Many of the analytical methods used to determine the concentration of fibrinogen in plasma are based on light scattering following its precipitation. For example, da Silva and colleagues describe a method in which fibrino- gen precipitates in the presence of ammonium sulfate in a guanidine hydrochloride buffer [da Silva, M. P.; Fernandez-Romero, J. M.; Luque de Castro, M. D. *Anal. Chim. Acta* **1996**, *327*, 101–106]. Light scattering is measured nephelometrically at a wavelength of 340 nm. Analysis of a set of external calibration standards gives the following calibration equation

$$I_s = -4.66 + 9907.63C$$

where I_s is the intensity of scattered light and C is the concentration of fibrinogen in g/L. A 9.00-mL sample of plasma is collected from a patient and mixed with 1.00 mL of an anticoagulating agent. A 1.00-mL aliquot of this solution is diluted to 250 mL in a volumetric flask and is found to have a scattering intensity of 44.70. What is the concentration of fibrinogen, in gram per liter, in the plasma sample?

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11.10: ADDITIONAL RESOURCES

The following set of experiments introduce students to the applications of spectroscopy. Experiments are grouped into five categories: UV/Vis spectroscopy, IR spectroscopy, atomic absorption and atomic emission, fluorescence and phosphorescence, and signal averaging.

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11.11: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

The spectrophotometric methods of analysis covered in this chapter include those based on the absorption, emission, or scattering of electromagnetic radiation. When a molecule absorbs UV/Vis radiation it undergoes a change in its valence shell electron configuration. A change in vibrational energy results from the absorption of IR radiation. Experimentally we measure the fraction of radiation transmitted, *T*, by the sample. Instrumentation for measuring absorption requires a source of electromagnetic radiation, a means for selecting a wavelength, and a detector for measuring transmittance. Beer's law relates absorbance to both transmittance and to the concentration of the absorbing species ($A = -\log T = \varepsilon bC$).

In atomic absorption we measure the absorption of radiation by gas phase atoms. Samples are atomized using thermal energy from either a flame or a graphite furnace. Because the width of an atom's absorption band is so narrow, the continuum sources common for molecular absorption are not used. Instead, a hollow cathode lamp provides the necessary line source of radiation. Atomic absorption suffers from a number of spectral and chemical interferences. The absorption or scattering of radiation from the sample's matrix are important spectral interferences that are minimized by background correction. Chemical interferences include the formation of nonvolatile forms of the analyte and ionization of the analyte. The former interference is minimized by using a releasing agent or a protecting agent, and an ionization suppressor helps minimize the latter interference.

When a molecule absorbs radiation it moves from a lower energy state to a higher energy state. In returning to the lower energy state the molecule may emit radiation. This process is called photoluminescence. One form of photoluminescence is fluorescence in which the analyte emits a photon without undergoing a change in its spin state. In phosphorescence, emission occurs with a change in the analyte's spin state. For low concentrations of analyte, both fluorescent and phosphorescent emission intensities are a linear function of the analyte's concentration. Thermally excited atoms also emit radiation, forming the basis for atomic emission spectroscopy. Thermal excitation is achieved using either a flame or a plasma.

Spectroscopic measurements also include the scattering of light by a particulate form of the analyte. In turbidimetry, the decrease in the radiation's transmission through the sample is measured and related to the ana- lyte's concentration through an equation similar to Beer's law. In nephelometry we measure the intensity of scattered radiation, which varies linearly with the analyte's concentration.

KEY TERMS

absorbance
amplitude
background correction
chromophore
double-beam
electromagnetic spectrum
excitation spectrum
fiber-optic probe
fluorescence
frequency
interferometer
ionization suppressor
line source
mole-ratio method
nephelometry
phosphorescence
photoluminescence
polychromatic
relaxation
self-absorption
signal-to-noise ratio
slope-ratio method
spectrophotometer
transducer
turbidimetry
wavenumber
absorbance spectrum
attenuated total reflectance
Beer's law
continuum source
effective bandwidth
emission
external conversion
filter
fluorescent quantum yield
graphite furnace
internal conversion
Jacquinot's advantage
method of continuous variations
monochromatic
nominal wavelength
phosphorescent quantum yield
photon
protecting agent
releasing agent
signal averaging
single-beam
spectral searching
spectroscopy
transmittance
vibrational relaxation
absorptivity
atomization
chemiluminescence
dark current
electromagnetic radiation
emission spectrum
Fellgett's advantage
filter photometer
fluorimeter
interferogram
intersystem crossing
lifetime
molar absorptivity
monochromator
phase angle
photodiode array
plasma
radiationless deactivation
resolution
signal processor
singlet excited state
spectrofluorometer
stray radiation
triplet excited state
wavelength

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CHAPTER OVERVIEW

12: CHROMATOGRAPHIC AND ELECTROPHORETIC METHODS

Drawing from an arsenal of analytical techniques—many of which were the subject of the preceding four chapters—analytical chemists design methods that detect increasingly smaller concentrations of analyte in increasingly more complex matrices. Despite the power of these analytical techniques, they often suffer from a lack of selectivity. For this reason, many analytical procedures include a step to separate the analyte from potential interferents. Although effective, each additional step in an analytical procedure increases the analysis time and the cost of the analysis, and introduces uncertainty. In this chapter we consider two analytical techniques that avoid these limitations by combining the separation and analysis: chromatography and electrophoresis.

12.1: General Theory of Separation Effiiciency
12.2: Classifying Separation Techniques
12.3: Liquid-Liquid Extractions
12.4: Separation Versus Preconcentration
12.5: Overview of Analytical Separations
12.6: General Theory of Column Chromatography
12.7: Optimizing Chromatographic Separations
12.8: Gas Chromatography
12.9: High-Performance Liquid Chromatography
12.10: Other Forms of Chromatography
12.11: Electrophoresis
12.12: Problems
12.13: Additional Resources
12.14: Chapter Summary and Key Terms

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12.1: GENERAL THEORY OF SEPARATION EFFIICIENCY

The goal of an analytical separation is to remove either the analyte or the interferent from the sample's matrix. To achieve this separation we must identify at least one significant difference between the analyte's and the interferent's chemical or physical properties. A significant difference in properties, however, is not sufficient to effect a separation if the conditions that favor the extraction of interferent from the sample also removes a small amount of analyte.

Two factors limit a separation's efficiency: failing to recover all the analyte and failing to remove all the interferent. We define the analyte's ***recovery***, R_A, as

$$R_A = \frac{C_A}{(C_A)_o} \tag{12.1.1}$$

where C_A is the concentration of analyte that remains after the separation, and $(C_A)_o$ is the analyte's initial concentration. A recovery of 1.00 means that no analyte is lost during the separation. The interferent's recovery, R_I, is defined in the same manner

$$R_I = \frac{C_I}{(C_I)_o} \tag{12.1.2}$$

where C_I is the concentration of interferent that remains after the separation, and $(C_I)_o$ is the interferent's initial concentration. We define the extent of the separation using a ***separation factor***, $S_{I,A}$ [(a) Sandell, E. B. *Colorimetric Determination of Trace Metals*, Interscience Publishers: New York, 1950, pp. 19–20; (b) Sandell, E. B. *Anal. Chem.* **1968**, *40*, 834–835].

$$S_{I,A} = \frac{R_I}{R_A} \tag{12.1.3}$$

In general, an $S_{I,A}$ of approximately 10^{-7} is needed for the quantitative analysis of a trace analyte in the presence of a macro interferent, and 10^{-3} when the analyte and interferent are present in approximately equal amounts.

> The meaning of trace and macro, as well as other terms for describing the concentrations of analytes and interferents, is presented in Chapter 2.

✔ EXAMPLE 7.5.1

An analytical method for determining Cu in an industrial plating bath gives poor results in the presence of Zn. To evaluate a method for separating the analyte from the interferent, samples with known concentrations of Cu or Zn were prepared and analyzed. When a sample of 128.6 ppm Cu was taken through the separation, the concentration of Cu that remained was 127.2 ppm. Taking a 134.9 ppm solution of Zn through the separation left behind a concentration of 4.3 ppm Zn. Calculate the recoveries for Cu and Zn, and the separation factor.

Solution

Using Equation 12.1.1 and Equation 12.1.2, the recoveries for the analyte and interferent are

$$R_{\text{Cu}} = \frac{127.2 \text{ ppm}}{128.6 \text{ ppm}} = 0.9891 \text{ or } 98.91\%$$

$$R_{\text{zn}} = \frac{4.3 \text{ ppm}}{134.9 \text{ ppm}} = 0.032 \text{ or } 3.2\%$$

and the separation factor is

$$S_{\text{Zn,Cu}} = \frac{R_{\text{Zn}}}{R_{\text{Cu}}} = \frac{0.032}{0.9891} = 0.032$$

Recoveries and separation factors are useful tools for evaluating a separation's potential effectiveness; they do not, however, give a direct indication of the error that results from failing to remove all the interferent or from failing to completely recover the analyte. The relative error due to the separation, E, is

$$E = \frac{S_{samp} - S^*_{samp}}{S_{samp}} \tag{12.1.4}$$

where S^*_{samp} is the sample's signal for an ideal separation in which we completely recover the analyte.

$$S^*_{samp} = k_A(C_A)_o \tag{12.1.5}$$

Substituting equation 7.4.4 and Equation 12.1.5 into Equation 12.1.4, and rearranging

$$E = \frac{k_A\left(C_A + K_{A,I} \times C_I\right) - k_A(C_A)_o}{k_A(C_A)_o}$$

$$E = \frac{C_A + K_{A,I} \times C_I - (C_A)_\circ}{(C_A)_\circ}$$

$$E = \frac{C_A}{(C_A)_\circ} - \frac{(C_A)_o}{(C_A)_o} + \frac{K_{A,I} \times C_I}{(C_A)_o}$$

leaves us with

$$E = (R_A - 1) + \frac{K_{A,I} \times C_I}{(C_A)_o} \tag{12.1.6}$$

A more useful equation is obtained by solving Equation 12.1.2 for C_I and substituting into Equation 12.1.6.

$$E = (R_A - 1) + \frac{K_{A,I} \times (C_I)_o}{(C_A)_o} \times R_I \tag{12.1.7}$$

The first term of Equation 12.1.7 accounts for the analyte's incomplete recovery and the second term accounts for a failure to remove all the interferent.

EXAMPLE 7.5.2

Following the separation outlined in Example 7.5.1 , an analysis is carried out to determine the concentration of Cu in an industrial plating bath. Analysis of standard solutions that contain either Cu or Zn give the following linear calibrations.

$$S_{\text{Cu}} = 1250\ \text{ppm}^{-1} \times C_{\text{Cu}} \text{ and } S_{\text{Zn}} = 2310\ \text{ppm}^{-1} \times C_{\text{Zn}}$$

(a) What is the relative error if we analyze a sample without removing the Zn? Assume the initial concentration ratio, Cu:Zn, is 7:1. (b) What is the relative error if we first complete the separation with the recoveries determined in Example 7.5.1 ? (c) What is the maximum acceptable recovery for Zn if the recovery for Cu is 1.00 and if the error due to the separation must be no greater than 0.10%?

Solution

(a) If we complete the analysis without separating Cu and Zn, then R_{Cu} and R_{Zn} are exactly 1 and Equation 12.1.7 simplifies to

$$E = \frac{K_{\text{Cu,Zn}} \times (C_{\text{Zn}})_\circ}{(C_{\text{Cu}})_\circ}$$

Using equation 7.4.3, we find that the selectivity coefficient is

$$K_{\text{Cu,Zn}} = \frac{k_{\text{Zn}}}{k_{\text{Cu}}} = \frac{2310\ \text{ppm}^{-1}}{1250\ \text{ppm}^{-1}} = 1.85$$

Given the initial concentration ratio of 7:1 for Cu and Zn, the relative error without the separation is

$$E = \frac{1.85 \times 1}{7} = 0.264 \text{ or } 26.4\%$$

(b) To calculate the relative error we substitute the recoveries from Example 7.5.1 into Equation 12.1.7, obtaining

$$E = (0.9891 - 1) + \frac{1.85 \times 1}{7} \times 0.032 = -0.0109 + 0.085 = -0.0024$$

or –0.24%. Note that the negative determinate error from failing to recover all the analyte is offset partially by the positive determinate error from failing to remove all the interferent.

(c) To determine the maximum recovery for Zn, we make appropriate substitutions into Equation 12.1.7

$$E = 0.0010 = (1 - 1) + \frac{1.85 \times 1}{7} \times R_{\text{Zn}}$$

and solve for R_{Zn}, obtaining a recovery of 0.0038, or 0.38%. Thus, we must remove at least

$$100.00\% - 0.38\% = 99.62\%$$

of the Zn to obtain an error of 0.10% when R_{Cu} is exactly 1.

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12.2: CLASSIFYING SEPARATION TECHNIQUES

We can separate an analyte and an interferent if there is a significant difference in at least one of their chemical or physical properties. Table 7.6.1 provides a partial list of separation techniques, organized by the chemical or physical property affecting the separation.

Table 7.6.1 . Classification of Separation Techniques

basis of separation	separation technique(s)
size	filtration; dialysis; size-exclusion chromatography
mass or density	centrifugation
complex formation	masking
change in physical state	distillation; sublimation; recrystalization
change in chemical state	precipitation; electrodeposition; volatilization
partitioning between phases	extraction; chromatography

SEPARATIONS BASED ON SIZE

Size is the simplest physical property we can exploit in a separation. To accomplish the separation we use a porous medium through which only the analyte or the interferent can pass. Examples of size-based separations include filtration, dialysis, and size-exclusion.

In a ***filtration*** we separate a particulate interferent from soluble analytes using a filter with a pore size that will retain the interferent. The solution that passes through the filter is called the ***filtrate***, and the material retained by the filter is the ***retentate***. Gravity filtration and suction filtration using filter paper are techniques with which you should already be familiar. A membrane filter is the method of choice for particulates that are too small to be retained by filter paper. Figure 7.6.1 provides information about three types of membrane filters. For applications of gravity filtration and suction filtration in gravimetric methods of analysis, see Chapter 8.

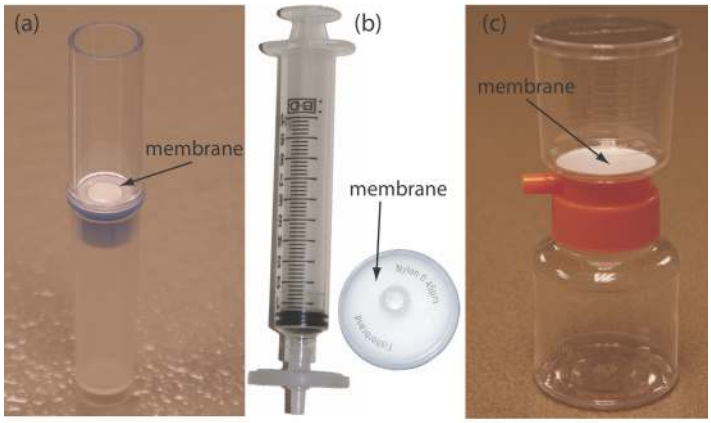


Figure 7.6.1 . Examples of three types of membrane filters for separating analytes and interferents. (a) A centrifugal filter for concentrating and desalting macromolecular solutions. The membrane has a nominal molecular weight cut-off of 1×10^6 g/mol. The sample is placed in the upper reservoir and the unit is placed in a centrifuge. Upon spinning the unit at $2000 \times g - 5000 \times g$ the filtrate collects in the bottom reservoir and the retentate remains in the upper reservoir. (b) A 0.45 μm membrane syringe filter. The photo on the right shows the membrane filter in its casing. In the photo on the left, the filter is attached to a syringe. Samples are placed in the syringe and pushed through the filter. The filtrate is collected in a test tube or other suitable container. (c) A disposable filter system with a 0.22 μm cellulose acetate membrane filter. The sample is added to the upper unit and vacuum suction is used to draw the filtrate through the membrane and into the lower unit. To store the filtrate, the top half of the unit is removed and a cap placed on the lower unit. The filter unit shown here has a capacity of 150 mL.

Dialysis is another example of a separation technique in which size is used to separate the analyte and the interferent. A dialysis membrane usually is made using cellulose and fashioned into tubing, bags, or cassettes. Figure 7.6.2 shows an example of a commercially available dialysis cassette. The sample is injected into the dialysis membrane, which is sealed tightly by a gasket, and the unit is placed in a container filled with a solution with a composition different from the sample. If there is a difference in a species' concentration on the membrane's two sides, the resulting concentration gradient provides a driving force for its diffusion across the membrane. While small species freely pass through the membrane, larger species are unable to pass. Dialysis frequently is used to purify proteins, hormones, and enzymes. During kidney dialysis, metabolic waste products, such as urea, uric acid, and creatinine, are removed from blood by passing it over a dialysis membrane.



Figure 7.6.2 . Example of a dialysis cassette. The dialysis membrane in this unit has a molecular weight cut-off of 10000 g/mol. Two sheets of the membrane are separated by a gasket and held in place by the plastic frame. Four ports, one of which is labeled, provide a means for injecting the sample between the dialysis membranes. The cassette is inverted and submerged in a beaker that contains the external solution. A foam buoy, used as a stand in the photo, serves as a float so that the unit remains suspended in the external solution. The external solution is stirred using a stir bar, and usually replaced several time during dialysis. When dialysis is complete, the solution in the cassette is removed through an injection port.

Size-exclusion chromatography is a third example of a separation technique that uses size as a means to effect a separation. In this technique a column is packed with small, approximately 10-μm, porous polymer beads of cross-linked dextrin or polyacrylamide. The pore size of the particles is controlled by the degree of cross-linking, with more cross-linking producing smaller pore sizes. The sample is placed into a stream of solvent that is pumped through the column at a fixed flow rate. Those species too large to enter the pores pass through the column at the same rate as the solvent. Species that enter into the pores take longer to pass through the column, with smaller species requiring more time to pass through the column. Size-exclusion chromatography is widely used in the analysis of polymers, and in biochemistry, where it is used for the separation of proteins. A more detailed treatment of size-exclusion chromatography, which also is called gel permeation chromatography, is in Chapter 12.

SEPARATIONS BASED ON MASS OR DENSITY

If the analyte and the interferent have different masses or densities, then a separation using ***centrifugation*** may be possible. The sample is placed in a centrifuge tube and spun at a high angular velocity, measured in revolutions per minute (rpm). The sample's constituents experience a centrifugal force that pulls them toward the bottom of the centrifuge tube. Those species that experience the greatest centrifugal force have the fastest sedimentation rate and are the first to reach the bottom of the centrifuge tube. If two species have the same density, their separation is based on a difference in mass, with the heavier species having the greater sedimentation rate. If the species are of equal mass, then the species with the larger density has the greatest sedimentation rate.

Centrifugation is an important separation technique in biochemistry. Table 7.6.2 , for example, lists conditions for separating selected cellular components. We can separate lysosomes from other cellular components by several differential centrifugations, in which we divide the sample into a solid residue and a supernatant solution. After destroying the cells, the solution is centrifuged for 20 minutes at $15000 \times g$ (a centrifugal force that is 15 000 times the earth's gravitational force), leaving a solid residue of cell membranes and mitochondria. The supernatant, which contains the lysosomes, is isolated by decanting it from the residue and then centrifuged for 30 minutes at $30000 \times g$, leaving a solid residue of lysosomes. Figure 7.6.3 shows a typical centrifuge capable of producing the centrifugal forces needed for biochemical separations.

Table 7.6.2 . Conditions for Separating Selected Cellular Components by Centrifugation

components	centrifugal force ($\times g$)	time (min)
eukaryotic cells	1000	5
cell membranes; nuclei	4000	10
mitochondria, bacterial cells	15000	20
lysosomes; bacterial membranes	30000	30
ribosomes	100000	180

Source: Adapted from Zubay, G. *Biochemistry*, 2nd ed. Macmillan: New York, 1988, p.120.



Figure 7.6.3 . Bench-top centrifuge capable of reaching speeds up to 14000 rpm and centrifugal forces of $20800 \times g$ This particular centrifuge is refrigerated, allowing samples to be cooled to temperatures as low as –4°C.

An alternative approach to differential centrifugation is a density gradient centrifugation. To prepare a sucrose density gradient, for example, a solution with a smaller concentration of sucrose—and, thus, of lower density—is gently layered upon a solution with a higher concentration of sucrose. Repeating this process several times, fills the centrifuge tube with a multi-layer density gradient. The sample is placed on top of the density gradient and centrifuged using a force greater than $150000 \times g$. During centrifugation, each of the sample's components moves through the gradient until it reaches a position where its density matches the surrounding sucrose solution. Each component is isolated as a separate band positioned where its density is equal to that of the local density within the gradient. Figure 7.6.4 provides an example of a typical sucrose density centrifugation for separating plant thylakoid membranes.

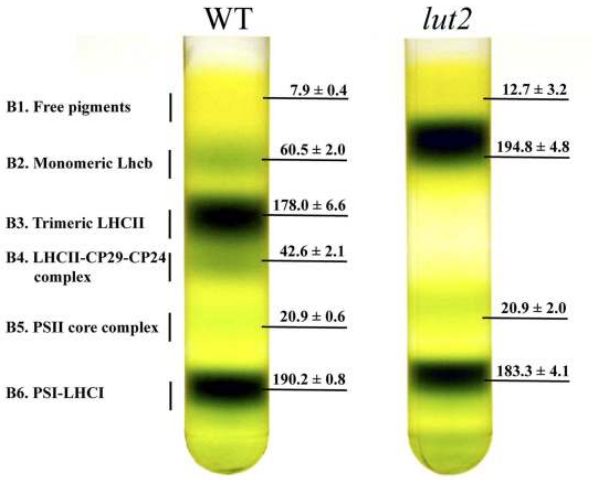


Figure 7.6.4 . Example of a sucrose density gradient centrifugation of thylakoid membranes from wild type (WT) and *lut2* plants. The thylakoid membranes were extracted from the plant's leaves and separated by centrifuging in a 0.1–1 M sucrose gradient for 22 h at $280000 \times g$and at 4°C. Six bands and their chlorophyll contents are shown. Adapted from Dall'Osto, L.; Lico, C.; Alric, J.; Giuliano, G.; Havaux, M.; Bassi, R. *BMC Plant Biology* **2006**, *6:32*.

SEPARATIONS BASED ON COMPLEXATION REACTIONS (MASKING)

One widely used technique for preventing an interference is to bind the interferent in a strong, soluble complex that prevents it from interfering in the analyte's determination. This process is known as ***masking***. As shown in Table 7.6.3 , a wide variety of ions and molecules are useful ***masking agents***, and, as a result, selectivity is usually not a problem.

> Technically, masking is not a separation technique because we do not physically separate the analyte and the interferent. We do, however, chemically isolate the interferent from the analyte, resulting in a pseudo-separation.

Table 7.6.3 . Selected Inorganic and Organic Masking Agents for Metal Ions

masking agent	elements whose ions are masked
CN^-	Ag, Au, Cd, Co, Cu, Fe, Hg, Mn, Ni, Pd, Pt, Zn
SCN^-	Ag, Cd, Co, Cu, Fe, Ni, Pd, Pt, Zn
NH_3	Ag, Co, Ni, Cu, Zn
F^-	Al, Co, Cr, Mg, Mn, Sn, Zn
$S_2O_3^{2-}$	Au, Ce, Co, Cu, Fe, Hg, Mn, Pb, Pd, Pt, Sb, Sn, Zn
tartrate	Al, Ba, Bi, Ca, Ce, Co, Cr, Cu, Fe, Hg, Mn, Pb, Pd, Pt, Sb, Sn, Zn
oxalate	Al, Fe, Mg, Mn
thioglycolic acid	Cu, Fe, Sn

Source: Meites, L. *Handbook of Analytical Chemistry*, McGraw-Hill: New York, 1963.

EXAMPLE 7.6.1

Using Table 7.6.3 , suggest a masking agent for the analysis of aluminum in the presence of iron.

Solution

A suitable masking agent must form a complex with the interferent, but not with the analyte. Oxalate, for example, is not a suitable masking agent because it binds both Al and Fe. Thioglycolic acid, on the other hand, is a selective masking agent for Fe in the presence of Al. Other acceptable masking agents are cyanide (CN^-) thiocyanate (SCN^-), and thiosulfate ($S_2O_3^{2-}$).

EXERCISE 7.6.1

Using Table 7.6, suggest a masking agent for the analysis of Fe in the presence of Al.

Answer

The fluoride ion, F^-, is a suitable masking agent as it binds with Al^{3+} to form the stable AlF_6^{3-} complex, leaving iron in solution.

As shown in Example 7.6.2 , we can judge a masking agent's effectiveness by considering the relevant equilibrium constants.

EXAMPLE 7.6.2

Show that CN^- is an appropriate masking agent for Ni^{2+} in a method where nickel's complexation with EDTA is an interference.

Solution

The relevant reactions and formation constants are

$$Ni^{2+}(aq) + Y^{4-}(aq) \rightleftharpoons NiY^{2-}(aq) \quad K_1 = 4.2 \times 10^{18}$$

$$Ni^{2+}(aq) + 4CN^-(aq) \rightleftharpoons Ni(CN)_4^{2-}(aq) \quad \beta_4 = 1.7 \times 10^{30}$$

where Y^{4-} is an abbreviation for EDTA. Cyanide is an appropriate masking agent because the formation constant for $Ni(CN)_4^{2-}$ is greater than that for the Ni–EDTA complex. In fact, the equilibrium constant for the reaction in which EDTA displaces the masking agent

$$Ni(CN)_4^{2-}(aq) + Y^{4-}(aq) \rightleftharpoons NiY^{2-}(aq) + 4CN^-(aq)$$

$$K = \frac{K_1}{\beta_4} = \frac{4.2 \times 10^{18}}{1.7 \times 10^{30}} = 2.5 \times 10^{-12}$$

is sufficiently small that $Ni(CN)_4^{2-}$ is relatively inert in the presence of EDTA.

EXERCISE 7.6.2

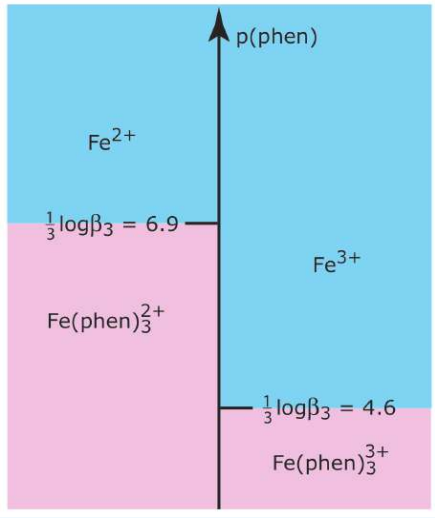
Use the formation constants in Appendix 12 to show that 1,10-phenanthroline is a suitable masking agent for Fe^{2+} in the presence of Fe^{3+}. Use a ladder diagram to define any limitations on using 1,10-phenanthroline as a masking agent. See Chapter 6 for a review of ladder diagrams.

Answer

The relevant reactions and equilibrium constants are

$$Fe^{2+}(aq) + 3\text{phen}(aq) \rightleftharpoons Fe(\text{phen})_3^{2+}(aq) \quad \beta_3 = 5 \times 10^{20}$$
$$Fe^{3+}(aq) + 3\text{phen}(aq) \rightleftharpoons Fe(\text{phen})_3^{3+}(aq) \quad \beta_3 = 6 \times 10^{13}$$

where phen is an abbreviation for 1,10-phenanthroline. Because β_3 is larger for the complex with Fe^{2+} than it is for the complex with Fe^{3+},1,10-phenanthroline will bind Fe^{2+} before it binds Fe^{3+}. A ladder diagram for this system (as shown below) suggests that an equilibrium p(phen) between 5.6 and 5.9 will fully complex Fe^{2+} without any significant formation of the $Fe(\text{phen})_3^{3+}$ complex. Adding a stoichiometrically equivalent amount of 1,10-phenanthroline to a solution of Fe^{2+} is sufficient to mask Fe^{2+} in the presence of Fe^{3+}. A large excess of 1,10-phenanthroline, however, decreases p(phen) and allows for the formation of both metal–ligand complexes.



SEPARATIONS BASED ON A CHANGE OF STATE

Because an analyte and its interferent are usually in the same phase, we can achieve a separation if one of them undergoes a change in its physical state or its chemical state.

CHANGES IN PHYSICAL STATE

When the analyte and the interferent are miscible liquids, separation by ***distillation*** is possible if their boiling points are significantly different. Figure 7.6.5 shows the progress of a distillation as a plot of temperature versus the composition of mixture's vapor-phase and liquid-phase. The initial liquid mixture (point A), contains more interferent than analyte. When this solution is brought to its boiling point, the vapor phase in equilibrium with the liquid phase is enriched in analyte (point B). The horizontal line that connects points A and B represents this vaporization equilibrium. Condensing the vapor phase at point B, by lowering the temperature, creates a new liquid phase with a composition identical to that in the vapor phase (point C). The vertical line that connects points B and C represents this condensation equilibrium. The liquid phase at point C has a lower boiling point than the original mixture, and is in equilibrium with the vapor phase at point D. This process of repeated vaporization and condensation gradually separates the analyte and the interferent.

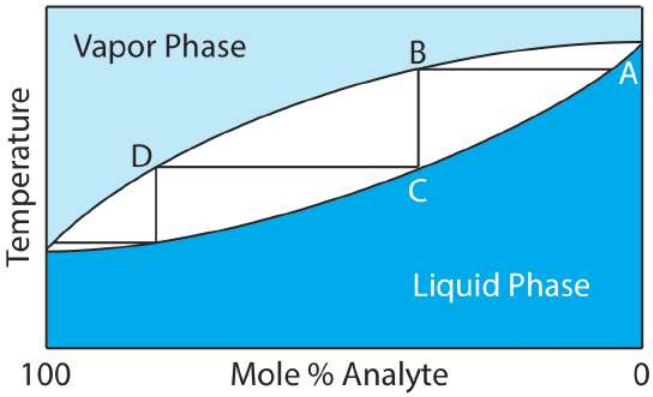


Figure 7.6.5 . Boiling point versus composition diagram for a near-ideal solution consisting of a low-boiling analyte and a high-boiling interferent. The horizontal lines represent vaporization equilibria and the vertical lines represent condensation equilibria. See the text for additional details.

Two experimental set-ups for distillations are shown in Figure 7.6.6 . The simple distillation apparatus shown in Figure 7.6.6 a is useful only for separating a volatile analyte (or interferent) from a non-volatile interferent (or analyte), or for separating an analyte and an interferent whose boiling points differ by more than 150ºC. A more efficient separation is achieved using the fractional distillation apparatus in Figure 7.6.6 b. Packing the fractionating column with a high surface area material, such as a steel sponge or glass beads, provides more opportunity for the repeated process of vaporization and condensation necessary to effect a complete separation.

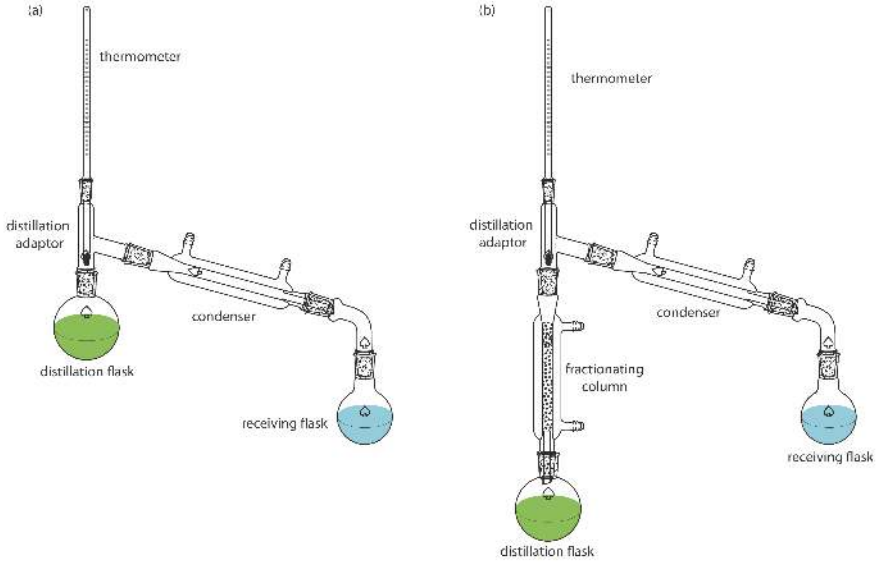


Figure 7.6.6 . Typical experimental set-up for (a) a simple distillation, and (b) a fractional distillation.

When the sample is a solid, ***sublimation*** may provide a useful separation of the analyte and the interferent. The sample is heated at a temperature and pressure below the analyte's triple point, allowing it to vaporize without passing through a liquid state. Condensing the vapor recovers the purified analyte (Figure 7.6.7). A useful analytical example of sublimation is the isolation of amino acids from fossil mollusk shells and deep-sea sediments [Glavin, D. P.; Bada, J. L. *Anal. Chem.* **1998**, *70*, 3119–3122].

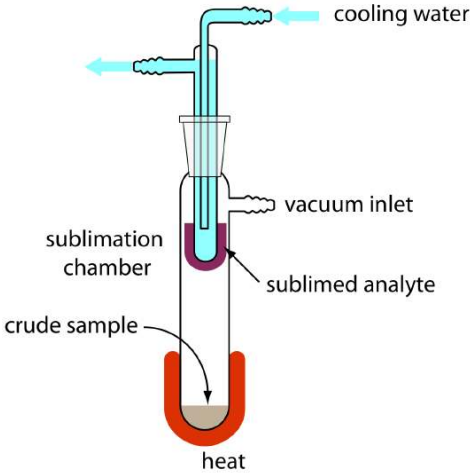


Figure 7.6.7 . Typical experimental set-up for a sublimation. The sample is placed in the sublimation chamber, which can be evacuated. Heating the sample causes the analyte to vaporize and sublime onto the cold finger, which is cooled using cold water.

Recrystallization is another method for purifying a solid. A solvent is chosen in which the analyte's solubility is significant when the solvent is hot and minimal when the solvent is cold. The interferents must be less soluble in the hot solvent than the analyte or present in much smaller amounts. After heating a portion of the solvent in an Erlenmeyer flask, small amounts of sample are added until undissolved sample is visible. Additional hot solvent is added until the sample redissolves, or until only insoluble impurities remain. This process of adding sample and solvent is repeated until the entire sample is added to the Erlenmeyer flask. Any insoluble impurities are removed by filtering the hot solution. The solution is allowed to cool slowly, which promotes the growth of large, pure crystals, and then cooled in an ice bath to minimize solubility losses. The purified sample is isolated by filtration and rinsed to remove any soluble impurities. Finally, the sample is dried to remove any remaining traces of the solvent. Further purification, if necessary, is accomplished by additional recrystallizations.

CHANGES IN CHEMICAL STATE

Distillation, sublimation, and recrystallization use a change in physical state to effect a separation. Chemical reactivity also is a useful tool for separating analytes and interferents. For example, we can separate SiO_2 from a sample by reacting it with HF to form SiF_4. Because SiF_4 is volatile, it is easy to remove by evaporation. If we wish to collect the reaction's volatile product, then a distillation is possible. For example, we can isolate the NH_4^+ in a sample by making the solution basic and converting it to NH_3. The ammonia is then removed by distillation. Table 7.6.4 provides additional examples of this approach for isolating inorganic ions.

Table 7.6.4 . Examples of Using a Chemical Reaction and a Distillation to Separate an Inorganic Analyte From Interferents

analyte	treatment	isolated species
CO_3^{2-}	$CO_3^{2-}(aq) + 2H_3O^+(aq) \rightarrow CO_2(g) + 3H_2O(l)$	CO_2
NH_4^+	$NH_4^+(aq) + OH^-(aq) \rightarrow NH_3(aq) + H_2O(l)$	NH_3
SO_3^-	$SO_3^{2-}(aq) + 2H_3O^+(aq) \rightarrow SO_2(g) + 3H_2O(l)$	SO_2
S^{2-}	$S^{2-}(aq) + 2H_3O^+(aq) \rightarrow H_2S(g) + 2H_2O(l)$	H_2S

Another reaction for separating analytes and interferents is precipitation. Two important examples of using a precipitation reaction in a separation are the pH-dependent solubility of metal oxides and hydroxides, and the pH-dependent solubility of metal sulfides.

Separations based on the pH-dependent solubility of oxides and hydroxides usually use a strong acid, a strong base, or an NH_3/NH_4Cl buffer to adjust the pH. Most metal oxides and hydroxides are soluble in hot concentrated HNO_3, although a few oxides, such as WO_3, SiO_2, and SnO_2 remain insoluble even under these harsh conditions. To determine the amount of Cu in brass, for example, we can avoid an interference from Sn by dissolving the sample with a strong acid and filtering to remove the solid residue of SnO_2.

Most metals form a hydroxide precipitate in the presence of concentrated NaOH. Those metals that form amphoteric hydroxides, however, do not precipitate because they react to form higher-order hydroxo-complexes. For example, Zn^{2+} and Al^{3+} do not precipitate in concentrated NaOH because they form the soluble complexes $Zn(OH)_3^-$ and $Al(OH)_4^-$. The solubility of Al^{3+} in concentrated NaOH allows us to isolate aluminum from impure samples of bauxite, an ore of Al_2O_3. After crushing the ore, we place it in a solution of concentrated NaOH, dissolving the Al_2O_3 and forming $Al(OH)_4^-$. Other oxides in the ore, such as Fe_2O_3 and SiO_2, remain insoluble. After filtering, we recover the aluminum as a precipitate of $Al(OH)_3$ by neutralizing some of the OH^- with acid.

The pH of an NH_3/NH_4Cl buffer (pK_a = 9.26) is sufficient to precipitate most metals as the hydroxide. The alkaline earths and alkaline metals, however, do not precipitate at this pH. In addition, metal ions that form soluble complexes with NH_3, such as Cu^{2+}, Zn^{2+}, Ni^{2+}, and Co^{2+} also do not precipitate under these conditions.

The use of S^{2-} as a precipitating reagent is one of the earliest examples of a separation technique. In Fresenius's 1881 text *A System of Instruction in Quantitative Chemical Analysis*, sulfide frequently is used to separate metal ions from the remainder of the sample's matrix [Fresenius. C. R. *A System of Instruction in Quantitative Chemical Analysis*, John Wiley and Sons: New York, 1881]. Sulfide is a useful reagent for separating metal ions for two reasons: (1) most metal ions, except for the alkaline earths and alkaline metals, form insoluble sulfides; and (2) these metal sulfides show a substantial variation in solubility. Because the concentration of S^{2-} is pH-dependent, we can control which metal ions precipitate by adjusting the pH. For example, in Fresenius's gravimetric procedure for the determination of Ni in ore samples (see Figure 1.1.1 for a schematic diagram of this procedure), sulfide is used three times to separate Co^{2+} and Ni^{2+} from Cu^{2+} and, to a lesser extent, from Pb^{2+}.

SEPARATIONS BASED ON A PARTITIONING BETWEEN PHASES

The most important group of separation techniques uses a selective partitioning of the analyte or interferent between two immiscible phases. If we bring a phase that contains the solute, *S*, into contact with a second phase, the solute will partition itself between the two phases, as shown by the following equilibrium reaction.

$$S_{\text{phase 1}} \rightleftharpoons S_{\text{phase 2}} \tag{12.2.1}$$

The equilibrium constant for reaction 12.2.1

$$K_D = \frac{[S_{\text{phase 2}}]}{[S_{\text{phase 1}}]}$$

is called the distribution constant or the ***partition coefficient***. If K_D is sufficiently large, then the solute moves from phase 1 to phase 2. The solute will remain in phase 1 if the partition coefficient is sufficiently small. When we bring a phase that contains two solutes into contact with a second phase, a separation of the solutes is possible if K_D is favorable for only one of the solutes. The physical states of the phases are identified when we describe the separation process, with the phase that contains the sample listed first. For example, if the sample is in a liquid phase and the second phase is a solid, then the separation involves liquid–solid partitioning.

EXTRACTION BETWEEN TWO PHASES

We call the process of moving a species from one phase to another phase an ***extraction***. Simple extractions are particularly useful for separations where only one component has a favorable partition coefficient. Several important separation techniques are based on a simple extraction, including liquid–liquid, liquid–solid, solid–liquid, and gas–solid extractions.

LIQUID-LIQUID EXTRACTIONS

A liquid–liquid extraction usually is accomplished using a separatory funnel (Figure 7.6.8). After placing the two liquids in the separatory funnel, we shake the funnel to increase the surface area between the phases. When the extraction is complete, we allow the liquids to separate. The stopcock at the bottom of the separatory funnel allows us to remove the two phases.

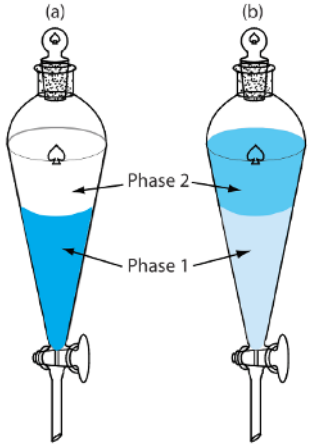


Figure 7.6.8 . Example of a liquid–liquid extraction using a separatory funnel. (a) Before the extraction, 100% of the analyte is in phase 1. (b) After the extraction, most of the analyte is in phase 2, although some analyte remains in phase 1. Although one liquid–liquid extraction can result in the complete transfer of analyte, a single extraction usually is not sufficient. See Chapter7.7 for a discussion of extraction efficiency and multiple extractions.

We also can carry out a liquid–liquid extraction without a separatory funnel by adding the extracting solvent to the sample's container. Pesticides in water, for example, are preserved in the field by extracting them into a small volume of hexane. A liquid–liquid microextraction, in which the extracting phase is a 1-µL drop suspended from a microsyringe (Figure 7.6.9), also has been described [Jeannot, M. A.; Cantwell, F. F. *Anal. Chem.* **1997**, *69*, 235–239]. Because of its importance, a more thorough discussion of liquid–liquid extractions is in Chapter7.7.

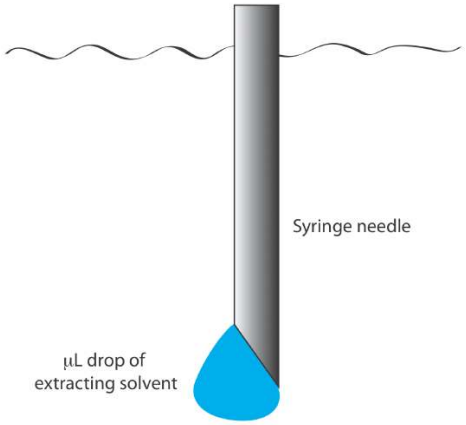


Figure 7.6.9 . Schematic of a liquid–liquid microextraction showing a syringe needle with a µL drop of the extracting solvent.

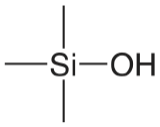
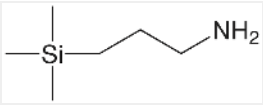
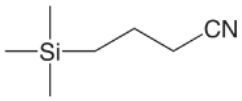
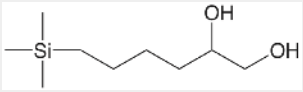
SOLID PHASE EXTRACTIONS

In a solid phase extraction of a liquid sample, we pass the sample through a cartridge that contains a solid adsorbent, several examples of which are shown in Figure 7.6.10 . The choice of adsorbent is determined by the species we wish to separate. Table 7.6.5 provides several representative examples of solid adsorbents and their applications.



Figure 7.6.10 . Selection of solid phase extraction cartridges for liquid samples. The solid adsorbent is the white or black material in each cartridge. From left-to-right, the absorbent materials are octadecylsilane, carbon, octadecylsilane, polyamide resin, and diol; see Table 7.6.5 for additional details. The size of the cartridges dictates the volume of sample used; from left-to-right, these cartridges use samples of 1 mL, 3 mL, 6 mL, 3 mL, and 1 mL.

Table 7.6.5 . Representative Adsorbents for the Solid Phase Extraction of Liquid Samples

absorbent	structure	properties and uses
silica		• retains low to moderate polarity species from organic matrices • fat soluble vitamins, steroids
aminopropyl		• retains polar compounds • carbohydrates, organic acids
cyanopropyl		• retains wide variety of species from aqueous and organic matrices • pesticides, hydrophobic peptides
diol		• retains wide variety of species from aqueous and organic matrices • proteins, peptides, fungicides
octadecyl (C–18)	—$C_{18}H_{37}$	• retains hydrophobic species from aqueous matrices • caffeine, sedatives, polyaromatic hydrocarbons, carbohydrates, pesticides
octyl (C–8)	—C_8H_{17}	• similar to C-18

As an example, let's examine a procedure for isolating the sedatives secobarbital and phenobarbital from serum samples using a C-18 solid adsorbent [Alltech Associates *Extract-Clean SPE Sample Preparation Guide*, Bulletin 83]. Before adding the sample, the solid phase cartridge is rinsed with 6 mL each of methanol and water. Next, a 500-µL sample of serum is pulled through the cartridge, with the sedatives and matrix interferents retained following a liquid–solid extraction (Figure 7.6.11 a). Washing the cartridge with distilled water removes any interferents (Figure 7.6.11 b). Finally, we elute the sedatives using 500 µL of acetone (Figure 7.6.11 c). In comparison to a liquid–liquid extraction, a solid phase extraction has the advantage of being easier, faster, and requires less solvent.

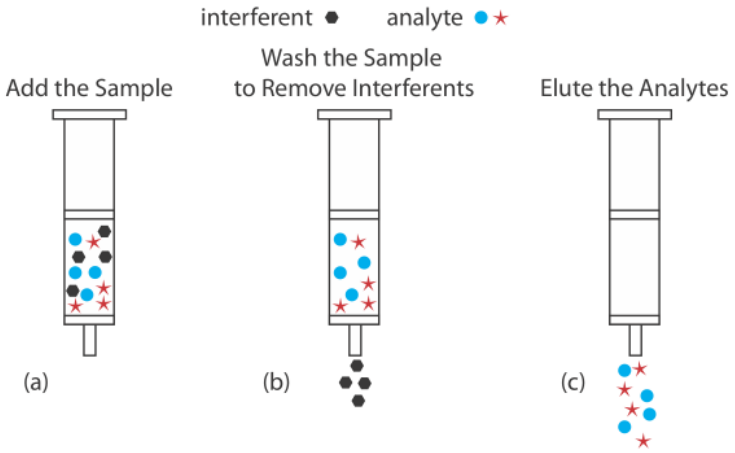


Figure 7.6.11 . Steps in a typical solid phase extraction. After preconditioning the solid phase cartridge with solvent, (a) the sample is added to the cartridge, (b) the sample is washed to remove interferents, and (c) the analytes are eluted.

CONTINUOUS EXTRACTIONS

An extraction is possible even if the analyte has an unfavorable partition coefficient, provided that the sample's other components have significantly smaller partition coefficients. Because the analyte's partition coefficient is unfavorable, a single extraction will not recover all the analyte. Instead we continuously pass the extracting phase through the sample until we achieve a quantitative extraction.

A continuous extraction of a solid sample is carried out using a ***Soxhlet extractor*** (Figure 7.6.12). The extracting solvent is placed in the lower reservoir and heated to its boiling point. Solvent in the vapor phase moves upward through the tube on the far right side of the apparatus, reaching the condenser where it condenses back to the liquid state. The solvent then passes through the sample, which is held in a porous cellulose filter thimble, collecting in the upper reservoir. When the solvent in the upper reservoir reaches the return tube's upper bend, the solvent and extracted analyte are siphoned back to the lower reservoir. Over time the analyte's concentration in the lower reservoir increases.

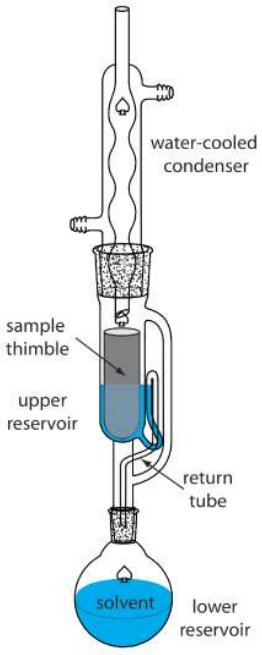


Figure 7.6.12 . Soxhlet extractor. See text for details.

Microwave-assisted extractions have replaced Soxhlet extractions in some applications [Renoe, B. W. *Am. Lab* August **1994**, 34–40]. The process is the same as that described earlier for a microwave digestion. After placing the sample and the solvent in a sealed digestion vessel, a microwave oven is used to heat the mixture. Using a sealed digestion vessel allows the extraction to take place at a higher temperature and pressure, reducing the amount of time needed for a quantitative extraction. In a Soxhlet extraction the temperature is limited by the solvent's boiling point at atmospheric pressure. When acetone is the solvent, for example, a Soxhlet extraction is limited to 56°C, but a microwave extraction can reach 150°C.

Two other continuous extractions deserve mention. Volatile organic compounds (VOCs) can be quantitatively removed from a liquid sample by a liquid–gas extraction. As shown in Figure 7.6.13 , an inert purging gas, such as He, is passed through the sample. The purge gas removes the VOCs, which are swept to a primary trap where they collect on a solid absorbent. When the extraction is complete, the VOCs are removed from the primary trap by rapidly heating the tube while flushing with He. This technique is known as a ***purge-and-trap***. Because the analyte's recovery may not be reproducible, an internal standard is required for quantitative work.

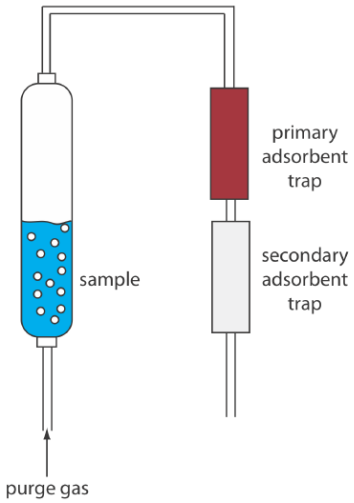


Figure 7.6.13 . Schematic diagram of a purge-and-trap system for extracting volatile analytes. The purge gas releases the analytes, which subsequently collect in the primary adsorbent trap. The secondary adsorption trap is monitored for evidence that the primary trap's capacity to absorb analyte is exceeded.

Continuous extractions also can be accomplished using supercritical fluids [McNally, M. E. *Anal. Chem.* **1995**, *67*, 308A–315A]. If we heat a substance above its critical temperature and pressure it forms a ***supercritical fluid*** whose properties are between those of a gas and a liquid. A supercritical fluid is a better solvent than a gas, which makes it a better reagent for extractions. In addition, a supercritical fluid's viscosity is significantly less than that of a liquid, which makes it easier to push it through a particulate sample. One example of a supercritical fluid extraction is the determination of total petroleum hydrocarbons (TPHs) in soils, sediments, and sludges using supercritical CO_2 ["TPH Extraction by SFE," ISCO, Inc. Lincoln, NE, Revised Nov. 1992]. An approximately 3-g sample is placed in a 10-mL stainless steel cartridge and supercritical CO_2 at a pressure of 340 atm and a temperature of 80°C is passed through the cartridge for 30 minutes at flow rate of 1–2 mL/min. To collect the TPHs, the effluent from the cartridge is passed through 3 mL of tetrachloroethylene at room temperature. At this temperature the CO_2 reverts to the gas phase and is released to the atmosphere.

CHROMATOGRAPHIC SEPARATIONS

In an extraction, the sample originally is in one phase and we extract the analyte or the interferent into a second phase. We also can separate the analyte and interferents by continuously passing one sample-free phase, called the mobile phase, over a second sample-free phase that remains fixed or stationary. The sample is injected into the mobile phase and the sample's components partition themselves between the mobile phase and the stationary phase. Those components with larger partition coefficients are more likely to move into the stationary phase and take longer time to pass through the system. This is the basis of all chromatographic separations. Chromatography provides both a separation of analytes and interferents, and a means for performing a qualitative or quantitative analysis for the analyte. For this reason a more thorough treatment of chromatography is found in Chapter 12.

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12.3: LIQUID-LIQUID EXTRACTIONS

A liquid–liquid extraction is an important separation technique for environmental, clinical, and industrial laboratories. A standard environmental analytical method illustrates the importance of liquid–liquid extractions. Municipal water departments routinely monitor public water supplies for trihalomethanes ($CHCl_3$, $CHBrCl_2$, $CHBr_2Cl$, and $CHBr_3$) because they are known or suspected carcinogens. Before their analysis by gas chromatography, trihalomethanes are separated from their aqueous matrix using a liquid–liquid extraction with pentane ["The Analysis of Trihalomethanes in Drinking Water by Liquid Extraction,"EPAMethod501.2 (EPA 500-Series, November 1979)].

> The Environmental Protection Agency (EPA) also publishes two additional methods for trihalomethanes. Method 501.1 and Method 501.3 use a purge-and-trap to collect the trihalomethanes prior to a gas chromatographic analysis with a halide-specific detector (Method 501.1) or a mass spectrometer as the detector (Method 501.3). You will find more details about gas chromatography, including detectors, in Chapter 12.

In a simple liquid–liquid extraction the solute partitions itself between two immiscible phases. One phase usually is an aqueous solvent and the other phase is an organic solvent, such as the pentane used to extract trihalomethanes from water. Because the phases are immiscible they form two layers, with the denser phase on the bottom. The solute initially is present in one of the two phases; after the extraction it is present in both phases. ***Extraction efficiency***—that is, the percentage of solute that moves from one phase to the other—is determined by the equilibrium constant for the solute's partitioning between the phases and any other side reactions that involve the solute. Examples of other reactions that affect extraction efficiency include acid–base reactions and complexation reactions.

PARTITION COEFFICIENTS AND DISTRIBUTION RATIOS

As we learned earlier in this chapter, a solute's partitioning between two phases is described by a partition coefficient, K_D. If we extract a solute from an aqueous phase into an organic phase

$$S_{aq} \rightleftharpoons S_{org}$$

then the partition coefficient is

$$K_D = \frac{[S_{org}]}{[S_{aq}]}$$

A large value for K_D indicates that extraction of solute into the organic phase is favorable.

To evaluate an extraction's efficiency we must consider the solute's total concentration in each phase, which we define as a ***distribution ratio***, D.

$$D = \frac{[S_{org}]_{\text{total}}}{[S_{aq}]_{\text{total}}}$$

The partition coefficient and the distribution ratio are identical if the solute has only one chemical form in each phase; however, if the solute exists in more than one chemical form in either phase, then K_D and D usually have different values. For example, if the solute exists in two forms in the aqueous phase, A and B, only one of which, A, partitions between the two phases, then

$$D = \frac{[S_{org}]_A}{[S_{aq}]_A + [S_{aq}]_B} \leq K_D = \frac{[S_{org}]_A}{[S_{aq}]_A}$$

This distinction between K_D and D is important. The partition coefficient is a thermodynamic equilibrium constant and has a fixed value for the solute's partitioning between the two phases. The distribution ratio's value, however, changes with solution conditions if the relative amounts of A and B change. If we know the solute's equilibrium reactions within each phase and between the two phases, we can derive an algebraic relationship between K_D and D.

LIQUID-LIQUID EXTRACTION WITH NO SECONDARY REACTIONS

In a simple liquid–liquid extraction, the only reaction that affects the extraction efficiency is the solute's partitioning between the two phases (Figure 7.7.1).

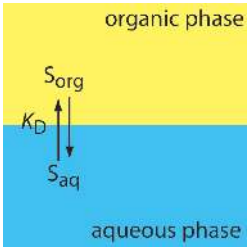


Figure 7.7.1 . Scheme for a simple liquid–liquid extraction in which the solute's partitioning depends only on the K_D equilibrium.

In this case the distribution ratio and the partition coefficient are equal.

$$D = \frac{[S_{org}]_{\text{total}}}{[S_{aq}]_{\text{total}}} = K_D = \frac{[S_{org}]}{[S_{aq}]} \tag{12.3.1}$$

Let's assume the solute initially is present in the aqueous phase and that we wish to extract it into the organic phase. A conservation of mass requires that the moles of solute initially present in the aqueous phase equal the combined moles of solute in the aqueous phase and the organic phase after the extraction.

$$(\text{mol } S_{aq})_0 = (\text{mol } S_{aq})_1 + (\text{mol } S_{org})_1 \tag{12.3.2}$$

where the subscripts indicate the extraction number with 0 representing the system before the extraction and 1 the system following the first extraction. After the extraction, the solute's concentration in the aqueous phase is

$$[S_{aq}]_1 = \frac{(\text{mol } S_{aq})_1}{V_{aq}} \tag{12.3.3}$$

and its concentration in the organic phase is

$$[S_{org}]_1 = \frac{(\text{mol } S_{org})_1}{V_{org}} \tag{12.3.4}$$

where V_{aq} and V_{org} are the volumes of the aqueous phase and the organic phase. Solving Equation 12.3.2 for (mol S_{org})$_1$ and substituting into Equation 12.3.4 leave us with

$$[S_{org}]_1 = \frac{(\text{mol } S_{aq})_0 - (\text{mol } S_{aq})_1}{V_{org}} \tag{12.3.5}$$

Substituting Equation 12.3.3 and Equation 12.3.5 into Equation 12.3.1 gives

$$D = \frac{\frac{(\text{mol } S_{aq})_0 - (\text{mol } S_{aq})_1}{V_{org}}}{\frac{(\text{mol } S_{aq})_1}{V_{aq}}} = \frac{(\text{mol } S_{aq})_0 \times V_{aq} - (\text{mol } S_{aq})_1 \times V_{aq}}{(\text{mol } S_{aq})_1 \times V_{org}}$$

Rearranging and solving for the fraction of solute that remains in the aqueous phase after one extraction, (q_{aq})$_1$, gives

$$(q_{aq})_1 = \frac{(\text{mol } S_{aq})_1}{(\text{mol } S_{aq})_0} = \frac{V_{aq}}{DV_{org} + V_{aq}} \tag{12.3.6}$$

The fraction present in the organic phase after one extraction, (q_{org})$_1$, is

$$(q_{org})_1 = \frac{(\text{mol } S_{org})_1}{(\text{mol } S_{aq})_0} = 1 - (q_{aq})_1 = \frac{DV_{org}}{DV_{org} + V_{aq}}$$

Example 7.7.1 shows how we can use Equation 12.3.6 to calculate the efficiency of a simple liquid-liquid extraction.

EXAMPLE 7.7.1

A solute has a K_D between water and chloroform of 5.00. Suppose we extract a 50.00-mL sample of a 0.050 M aqueous solution of the solute using 15.00 mL of chloroform. (a) What is the separation's extraction efficiency? (b) What volume of chloroform do we need if we wish to extract 99.9% of the solute?

Solution

For a simple liquid–liquid extraction the distribution ratio, D, and the partition coefficient, K_D, are identical.

(a) The fraction of solute that remains in the aqueous phase after the extraction is given by Equation 12.3.6.

$$(q_{aq})_1 = \frac{V_{aq}}{DV_{org} + V_{aq}} = \frac{50.00\ \text{mL}}{(5.00)(15.00\ \text{mL}) + 50.00\ \text{mL}} = 0.400$$

The fraction of solute in the organic phase is 1–0.400, or 0.600. Extraction efficiency is the percentage of solute that moves into the extracting phase; thus, the extraction efficiency is 60.0%.

(b) To extract 99.9% of the solute $(q_{aq})_1$ must be 0.001. Solving Equation 12.3.6 for V_{org}, and making appropriate substitutions for $(q_{aq})_1$ and V_{aq} gives

$$V_{org} = \frac{V_{aq} - (q_{aq})_1 V_{aq}}{(q_{aq})_1 D} = \frac{50.00\ \text{mL} - (0.001)(50.00\ \text{mL})}{(0.001)(5.00\ \text{mL})} = 999\ \text{mL}$$

This is large volume of chloroform. Clearly, a single extraction is not reasonable under these conditions.

In Example 7.7.1 , a single extraction provides an extraction efficiency of only 60%. If we carry out a second extraction, the fraction of solute remaining in the aqueous phase, $(q_{aq})_2$, is

$$(q_{aq})_2 = \frac{(\text{mol } S_{aq})_2}{(\text{mol } S_{aq})_1} = \frac{V_{aq}}{DV_{org} + V_{aq}}$$

If V_{aq} and V_{org} are the same for both extractions, then the cumulative fraction of solute that remains in the aqueous layer after two extractions, $(Q_{aq})_2$, is the product of $(q_{aq})_1$ and $(q_{aq})_2$, or

$$(Q_{aq})_2 = \frac{(\text{mol } S_{aq})_2}{(\text{mol } S_{aq})_0} = (q_{aq})_1 \times (q_{aq})_2 = \left(\frac{V_{aq}}{DV_{org} + V_{aq}}\right)^2$$

In general, for a series of n identical extractions, the fraction of analyte that remains in the aqueous phase after the last extraction is

$$(Q_{aq})_n = \left(\frac{V_{aq}}{DV_{org} + V_{aq}}\right)^n \tag{12.3.7}$$

EXAMPLE 7.7.2

For the extraction described in Example 7.7.1 , determine (a) the extraction efficiency for two identical extractions and for three identical extractions; and (b) the number of extractions required to ensure that we extract 99.9% of the solute.

Solution

(a) The fraction of solute remaining in the aqueous phase after two extractions and three extractions is

$$(Q_{aq})_2 = \left(\frac{50.00\ \text{mL}}{(5.00)(15.00\ \text{mL}) + 50.00\ \text{mL}}\right)^2 = 0.160$$

$$(Q_{aq})_3 = \left(\frac{50.0\ \text{mL}}{(5.00)(15.00\ \text{mL}) + 50.00\ \text{mL}}\right)^3 = 0.0640$$

The extraction efficiencies are 84.0% for two extractions and 93.6% for three extractions.

(b) To determine the minimum number of extractions for an efficiency of 99.9%, we set $(Q_{aq})_n$ to 0.001 and solve for n using Equation 12.3.7.

$$0.001 = \left(\frac{50.00\ \text{mL}}{(5.00)(15.00\ \text{mL}) + 50.00\ \text{mL}}\right)^n = (0.400)^n$$

Taking the log of both sides and solving for n

$$\log(0.001) = n\log(0.400)$$
$$n = 7.54$$

we find that a minimum of eight extractions is necessary.

The last two examples provide us with an important observation—for any extraction efficiency, we need less solvent if we complete several extractions using smaller portions of solvent instead of one extraction using a larger volume of solvent. For the conditions in Example 7.7.1 and Example 7.7.2 , an extraction efficiency of 99.9% requires one extraction with 9990 mL of chloroform, or 120 mL when using eight 15-mL portions of chloroform. Although extraction efficiency increases dramatically with the first few multiple, the effect diminishes quickly as we increase the number of extractions (Figure 7.7.2). In most cases there is little improvement in extraction efficiency after five or six

extractions. For the conditions in Example 7.7.2 , we reach an extraction efficiency of 99% after five extractions and need three additional extractions to obtain the extra 0.9% increase in extraction efficiency.

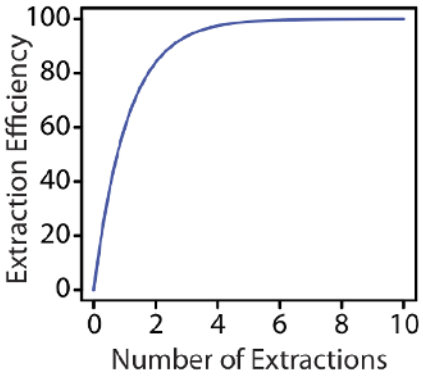


Figure 7.7.2 . Plot of extraction efficiency versus the number of extractions for the liquid–liquid extraction in Example 7.7.2 .

? EXERCISE 7.7.1

To plan a liquid–liquid extraction we need to know the solute's distribution ratio between the two phases. One approach is to carry out the extraction on a solution that contains a known amount of solute. After the extraction, we isolate the organic phase and allow it to evaporate, leaving behind the solute. In one such experiment, 1.235 g of a solute with a molar mass of 117.3 g/mol is dissolved in 10.00 mL of water. After extracting with 5.00 mL of toluene, 0.889 g of the solute is recovered in the organic phase. (a) What is the solute's distribution ratio between water and toluene? (b) If we extract 20.00 mL of an aqueous solution that contains the solute using 10.00 mL of toluene, what is the extraction efficiency? (c) How many extractions will we need to recover 99.9% of the solute?

Answer

(a) The solute's distribution ratio between water and toluene is

$$D = \frac{[S_{org}]}{[S_{aq}]} = \frac{0.889\text{ g} \times \frac{1\text{ mol}}{117.3\text{ g}} \times \frac{1}{0.00500\text{ L}}}{(1.235\text{ g} - 0.889\text{ g}) \times \frac{1\text{ mol}}{117.3\text{ g}} \times \frac{1}{0.01000\text{ L}}} = 5.14$$

(b) The fraction of solute remaining in the aqueous phase after one extraction is

$$(q_{aq})_1 = \frac{V_{aq}}{DV_{org} + V_{aq}} = \frac{20.00\text{ mL}}{(5.14)(10.00\text{ mL}) + 20.00\text{ mL}} = 0.280$$

The extraction efficiency, therefore, is 72.0%.

(c) To extract 99.9% of the solute requires

$$(Q_{aq})_n = 0.001 = \left(\frac{20.00\text{ mL}}{(5.14)(10.00\text{ mL}) + 20.00\text{ mL}}\right)^n = (0.280)^n$$

$$\log(0.001) = n\log(0.280)$$

$$n = 5.4$$

a minimum of six extractions.

LIQUID-LIQUID EXTRACTIONS INVOLVING ACID-BASE EQUILIBRIA

As we see in Equation 12.3.1, in a simple liquid–liquid extraction the distribution ratio and the partition coefficient are identical. As a result, the distribution ratio does not depend on the composition of the aqueous phase or the organic phase. A change in the pH of the aqueous phase, for example, will not affect the solute's extraction efficiency when K_D and D have the same value.

If the solute participates in one or more additional equilibrium reactions within a phase, then the distribution ratio and the partition coefficient may not be the same. For example, Figure 7.7.3 shows the equilibrium reactions that affect the extraction of the weak acid, HA, by an organic phase in which ionic species are not soluble.

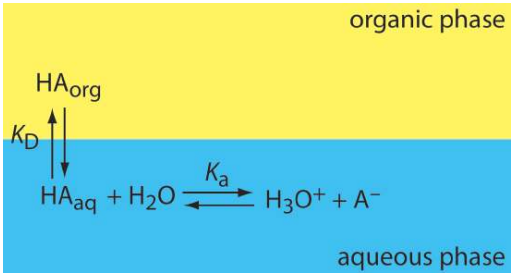


Figure 7.7.3 . Scheme for the liquid–liquid extraction of a weak acid, HA. Although the weak acid is soluble in both phases, its conjugate weak base, A^-, is soluble in the aqueous phase only. The K_a reaction for HA, which is called a ***secondary equilibrium reaction***, affects weak acid's extraction efficiency because it determines the relative abundance of HA in solution.

In this case the partition coefficient and the distribution ratio are

$$K_D = \frac{[HA_{org}]}{[HA_{aq}]} \tag{12.3.8}$$

$$D = \frac{[HA_{org}]_{\text{total}}}{[HA_{aq}]_{\text{total}}} = \frac{[HA_{org}]}{[HA_{aq}] + [A^-_{aq}]} \tag{12.3.9}$$

Because the position of an acid–base equilibrium depends on pH, the distribution ratio, D, is pH-dependent. To derive an equation for D that shows this dependence, we begin with the acid dissociation constant for HA.

$$K_a = \frac{[H_3O^+_{aq}]\,[A^-_{aq}]}{[HA_{aq}]} \tag{12.3.10}$$

Solving Equation 12.3.10 for the concentration of A^- in the aqueous phase

$$[A^-_{aq}] = \frac{K_a \times [HA_{aq}]}{[H_3O^+_{aq}]}$$

and substituting into Equation 12.3.9 gives

$$D = \frac{[HA_{org}]}{[HA_{aq}] + \frac{K_a \times [HA_{aq}]}{[H_3O^+_{aq}]}}$$

Factoring $[HA_{aq}]$ from the denominator, replacing $[HA_{org}]/[HA_{aq}]$ with K_D (Equation 12.3.8), and simplifying leaves us with the following relationship between the distribution ratio, D, and the pH of the aqueous solution.

$$D = \frac{K_D\,[H_3O^+_{aq}]}{[H_3O^+_{aq}] + K_a} \tag{12.3.11}$$

EXAMPLE 7.7.3

An acidic solute, HA, has a K_a of 1.00×10^{-5} and a K_D between water and hexane of 3.00. Calculate the extraction efficiency if we extract a 50.00 mL sample of a 0.025 M aqueous solution of HA, buffered to a pH of 3.00, with 50.00 mL of hexane. Repeat for pH levels of 5.00 and 7.00.

Solution

When the pH is 3.00, $[H_3O^+_{aq}]$ is 1.0×10^{-3} and the distribution ratio is

$$D = \frac{(3.00)\left(1.0 \times 10^{-3}\right)}{1.0 \times 10^{-3} + 1.00 \times 10^{-5}} = 2.97$$

The fraction of solute that remains in the aqueous phase is

$$(Q_{aq})_1 = \frac{50.00\ \text{mL}}{(2.97)(50.00\ \text{mL}) + 50.00\ \text{mL}} = 0.252$$

The extraction efficiency, therefore, is almost 75%. The same calculation at a pH of 5.00 gives the extraction efficiency as 60%. At a pH of 7.00 the extraction efficiency is just 3% .

The extraction efficiency in Example 7.7.3 is greater at more acidic pH levels because HA is the solute's predominate form in the aqueous phase. At a more basic pH, where A^- is the solute's predominate form, the extraction efficiency is smaller. A graph of extraction efficiency versus pH is shown in Figure 7.7.4 . Note that extraction efficiency essentially is independent of pH for pH levels more acidic than the HA's pK_a, and that it is essentially zero for pH levels more basic than HA's pK_a. The greatest change in extraction efficiency occurs at pH levels where both HA and A^- are predominate species. The ladder diagram for HA along the graph's *x*-axis helps illustrate this effect.

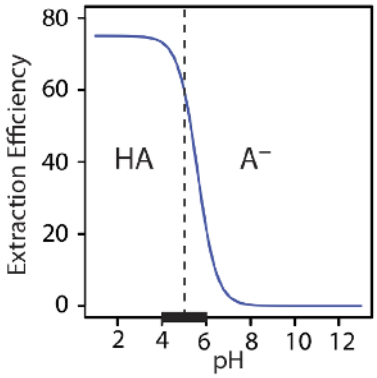


Figure 7.7.4 . Plot of extraction efficiency versus pH of the aqueous phase for the extraction in Example 7.7.3 . A ladder diagram for HA is superimposed along the *x*-axis, which divides the pH scale into regions where HA and A^- are the predominate aqueous phase species. The greatest change in extraction efficiency occurs as the pH moves through HA's buffer region.

EXERCISE 7.7.2

The liquid–liquid extraction of the weak base B is governed by the following equilibrium reactions:

$$\mathrm{B}(aq) \rightleftharpoons \mathrm{B}(org) \quad K_D = 5.00$$

$$\mathrm{B}(aq) + \mathrm{H_2O}(l) \rightleftharpoons \mathrm{OH^-}(aq) + \mathrm{HB^+}(aq) \quad K_b = 1.0 \times 10^{-4}$$

Derive an equation for the distribution ratio, *D*, and calculate the extraction efficiency if 25.0 mL of a 0.025 M solution of B, buffered to a pH of 9.00, is extracted with 50.0 mL of the organic solvent.

Answer

Because the weak base exists in two forms, only one of which extracts into the organic phase, the partition coefficient, K_D, and the distribution ratio, *D*, are not identical.

$$K_\mathrm{D} = \frac{[\mathrm{B}_{org}]}{[\mathrm{B}_{aq}]}$$

$$D = \frac{[\mathrm{B}_{org}]}{[\mathrm{B}_{aq}]} = \frac{[\mathrm{B}_{org}]}{[\mathrm{B}_{aq}] + [\mathrm{HB}^+_{aq}]}$$

Using the K_b expression for the weak base

$$K_\mathrm{b} = \frac{\left[\mathrm{OH}^-_{aq}\right]\left[\mathrm{HB}^+_{aq}\right]}{[\mathrm{B}_{aq}]}$$

we solve for the concentration of HB^+ and substitute back into the equation for *D*, obtaining

$$D = \frac{[\mathrm{B}_{org}]}{[\mathrm{B}_{aq}] + \frac{K_b \times [\mathrm{B}_{aq}]}{[\mathrm{OH}^-_{aq}]}} = \frac{[\mathrm{B}_{org}]}{[\mathrm{B}_{aq}]\left(1 + \frac{K_b}{[\mathrm{OH}^+_{aq}]}\right)} = \frac{K_D\left[\mathrm{OH}^-_{aq}\right]}{\left[\mathrm{OH}^-_{aq}\right] + K_\mathrm{b}}$$

At a pH of 9.0, the $[OH^-]$ is 1×10^{-5} M and the distribution ratio has a value of

$$D = \frac{K_D\left[\mathrm{OH}^-_{aq}\right]}{\left[\mathrm{OH}^-_{aq}\right] + K_\mathrm{b}} = \frac{(5.00)\left(1.0 \times 10^{-5}\right)}{1.0 \times 10^{-5} + 1.0 \times 10^{-4}} = 0.455$$

After one extraction, the fraction of B remaining in the aqueous phase is

$$(q_{aq})_1 = \frac{25.00\ \mathrm{mL}}{(0.455)(50.00\ \mathrm{mL}) + 25.00\ \mathrm{mL}} = 0.524$$

The extraction efficiency, therefore, is 47.6%. At a pH of 9, most of the weak base is present as HB^+, which explains why the overall extraction efficiency is so poor.

LIQUID-LIQUID EXTRACTION OF A METAL-LIGAND COMPLEX

One important application of a liquid–liquid extraction is the selective extraction of metal ions using an organic ligand. Unfortunately, many organic ligands are not very soluble in water or undergo hydrolysis or oxidation reactions in aqueous solutions. For these reasons the ligand is added to the organic solvent instead of the aqueous phase. Figure 7.7.5 shows the relevant equilibrium reactions (and equilibrium constants) for the extraction of M^{n+} by the ligand HL, including the ligand's extraction into the aqueous phase ($K_{D,HL}$), the ligand's acid dissociation reaction (K_a), the formation of the metal–ligand complex (β_n), and the complex's extraction into the organic phase ($K_{D,c}$).

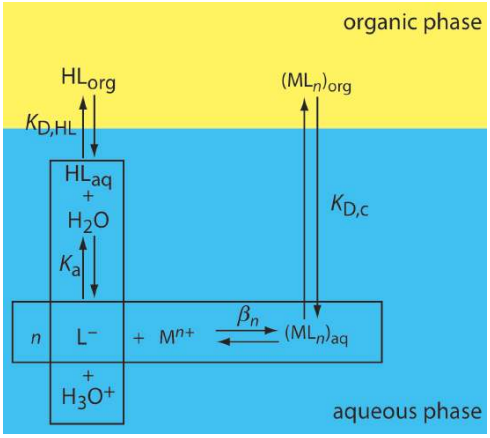


Figure 7.7.5 . Scheme for the liquid–liquid extraction of a metal ion, M^{n+}, by the ligand L^-. The ligand initially is present in the organic phase as HL. Four equilibrium reactions are needed to explain the extraction efficiency.

If the ligand's concentration is much greater than the metal ion's concentration, then the distribution ratio is

$$D = \frac{\beta_n K_{D,c} (K_a)^n (C_{HL})^n}{(K_{D,HL})^n \left[H_3O^+\right]^n + \beta_n (K_a)^n (C_{HL})^n} \tag{12.3.12}$$

where C_{HL} is the ligand's initial concentration in the organic phase. As shown in Example 7.7.4 , the extraction efficiency for metal ions shows a marked pH dependency.

EXAMPLE 7.7.4

A liquid–liquid extraction of the divalent metal ion, M^{2+}, uses the scheme outlined in Figure 7.7.5 . The partition coefficients for the ligand, $K_{D,HL}$, and for the metal–ligand complex, $K_{D,c}$, are 1.0×10^4 and 7.0×10^4, respectively. The ligand's acid dissociation constant, K_a, is 5.0×10^{-5}, and the formation constant for the metal–ligand complex, β_2, is 2.5×10^{16}. What is the extraction efficiency if we extract 100.0 mL of a 1.0×10^{-6} M aqueous solution of M^{2+}, buffered to a pH of 1.00, with 10.00 mL of an organic solvent that is 0.1 mM in the chelating agent? Repeat the calculation at a pH of 3.00.

Solution

When the pH is 1.00 the distribution ratio is

$$D = \frac{\left(2.5 \times 10^{16}\right)\left(7.0 \times 10^4\right)\left(5.0 \times 10^{-5}\right)^2\left(1.0 \times 10^{-4}\right)^2}{\left(1.0 \times 10^4\right)^2(0.10)^2 + \left(2.5 \times 10^{16}\right)\left(5.0 \times 10^{-5}\right)^2\left(1.0 \times 10^{-4}\right)^2}$$

or a D of 0.0438. The fraction of metal ion that remains in the aqueous phase is

$$(Q_{aq})_1 = \frac{100.0 \text{ mL}}{(0.0438)(10.00 \text{ mL}) + 100.0 \text{ mL}} = 0.996$$

At a pH of 1.00, we extract only 0.40% of the metal into the organic phase. Changing the pH to 3.00, however, increases the extraction efficiency to 97.8%. Figure 7.7.6 shows how the pH of the aqueous phase affects the extraction efficiency for M^{2+}.

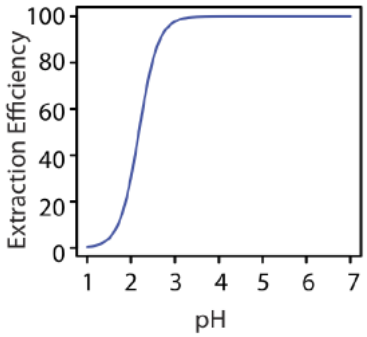


Figure 7.7.6 . Plot of extraction efficiency versus pH for the extraction of the metal ion, M^{2+}, in Example 7.7.4 .

One advantage of using a ligand to extract a metal ion is the high degree of selectivity that it brings to a liquid–liquid extraction. As seen in Figure 7.7.6 , a divalent metal ion's extraction efficiency increases from approximately 0% to 100% over a range of 2 pH units. Because a ligand's ability to form a metal–ligand complex varies substantially from metal ion to metal ion, significant selectivity is possible if we carefully control the pH. Table 7.7.1 shows the minimum pH for extracting 99% of a metal ion from an aqueous solution using an equal volume of 4 mM dithizone in CCl_4.

Table 7.7.1 . Minimum pH for Extracting 99% of an Aqueous Metal Ion Using 4.0 mM Dithizone in CCl_4 $V_{aq} = V_{org}$

metal ion	minimum pH
Hg^{2+}	–8.7
Ag^{+}	–1.7
Cu^{2+}	–0.8
Bi^{3+}	0.9
Zn^{2+}	2.3
Cd^{2+}	3.6
Co^{2+}	3.6
Pb^{2+}	4.1
Ni^{2+}	6.0
Tl^{+}	8.7

EXAMPLE 7.7.5

Using Table 7.7.1 , explain how we can separate the metal ions in an aqueous mixture of Cu^{2+}, Cd^{2+}, and Ni^{2+} by extracting with an equal volume of dithizone in CCl_4.

Solution

From Table 7.7.1 , a quantitative separation of Cu^{2+} from Cd^{2+} and from Ni^{2+} is possible if we acidify the aqueous phase to a pH of less than 1. This pH is greater than the minimum pH for extracting Cu^{2+} and significantly less than the minimum pH for extracting either Cd^{2+} or Ni^{2+}. After the extraction of Cu^{2+} is complete, we shift the pH of the aqueous phase to 4.0, which allows us to extract Cd^{2+} while leaving Ni^{2+} in the aqueous phase.

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12.4: SEPARATION VERSUS PRECONCENTRATION

Two common analytical problems are matrix components that interfere with an analyte's analysis and an analyte with a concentration that is too small to analyze accurately. As we have learned in this chapter, we can use a separation to solve the first problem. Interestingly, we often can use a separation to solve the second problem as well. For a separation in which we recover the analyte in a new phase, it may be possible to increase the analyte's concentration if we can extract the analyte from a larger volume into a smaller volume. This step in an analytical procedure is known as a ***preconcentration***.

An example from the analysis of water samples illustrates how we can simultaneously accomplish a separation and a preconcentration. In the gas chromatographic analysis for organophosphorous pesticides in environmental waters, the analytes in a 1000-mL sample are separated from their aqueous matrix by a solid-phase extraction that uses 15 mL of ethyl acetate [Aguilar, C.; Borrul, F.; Marcé, R. M. *LC•GC* **1996**, *14*, 1048–1054]. After the extraction, the analytes in the ethyl acetate have a concentration that is 67 times greater than that in the original sample (assuming the extraction is 100% efficient).

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12.5: OVERVIEW OF ANALYTICAL SEPARATIONS

In Chapter 7 we examined several methods for separating an analyte from potential interferents. For example, in a liquid–liquid extraction the analyte and interferent initially are present in a single liquid phase. We add a second, immiscible liquid phase and thoroughly mix them by shaking. During this process the analyte and interferents partition between the two phases to different extents, effecting their separation. After allowing the phases to separate, we draw off the phase enriched in analyte. Despite the power of liquid–liquid extractions, there are significant limitations.

TWO LIMITATIONS OF LIQUID-LIQUID EXTRACTIONS

Suppose we have a sample that contains an analyte in a matrix that is incompatible with our analytical method. To determine the analyte's concentration we first separate it from the matrix using a simple liquid–liquid extraction. If we have several analytes, we may need to complete a separate extraction for each analyte. For a complex mixture of analytes this quickly becomes a tedious process. This is one limitation to a liquid–liquid extraction.

A more significant limitation is that the extent of a separation depends on the distribution ratio of each species in the sample. If the analyte's distribution ratio is similar to that of another species, then their separation becomes impossible. For example, let's assume that an analyte, *A*, and an interferent, *I*, have distribution ratios of, respectively, 5 and 0.5. If we use a liquid–liquid extraction with equal volumes of sample and extractant, then it is easy to show that a single extraction removes approximately 83% of the analyte and 33% of the interferent. Although we can remove 99% of the analyte with three extractions, we also remove 70% of the interferent. In fact, there is no practical combination of number of extractions or volumes of sample and extractant that produce an acceptable separation.

From Chapter 7 we know that the distribution ratio, *D*, for a solute, *S*, is

$$D = \frac{[S]_{\text{ext}}}{[S]_{\text{samp}}}$$

where $[S]_{\text{ext}}$ is its equilibrium concentration in the extracting phase and $[S]_{\text{samp}}$ is its equilibrium concentration in the sample. We can use the distribution ratio to calculate the fraction of *S* that remains in the sample, q_{samp}, after an extraction

$$q_{\text{samp}} = \frac{V_{\text{samp}}}{DV_{\text{ext}} + V_{\text{samp}}}$$

where V_{samp} is the volume of sample and V_{ext} is the volume of the extracting phase. For example, if $D = 10$, $V_{\text{samp}} = 20$, and $V_{\text{ext}} = 5$, the fraction of *S* remaining in the sample after the extraction is

$$q_{\text{sanp}} = \frac{20}{10 \times 5 + 20} = 0.29$$

or 29%. The remaining 71% of the analyte is in the extracting phase.

A BETTER WAY TO SEPARATE MIXTURES

The problem with a liquid–liquid extraction is that the separation occurs in one direction only: from the sample to the extracting phase. Let's take a closer look at the liquid–liquid extraction of an analyte and an interferent with distribution ratios of, respectively, 5 and 0.5. Figure 12.1.1 shows that a single extraction using equal volumes of sample and extractant transfers 83% of the analyte and 33% of the interferent to the extracting phase. If the original concentrations of *A* and *I* are identical, then their concentration ratio in the extracting phase after one extraction is

$$\frac{[A]}{[I]} = \frac{0.83}{0.33} = 2.5$$

A single extraction, therefore, enriches the analyte by a factor of $2.5\times$. After completing a second extraction (Figure 12.1.1) and combining the two extracting phases, the separation of the analyte and the interferent, surprisingly, is less efficient.

$$\frac{[A]}{[I]} = \frac{0.97}{0.55} = 1.8$$

Figure 12.1.1 makes it clear why the second extraction results in a poorer overall separation: the second extraction actually favors the interferent!

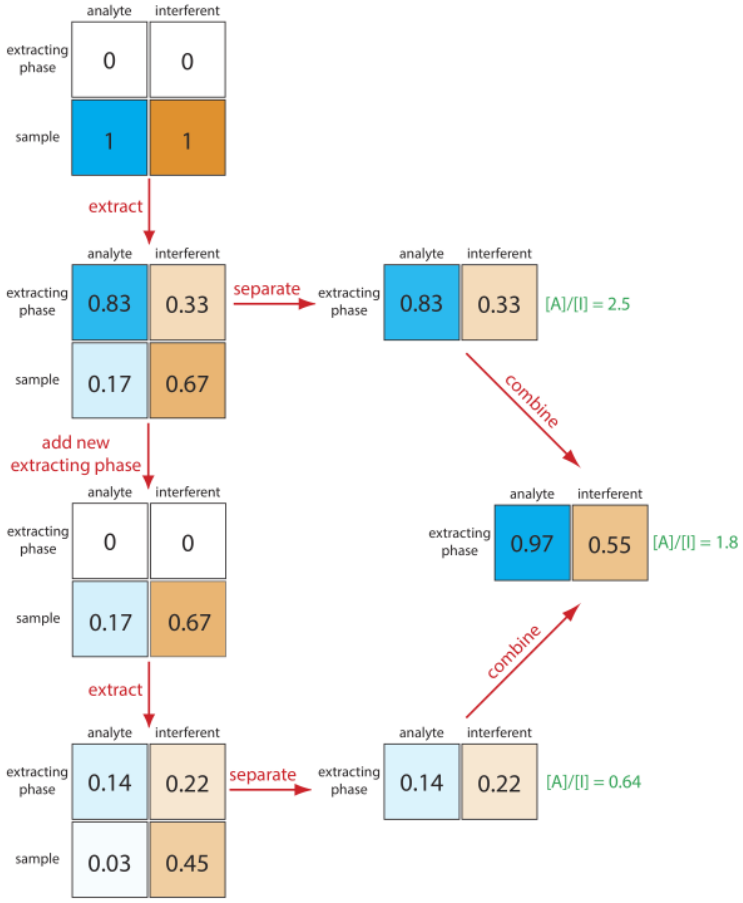


Figure 12.1.1 . Progress of a traditional liquid–liquid extraction using two identical extractions of a single sample using fresh portions of the extractant. The numbers give the fraction of analyte and interferent in each phase assuming equal volumes of sample and extractant and distribution ratios of 5 and 0.5 for the analyte and the interferent, respectively. The opacity of the colors equals the fraction of analyte and interferent present.

We can improve the separation by first extracting the solutes from the sample into the extracting phase and then extracting them back into a fresh portion of solvent that matches the sample's matrix (Figure 12.1.2). Because the analyte has the larger distribution ratio, more of it moves into the extractant during the first extraction and less of it moves back to the sample phase during the second extraction. In this case the concentration ratio in the extracting phase after two extractions is significantly greater.

$$\frac{[A]}{[I]} = \frac{0.69}{0.11} = 6.3$$

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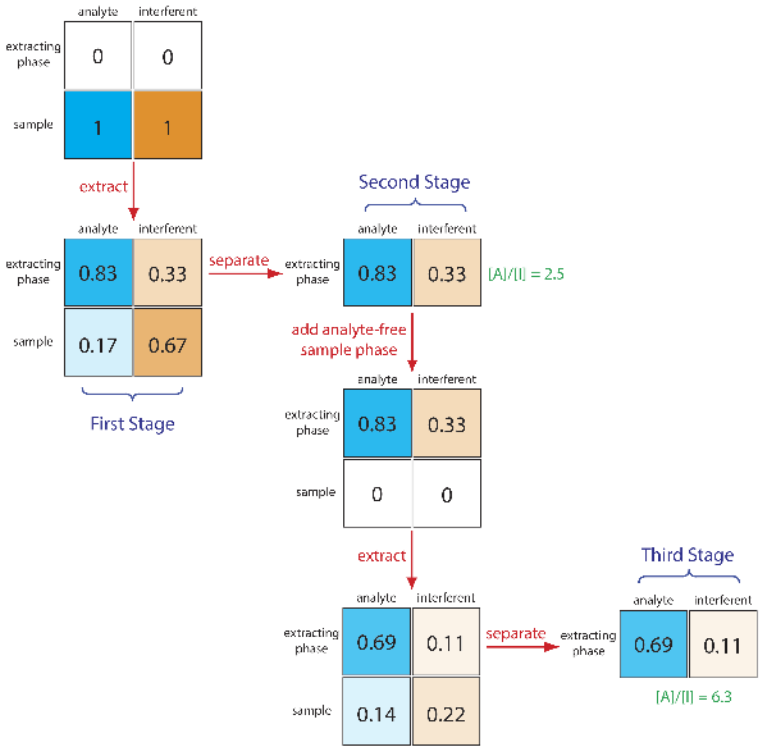


Figure 12.1.2 . Progress of a liquid–liquid extraction in which we first extract the solutes into the extracting phase and then extract them back into an analyte-free portion of the sample's phase. The numbers give the fraction of analyte and interferent in each phase assuming equal volumes of sample and extractant and distribution ratios of 5 and 0.5 for the analyte and the interferent, respectively. The opacity of the colors equals the fraction of analyte and interferent present.

Not shown in Figure 12.2 is that we can add a fresh portion of the extracting phase to the sample that remains after the first extraction (the bottom row of the first stage in Figure 12.2, beginning the process anew. As we increase the number of extractions, the analyte and the interferent each spread out in space over a series of stages. Because the interferent's distribution ratio is smaller than the analyte's, the interferent lags behind the analyte. With a sufficient number of extractions—that is, a sufficient number of stages—a complete separation of the analyte and interferent is possible. This process of extracting the solutes back and forth between fresh portions of the two phases, which we call a ***countercurrent extraction***, was developed by Craig in the 1940s [Craig, L. C. *J. Biol. Chem.* **1944**, *155*, 519–534]. The same phenomenon forms the basis of modern chromatography.

> See Appendix 16 for a more detailed consideration of the mathematics behind a countercurrent extraction.

CHROMATOGRAPHIC SEPARATIONS

In ***chromatography*** we pass a sample-free phase, which we call the ***mobile phase***, over a second sample-free ***stationary phase*** that remains fixed in space (Figure 12.1.3). We inject or place the sample into the mobile phase. As the sample moves with the mobile phase, its components partition between the mobile phase and the stationary phase. A component whose distribution ratio favors the stationary phase requires more time to pass through the system. Given sufficient time and sufficient stationary and mobile phase, we can separate solutes even if they have similar distribution ratios.

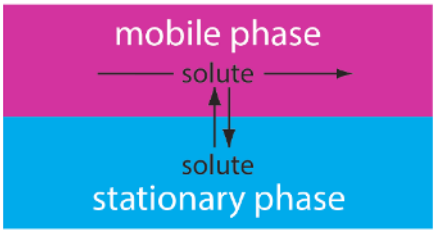


Figure 12.1.3 . In chromatography we pass a mobile phase over a stationary phase. When we inject a sample into the mobile phase, the sample's components both move with the mobile phase and partition into the stationary phase. The solute that spends the most time in the stationary phase takes the longest time to move through the system.

There are many ways in which we can identify a chromatographic separation: by describing the physical state of the mobile phase and the stationary phase; by describing how we bring the stationary phase and the mobile phase into contact with each other; or by describing the chemical or physical interactions between the solute and the stationary phase. Let's briefly consider how we might use each of these classifications.

> We can trace the history of chromatography to the turn of the century when the Russian botanist Mikhail Tswett used a column packed with calcium carbonate and a mobile phase of petroleum ether to separate colored pigments from plant extracts. As the sample moved through the column, the plant's pigments separated into individual colored bands. After effecting the separation, the calcium carbonate was removed from the column, sectioned, and the pigments recovered. Tswett named the technique chromatography, combining the Greek words for "color" and "to write." There was little interest in Tswett's technique until Martin and Synge's pioneering development of a theory of chromatography (see Martin, A. J. P.; Synge, R. L. M. "A New Form of Chromatogram Employing Two Liquid Phases," *Biochem. J.* **1941**, *35*, 1358–1366). Martin and Synge were awarded the 1952 Nobel Prize in Chemistry for this work.

TYPES OF MOBILE PHASES AND STATIONARY PHASES

The mobile phase is a liquid or a gas, and the stationary phase is a solid or a liquid film coated on a solid substrate. We often name chromatographic techniques by listing the type of mobile phase followed by the type of stationary phase. In gas–liquid chromatography, for example, the mobile phase is a gas and the stationary phase is a liquid film coated on a solid substrate. If a technique's name includes only one phase, as in gas chromatography, it is the mobile phase.

CONTACT BETWEEN THE MOBILE PHASE AND THE STATIONARY PHASE

There are two common methods for bringing the mobile phase and the stationary phase into contact. In ***column chromatography*** we pack the stationary phase into a narrow column and pass the mobile phase through the column using gravity or by applying pressure. The stationary phase is a solid particle or a thin liquid film coated on either a solid particulate packing material or on the column's walls.

In ***planar chromatography*** the stationary phase is coated on a flat surface—typically, a glass, metal, or plastic plate. One end of the plate is placed in a reservoir that contains the mobile phase, which moves through the stationary phase by capillary action. In paper chromatography, for example, paper is the stationary phase.

INTERACTION BETWEEN THE SOLUTE AND THE STATIONARY PHASE

The interaction between the solute and the stationary phase provides a third method for describing a separation (Figure 12.1.4). In ***adsorption chromatography***, solutes separate based on their ability to adsorb to a solid stationary phase. In ***partition chromatography***, the stationary phase is a thin liquid film on a solid support. Separation occurs because there is a difference in the equilibrium partitioning of solutes between the stationary phase and the mobile phase. A stationary phase that consists of a solid support with covalently attached anionic (e.g., $-SO_3^-$) or cationic (e.g., $-N(CH_3)_3^+$) functional groups is the basis for ion-exchange chromatography in which ionic solutes are attracted to the stationary phase by electrostatic forces. In size-exclusion chromatography the stationary phase is a porous particle or gel, with separation based on the size of the solutes. Larger solutes are unable to penetrate as deeply into the porous stationary phase and pass more quickly through the column.

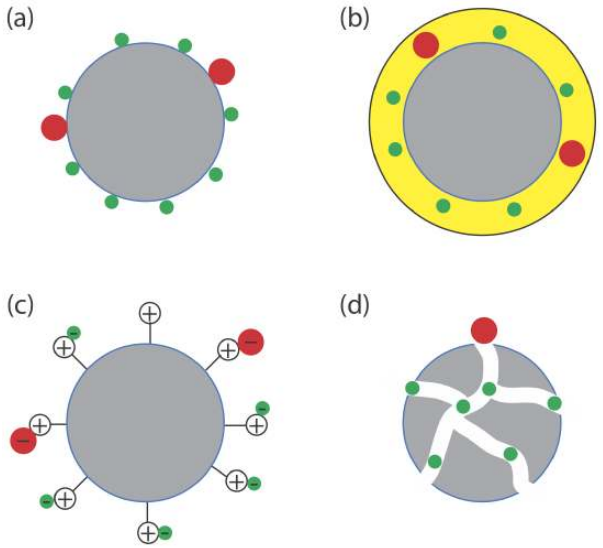


Figure 12.1.4 . Four examples of interactions between a solute and the stationary phase: (a) adsorption on a solid surface, (b) partitioning into a liquid phase, (c) ion-exchange, and (d) size exclusion. For each example, the smaller, green solute is more strongly retained than the larger, red solute.

There are other interactions that can serve as the basis of a separation. In affinity chromatography the interaction between an antigen and an antibody, between an enzyme and a substrate, or between a receptor and a ligand forms the basis of a separation. See this chapter's additional resources for some suggested readings.

ELECTROPHORETIC SEPARATIONS

In chromatography, a separation occurs because there is a difference in the equilibrium partitioning of solutes between the mobile phase and the stationary phase. Equilibrium partitioning, however, is not the only basis for effecting a separation. In an electrophoretic separation, for example, charged solutes migrate under the influence of an applied potential. A separation occurs because of differences in the charges and the sizes of the solutes (Figure 12.1.5).

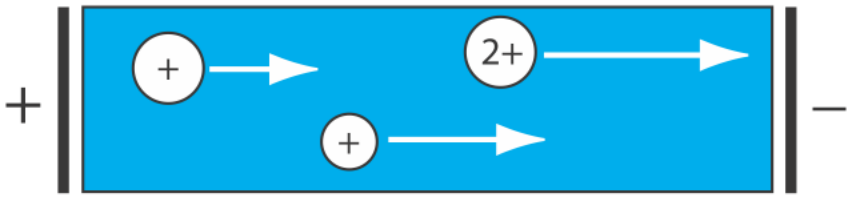


Figure 12.1.5 . Movement of charged solutes under the influence of an applied potential. The lengths of the arrows indicate the relative speed of the solutes. In general, a larger solute moves more slowly than a smaller solute of equal charge, and a solute with a larger charge move more quickly than a solute with a smaller charge.

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12.6: GENERAL THEORY OF COLUMN CHROMATOGRAPHY

Of the two methods for bringing the stationary phase and the mobile phases into contact, the most important is column chromatography. In this section we develop a general theory that we may apply to any form of column chromatography.

Figure 12.2.1 provides a simple view of a liquid–solid column chromatography experiment. The sample is introduced as a narrow band at the top of the column. Ideally, the solute's initial concentration profile is rectangular (Figure 12.2.2 a). As the sample moves down the column, the solutes begin to separate (Figure 12.2.1 b,c) and the individual solute bands begin to broaden and develop a Gaussian profile (Figure 12.2.2 b,c). If the strength of each solute's interaction with the stationary phase is sufficiently different, then the solutes separate into individual bands (Figure 12.2.1 d and Figure 12.2.2 d).

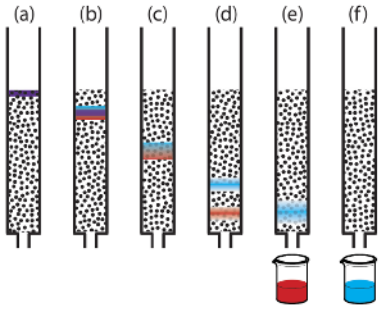


Figure 12.2.1 . Progress of a column chromatographic separation of a two-component mixture. In (a) the sample is layered on top of the stationary phase. As mobile phase passes through the column, the sample separates into two solute bands (b–d). In (e) and (f), we collect each solute as it elutes from the column.

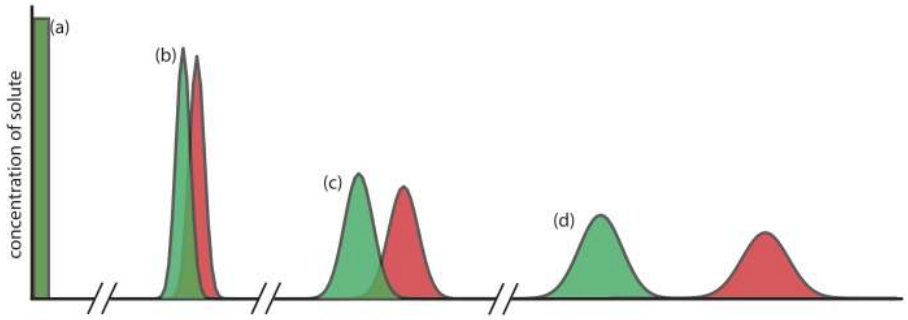


Figure 12.2.2 . An alternative view of the separation in Figure 12.2.1 showing the concentration of each solute as a function of distance down the column.

We can follow the progress of the separation by collecting fractions as they elute from the column (Figure 12.2.1 e,f), or by placing a suitable detector at the end of the column. A plot of the detector's response as a function of elution time, or as a function of the volume of mobile phase, is known as a ***chromatogram*** (Figure 12.2.3), and consists of a peak for each solute.

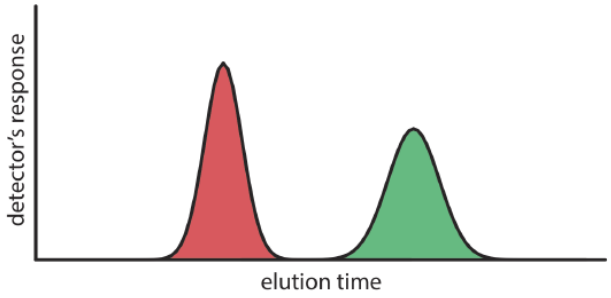


Figure 12.2.3 . Chromatogram for the separation shown in Figure 12.2.1 and Figure 12.2.2 , showing the detector's response as a function of the elution time.

> There are many possible detectors that we can use to monitor the separation. Later sections of this chapter describe some of the most popular.

We can characterize a chromatographic peak's properties in several ways, two of which are shown in Figure 12.2.4 . ***Retention time***, t_r, is the time between the sample's injection and the maximum response for the solute's peak. A chromatographic peak's ***baseline width***, w, as shown in Figure 12.2.4 , is determined by extending tangent lines from the inflection points on either side of the peak through the baseline. Although usually we report t_r and w using units of time, we can report them using units of volume by multiplying each by the mobile phase's velocity, or report them in linear units by measuring distances with a ruler.

> For example, a solute's retention volume, V_r, is $t_r \times u$ where u is the mobile phase's velocity through the column.

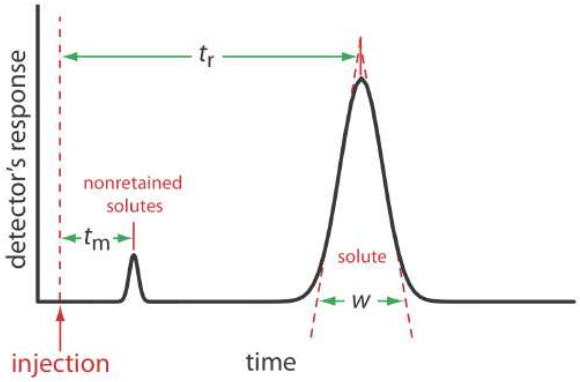


Figure 12.2.4 . Chromatogram showing a solute's retention time, t_r, and baseline width, w, and the column's void time, t_m, for nonretained solutes.

In addition to the solute's peak, Figure 12.2.4 also shows a small peak that elutes shortly after the sample is injected into the mobile phase. This peak contains all ***nonretained solutes***, which move through the column at the same rate as the mobile phase. The time required to elute the nonretained solutes is called the column's ***void time***, t_m.

CHROMATOGRAPHIC RESOLUTION

The goal of chromatography is to separate a mixture into a series of chromatographic peaks, each of which constitutes a single component of the mixture. The ***resolution*** between two chromatographic peaks, R_{AB}, is a quantitative measure of their separation, and is defined as

$$R_{AB} = \frac{t_{t,B} - t_{t,A}}{0.5\,(w_B + w_A)} = \frac{2\Delta t_r}{w_B + w_A} \tag{12.6.1}$$

where B is the later eluting of the two solutes. As shown in Figure 12.2.5 , the separation of two chromatographic peaks improves with an increase in R_{AB}. If the areas under the two peaks are identical—as is the case in Figure 12.2.5 —then a resolution of 1.50 corresponds to an overlap of only 0.13% for the two elution profiles. Because resolution is a quantitative measure of a separation's success, it is a useful way to determine if a change in experimental conditions leads to a better separation.

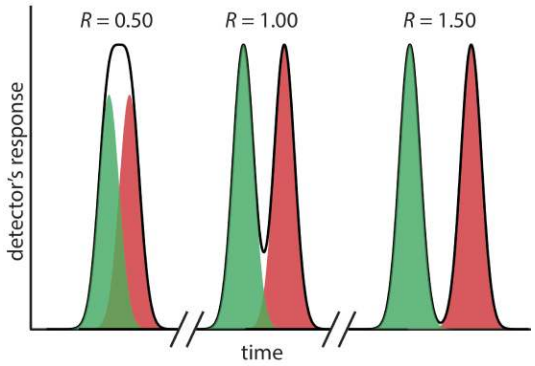


Figure 12.2.5 . Three examples that show the relationship between resolution and the separation of a two component mixture. The green peak and the red peak are the elution profiles for the two components. The chromatographic peak— which is the sum of the two elution profiles—is shown by the solid black line.

EXAMPLE 12.2.1

In a chromatographic analysis of lemon oil a peak for limonene has a retention time of 8.36 min with a baseline width of 0.96 min. γ-Terpinene elutes at 9.54 min with a baseline width of 0.64 min. What is the resolution between the two peaks?

Solution

Using Equation 12.6.1 we find that the resolution is

$$R_{AB} = \frac{2\Delta t_r}{w_B + w_A} = \frac{2(9.54\text{ min} - 8.36\text{ min})}{0.64\text{ min} + 0.96\text{ min}} = 1.48$$

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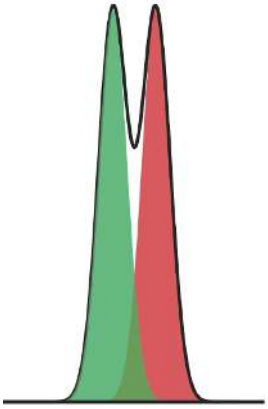


Figure 12.2.6 . Chromatogram for Exercise 12.2.1 .

? EXERCISE 12.2.1

Figure 12.2.6 shows the separation of a two-component mixture. What is the resolution between the two components? Use a ruler to measure Δt_r, w_A, and w_B in millimeters.

Answer

Because the relationship between elution time and distance is proportional, we can measure Δt_r, w_A, and w_B using a ruler. My measurements are 8.5 mm for Δt_r, and 12.0 mm each for w_A and w_B. Using these values, the resolution is

$$R_{AB} = \frac{2\Delta t_t}{w_A + w_B} = \frac{2(8.5\text{ mm})}{12.0\text{ mm} + 12.0\text{ mm}} = 0.70$$

Your measurements for Δt_r, w_A, and w_B will depend on the relative size of your monitor or printout; however, your value for the resolution should be similar to the answer above.

Equation 12.6.1 suggests that we can improve resolution by increasing Δt_r, or by decreasing w_A and w_B (Figure 12.2.7). To increase Δt_r we can use one of two strategies. One approach is to adjust the separation conditions so that both solutes spend less time in the mobile phase —that is, we increase each *solute's retention factor*—which provides more time to effect a separation. A second approach is to increase *selectivity* by adjusting conditions so that only one solute experiences a significant change in its retention time. The baseline width of a solute's peak depends on the solutes movement within and between the mobile phase and the stationary phase, and is governed by several factors that collectively we call *column efficiency*. We will consider each of these approaches for improving resolution in more detail, but first we must define some terms.

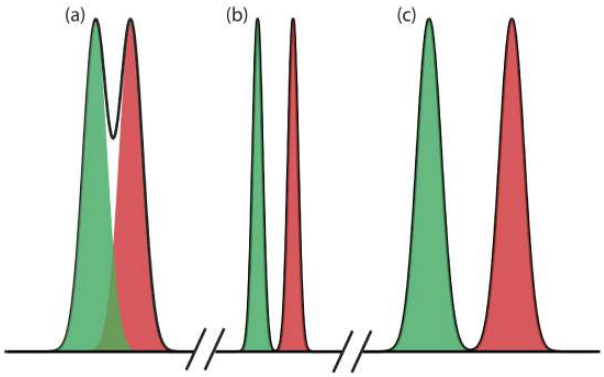


Figure 12.2.7 . Two method for improving chromatographic resolution: (a) original chromatogram; (b) chromatogram after decreasing w_A and w_B by $4\times$; and (c) chromatogram after increasing Δt_r by $2\times$.

SOLUTE RETENTION FACTOR

Let's assume we can describe a solute's distribution between the mobile phase and stationary phase using the following equilibrium reaction

$$S_m \rightleftharpoons S_s$$

where S_m is the solute in the mobile phase and S_s is the solute in the stationary phase. Following the same approach we used in Chapter 7.7 for liquid–liquid extractions, the equilibrium constant for this reaction is an equilibrium partition coefficient, K_D.

$$K_D = \frac{[S_s]}{[S_m]}$$

> This is not a trivial assumption. In this section we are, in effect, treating the solute's equilibrium between the mobile phase and the stationary phase as if it is identical to the equilibrium in a liquid–liquid extraction. You might question whether this is a reasonable assumption. There is an important difference between the two experiments that we need to consider. In a liquid–liquid extraction, which takes place in a separatory funnel, the two phases remain in contact with each other at all times, allowing for a true equilibrium. In chromatography, however, the mobile phase is in constant motion. A solute that moves into the stationary phase from the mobile phase will equilibrate back into a different portion of the mobile phase; this does not describe a true equilibrium.
>
> So, we ask again: Can we treat a solute's distribution between the mobile phase and the stationary phase as an equilibrium process? The answer is yes, if the mobile phase velocity is slow relative to the kinetics of the solute's movement back and forth between the two phase. In general, this is a reasonable assumption.

In the absence of any additional equilibrium reactions in the mobile phase or the stationary phase, K_D is equivalent to the distribution ratio, D,

$$D = \frac{[S_0]}{[S_m]} = \frac{(\text{mol S})_s / V_s}{(\text{mol S})_m / V_m} = K_D \tag{12.6.2}$$

where V_s and V_m are the volumes of the stationary phase and the mobile phase, respectively.

A conservation of mass requires that the total moles of solute remain constant throughout the separation; thus, we know that the following equation is true.

$$(\text{mol S})_{tot} = (\text{mol S})_m + (\text{mol S})_s \tag{12.6.3}$$

Solving Equation 12.6.3 for the moles of solute in the stationary phase and substituting into Equation 12.6.2 leaves us with

$$D = \frac{\{(\text{mol S})_{tot} - (\text{mol S})_m\} / V_s}{(\text{mol S})_m / V_m}$$

Rearranging this equation and solving for the fraction of solute in the mobile phase, f_m, gives

$$f_m = \frac{(\text{mol S})_m}{(\text{mol S})_{tot}} = \frac{V_m}{DV_s + V_m} \tag{12.6.4}$$

which is identical to the result for a liquid-liquid extraction (see Chapter 7). Because we may not know the exact volumes of the stationary phase and the mobile phase, we simplify Equation 12.6.4 by dividing both the numerator and the denominator by V_m; thus

$$f_m = \frac{V_m / V_m}{DV_s / V_m + V_m / V_m} = \frac{1}{DV_s / V_m + 1} = \frac{1}{1 + k} \tag{12.6.5}$$

where k

$$k = D \times \frac{V_s}{V_m} \tag{12.6.6}$$

is the solute's ***retention factor***. Note that the larger the retention factor, the more the distribution ratio favors the stationary phase, leading to a more strongly retained solute and a longer retention time.

> Other (older) names for the retention factor are capacity factor, capacity ratio, and partition ratio, and it sometimes is given the symbol k'. Keep this in mind if you are using other resources. Retention factor is the approved name from the IUPAC Gold Book.

We can determine a solute's retention factor from a chromatogram by measuring the column's void time, t_m, and the solute's retention time, t_r (see Figure 12.2.4). Solving Equation 12.6.5 for k, we find that

$$k = \frac{1 - f_m}{f_m} \tag{12.6.7}$$

Earlier we defined f_m as the fraction of solute in the mobile phase. Assuming a constant mobile phase velocity, we also can define f_m as

$$f_{\text{m}} = \frac{\text{time spent in the mobile phase}}{\text{time spent in the stationary phase}} = \frac{t_{\text{m}}}{t_{\text{r}}}$$

Substituting back into Equation 12.6.7 and rearranging leaves us with

$$k = \frac{1 - \frac{t_m}{t_t}}{\frac{t_{\text{m}}}{t_{\text{r}}}} = \frac{t_{\text{t}} - t_{\text{m}}}{t_{\text{m}}} = \frac{t'_{\text{r}}}{t_{\text{m}}} \tag{12.6.8}$$

where t'_{r} is the ***adjusted retention time***.

EXAMPLE 12.2.2

In a chromatographic analysis of low molecular weight acids, butyric acid elutes with a retention time of 7.63 min. The column's void time is 0.31 min. Calculate the retention factor for butyric acid.

Solution

$$k_{\text{but}} = \frac{t_{\text{r}} - t_{\text{m}}}{t_{\text{m}}} = \frac{7.63 \text{ min} - 0.31 \text{ min}}{0.31 \text{ min}} = 23.6$$

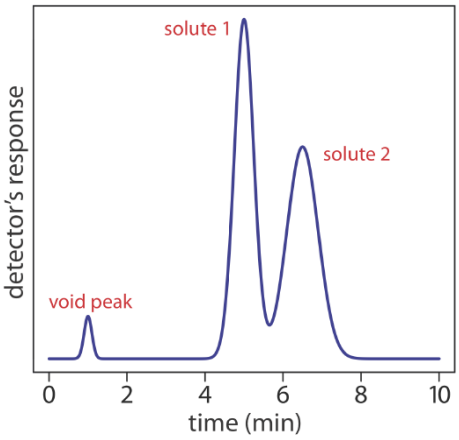


Figure 12.2.8 . Chromatogram for Exercise 12.2.2 .

EXERCISE 12.2.2

Figure 12.2.8 is the chromatogram for a two-component mixture. Determine the retention factor for each solute assuming the sample was injected at time $t = 0$.

Answer

Because the relationship between elution time and distance is proportional, we can measure t_m, $t_{\text{r},1}$, and $t_{\text{r},2}$ using a ruler. My measurements are 7.8 mm, 40.2 mm, and 51.5 mm, respectively. Using these values, the retention factors for solute A and solute B are

$$k_1 = \frac{t_{\text{r}1} - t_{\text{m}}}{t_{\text{m}}} = \frac{40.2 \text{ mm} - 7.8 \text{ mm}}{7.8 \text{ mm}} = 4.15$$

$$k_2 = \frac{t_{\text{r}2} - t_{\text{m}}}{t_{\text{m}}} = \frac{51.5 \text{ mm} - 7.8 \text{ mm}}{7.8 \text{ mm}} = 5.60$$

Your measurements for t_m, $t_{\text{r},1}$, and $t_{\text{r},2}$ will depend on the relative size of your monitor or printout; however, your value for the resolution should be similar to the answer above.

SELECTIVITY

Selectivity is a relative measure of the retention of two solutes, which we define using a selectivity factor, α

$$\alpha = \frac{k_B}{k_A} = \frac{t_{r,B} - t_{\text{m}}}{t_{r,A} - t_{\text{m}}} \tag{12.6.9}$$

where solute *A* has the smaller retention time. When two solutes elute with identical retention time, $\alpha = 1.00$; for all other conditions $\alpha > 1.00$.

EXAMPLE 12.2.3

In the chromatographic analysis for low molecular weight acids described in Example 12.2.2 , the retention time for isobutyric acid is 5.98 min. What is the selectivity factor for isobutyric acid and butyric acid?

Solution

First we must calculate the retention factor for isobutyric acid. Using the void time from Example 12.2.2 we have

$$k_{\text{iso}} = \frac{t_{\text{r}} - t_{\text{m}}}{t_{\text{m}}} = \frac{5.98 \text{ min} - 0.31 \text{ min}}{0.31 \text{ min}} = 18.3$$

The selectivity factor, therefore, is

$$\alpha = \frac{k_{\text{but}}}{k_{\text{iso}}} = \frac{23.6}{18.3} = 1.29$$

EXERCISE 12.2.3

Determine the selectivity factor for the chromatogram in Exercise 12.2.2 .

Answer

Using the results from Exercise 12.2.2 , the selectivity factor is

$$\alpha = \frac{k_2}{k_1} = \frac{5.60}{4.15} = 1.35$$

Your answer may differ slightly due to differences in your values for the two retention factors.

COLUMN EFFICIENCY

Suppose we inject a sample that has a single component. At the moment we inject the sample it is a narrow band of finite width. As the sample passes through the column, the width of this band continually increases in a process we call ***band broadening***. Column efficiency is a quantitative measure of the extent of band broadening.

> See Figure 12.2.1 and Figure 12.2.2 . When we inject the sample it has a uniform, or rectangular concentration profile with respect to distance down the column. As it passes through the column, the band broadens and takes on a Gaussian concentration profile.

In their original theoretical model of chromatography, Martin and Synge divided the chromatographic column into discrete sections, which they called theoretical plates. Within each theoretical plate there is an equilibrium between the solute present in the stationary phase and the solute present in the mobile phase [Martin, A. J. P.; Synge, R. L. M. *Biochem. J.* **1941**, *35*, 1358–1366]. They described column efficiency in terms of the number of ***theoretical plates***, *N*,

$$N = \frac{L}{H} \tag{12.6.10}$$

where *L* is the column's length and *H* is the height of a theoretical plate. For any given column, the column efficiency improves—and chromatographic peaks become narrower—when there are more theoretical plates.

If we assume that a chromatographic peak has a Gaussian profile, then the extent of band broadening is given by the peak's variance or standard deviation. The height of a theoretical plate is the peak's variance per unit length of the column

$$H = \frac{\sigma^2}{L} \tag{12.6.11}$$

where the standard deviation, σ, has units of distance. Because retention times and peak widths usually are measured in seconds or minutes, it is more convenient to express the standard deviation in units of time, τ, by dividing σ by the solute's average linear velocity, $\bar{u}$, which is equivalent to dividing the distance it travels, *L*, by its retention time, t_{r}.

$$\tau = \frac{\sigma}{\bar{u}} = \frac{\sigma t_r}{L} \tag{12.6.12}$$

For a Gaussian peak shape, the width at the baseline, w, is four times its standard deviation, τ.

$$w = 4\tau \tag{12.6.13}$$

Combining Equation 12.6.11, Equation 12.6.12, and Equation 12.6.13 defines the height of a theoretical plate in terms of the easily measured chromatographic parameters t_r and w.

$$H = \frac{Lw^2}{16t_r^2} \tag{12.6.14}$$

Combing Equation 12.6.14 and Equation 12.6.10 gives the number of theoretical plates.

$$N = 16\frac{t_r^2}{w^2} = 16\left(\frac{t_r}{w}\right)^2 \tag{12.6.15}$$

EXAMPLE 12.2.4

A chromatographic analysis for the chlorinated pesticide Dieldrin gives a peak with a retention time of 8.68 min and a baseline width of 0.29 min. Calculate the number of theoretical plates? Given that the column is 2.0 m long, what is the height of a theoretical plate in mm?

Solution

Using Equation 12.6.15, the number of theoretical plates is

$$N = 16\frac{t_r^2}{w^2} = 16 \times \frac{(8.68\text{ min})^2}{(0.29\text{ min})^2} = 14300\text{ plates}$$

Solving Equation 12.6.10 for H gives the average height of a theoretical plate as

$$H = \frac{L}{N} = \frac{2.00\text{ m}}{14300\text{ plates}} \times \frac{1000\text{ mm}}{\text{m}} = 0.14\text{ mm/plate}$$

EXERCISE 12.2.4

For each solute in the chromatogram for Exercise 12.2.2 , calculate the number of theoretical plates and the average height of a theoretical plate. The column is 0.5 m long.

Answer

Because the relationship between elution time and distance is proportional, we can measure $t_{r,1}$, $t_{r,2}$, w_1, and w_2 using a ruler. My measurements are 40.2 mm, 51.5 mm, 8.0 mm, and 13.5 mm, respectively. Using these values, the number of theoretical plates for each solute is

$$N_1 = 16\frac{t_{r,1}^2}{w_1^2} = 16 \times \frac{(40.2\text{ mm})^2}{(8.0\text{ mm})^2} = 400\text{ theoretical plates}$$

$$N_2 = 16\frac{t_{r,2}^2}{w_2^2} = 16 \times \frac{(51.5\text{ mm})^2}{(13.5\text{ mm})^2} = 233\text{ theoretical plates}$$

The height of a theoretical plate for each solute is

$$H_1 = \frac{L}{N_1} = \frac{0.500\text{ m}}{400\text{ plates}} \times \frac{1000\text{ mm}}{\text{m}} = 1.2\text{ mm/plate}$$

$$H_2 = \frac{L}{N_2} = \frac{0.500\text{ m}}{233\text{ plates}} \times \frac{1000\text{ mm}}{\text{m}} = 2.15\text{ mm/plate}$$

Your measurements for $t_{r,1}$, $t_{r,2}$, w_1, and w_2 will depend on the relative size of your monitor or printout; however, your values for N and for H should be similar to the answer above.

It is important to remember that a theoretical plate is an artificial construct and that a chromatographic column does not contain physical plates. In fact, the number of theoretical plates depends on both the properties of the column and the solute. As a result, the number of theoretical plates for a column may vary from solute to solute.

PEAK CAPACITY

One advantage of improving column efficiency is that we can separate more solutes with baseline resolution. One estimate of the number of solutes that we can separate is

$$n_c = 1 + \frac{\sqrt{N}}{4} \ln \frac{V_{max}}{V_{min}} \tag{12.6.16}$$

where n_c is the column's ***peak capacity***, and V_{min} and V_{max} are the smallest and the largest volumes of mobile phase in which we can elute and detect a solute [Giddings, J. C. *Unified Separation Science*, Wiley-Interscience: New York, 1991]. A column with 10 000 theoretical plates, for example, can resolve no more than

$$n_c = 1 + \frac{\sqrt{10000}}{4} \ln \frac{30\text{mL}}{1\text{mL}} = 86 \text{ solutes}$$

if V_{min} and V_{max} are 1 mL and 30 mL, respectively. This estimate provides an upper bound on the number of solutes and may help us exclude from consideration a column that does not have enough theoretical plates to separate a complex mixture. Just because a column's theoretical peak capacity is larger than the number of solutes, however, does not mean that a separation is feasible. In most situations the practical peak capacity is less than the theoretical peak capacity because the retention characteristics of some solutes are so similar that a separation is impossible. Nevertheless, columns with more theoretical plates, or with a greater range of possible elution volumes, are more likely to separate a complex mixture.

> The smallest volume we can use is the column's void volume. The largest volume is determined either by our patience—the maximum analysis time we can tolerate—or by our inability to detect solutes because there is too much band broadening.

ASYMMETRIC PEAKS

Our treatment of chromatography in this section assumes that a solute elutes as a symmetrical Gaussian peak, such as that shown in Figure 12.2.4 . This ideal behavior occurs when the solute's partition coefficient, K_D

$$K_D = \frac{[S_s]}{[S_m]}$$

is the same for all concentrations of solute. If this is not the case, then the chromatographic peak has an asymmetric peak shape similar to those shown in Figure 12.2.9 . The chromatographic peak in Figure 12.2.9 a is an example of ***peak tailing***, which occurs when some sites on the stationary phase retain the solute more strongly than other sites. Figure 12.2.9 b, which is an example of ***peak fronting*** most often is the result of overloading the column with sample.

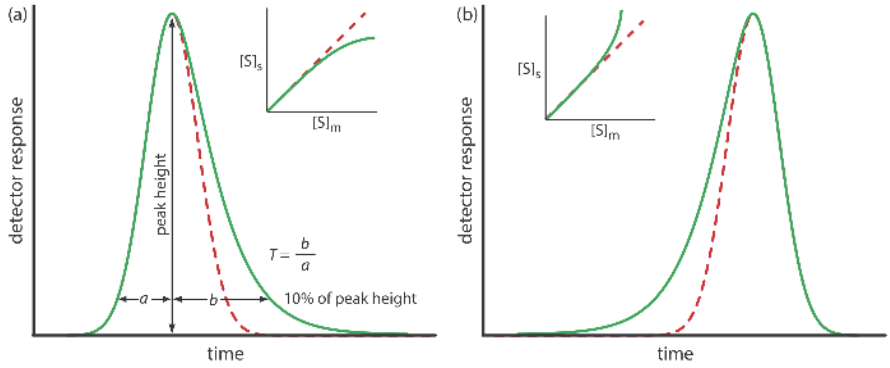


Figure 12.2.9 . Examples of asymmetric chromatographic peaks showing (a) peak tailing and (b) peak fronting. For both (a) and (b) the green chromatogram is the asymmetric peak and the red dashed chromatogram shows the ideal, Gaussian peak shape. The insets show the relationship between the concentration of solute in the stationary phase, $[S]_s$, and its concentration in the mobile phase, $[S]_m$. The dashed red lines show ideal behavior (K_D is constant for all conditions) and the green lines show nonideal behavior (K_D decreases or increases for higher total concentrations of solute). A quantitative measure of peak tailing, T, is shown in (a).

As shown in Figure 12.2.9 a, we can report a peak's asymmetry by drawing a horizontal line at 10% of the peak's maximum height and measuring the distance from each side of the peak to a line drawn vertically through the peak's maximum. The asymmetry factor, T, is defined as

$$T = \frac{b}{a}$$

The number of theoretical plates for an asymmetric peak shape is approximately

$$N \approx \frac{41.7 \times \frac{t_r^2}{(w_{0.1})^2}}{T + 1.25} = \frac{41.7 \times \frac{t_r^2}{(a+b)^2}}{T + 1.25}$$

where $w_{0.1}$ is the width at 10% of the peak's height [Foley, J. P.; Dorsey, J. G. *Anal. Chem.* **1983**, *55*, 730–737].

Asymmetric peaks have fewer theoretical plates, and the more asymmetric the peak the smaller the number of theoretical plates. For example, the following table gives values for *N* for a solute eluting with a retention time of 10.0 min and a peak width of 1.00 min.

b	*a*	*T*	*N*
0.5	0.5	1.00	1850
0.6	0.4	1.50	1520
0.7	0.3	2.33	1160
0.8	0.2	4.00	790

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12.7: OPTIMIZING CHROMATOGRAPHIC SEPARATIONS

Now that we have defined the solute retention factor, selectivity, and column efficiency we are able to consider how they affect the resolution of two closely eluting peaks. Because the two peaks have similar retention times, it is reasonable to assume that their peak widths are nearly identical. If the number of theoretical plates is the same for all solutes—not strictly true, but not a bad assumption—then from equation 12.2.15, the ratio t_r/w is a constant. If two solutes have similar retention times, then their peak widths must be similar. Equation 12.2.1, therefore, becomes

$$R_{AB} = \frac{t_{r,B} - t_{r,A}}{0.5\,(w_B + w_A)} \approx \frac{t_{r,B} - t_{r,A}}{0.5\,(2w_B)} = \frac{t_{r,B} - t_{r,A}}{w_B} \tag{12.7.1}$$

where *B* is the later eluting of the two solutes. Solving equation 12.2.15 for w_B and substituting into Equation 12.7.1 leaves us with the following result.

$$R_{AB} = \frac{\sqrt{N_B}}{4} \times \frac{t_{r,B} - t_{r,A}}{t_{r,B}} \tag{12.7.2}$$

Rearranging equation 12.2.8 provides us with the following equations for the retention times of solutes *A* and *B*.

$$t_{r,A} = k_A t_\mathrm{m} + t_\mathrm{m} \quad \text{and} \quad t_{r,B} = k_B t_\mathrm{m} + t_\mathrm{m}$$

After substituting these equations into Equation 12.7.2 and simplifying, we have

$$R_{AB} = \frac{\sqrt{N_B}}{4} \times \frac{k_B - k_A}{1 + k_B}$$

Finally, we can eliminate solute *A*'s retention factor by substituting in equation 12.2.9. After rearranging, we end up with the following equation for the resolution between the chromatographic peaks for solutes A and B.

$$R_{AB} = \frac{\sqrt{N_B}}{4} \times \frac{\alpha - 1}{\alpha} \times \frac{k_B}{1 + k_B} \tag{12.7.3}$$

In addition to resolution, another important factor in chromatography is the amount of time needed to elute a pair of solutes, which we can approximate using the retention time for solute *B*.

$$t_{r,s} = \frac{16 R_{AB}^2 H}{u} \times \left(\frac{\alpha}{\alpha - 1}\right)^2 \times \frac{(1 + k_B)^3}{k_B^2} \tag{12.7.4}$$

where *u* is the mobile phase's velocity.

> Although Equation 12.7.3 is useful for considering how a change in *N*, α, or *k* qualitatively affects resolution—which suits our purpose here—it is less useful for making accurate quantitative predictions of resolution, particularly for smaller values of *N* and for larger values of *R*. For more accurate predictions use the equation
>
> $$R_{AB} = \frac{\sqrt{N}}{4} \times (\alpha - 1) \times \frac{k_B}{1 + k_{\text{avg}}}$$
>
> where k_{avg} is (k_A + k_B)/2. For a derivation of this equation and for a deeper discussion of resolution in column chromatography, see Foley, J. P. "Resolution Equations for Column Chromatography," *Analyst*, **1991**, *116*, 1275-1279.

Equation 12.7.3 and Equation 12.7.4 contain terms that correspond to column efficiency, selectivity, and the solute retention factor. We can vary these terms, more or less independently, to improve resolution and analysis time. The first term, which is a function of the number of theoretical plates (for Equation 12.7.3) or the height of a theoretical plate (for Equation 12.7.4), accounts for the effect of column efficiency. The second term is a function of α and accounts for the influence of column selectivity. Finally, the third term in both equations is a function of k_B and accounts for the effect of solute *B*'s retention factor. A discussion of how we can use these parameters to improve resolution is the subject of the remainder of this section.

USING THE RETENTION FACTOR TO OPTIMIZE RESOLUTION

One of the simplest ways to improve resolution is to adjust the retention factor for solute *B*. If all other terms in Equation 12.7.3 remain constant, an increase in k_B will improve resolution. As shown by the green curve in Figure 12.3.1 , however, the improvement is greatest if the initial value of k_B is small. Once k_B exceeds a value of approximately 10, a further increase produces only a marginal improvement in

resolution. For example, if the original value of k_B is 1, increasing its value to 10 gives an 82% improvement in resolution; a further increase to 15 provides a net improvement in resolution of only 87.5%.

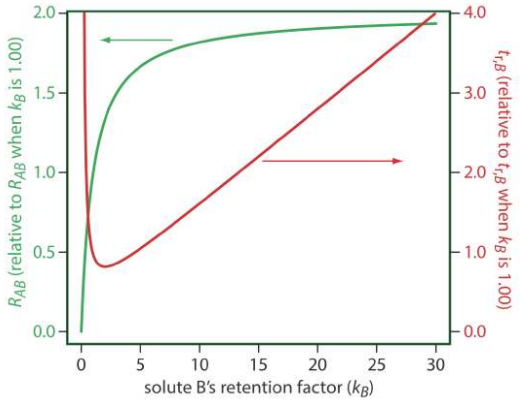


Figure 12.3.1 . Effect of k_B on the resolution for a pair of solutes, R_{AB}, and the retention time for the later eluting solute, $t_{r,B}$. The *y*-axes display the resolution and retention time relative to their respective values when k_B is 1.00.

Any improvement in resolution from increasing the value of k_B generally comes at the cost of a longer analysis time. The red curve in Figure 12.3.1 shows the relative change in the retention time for solute *B* as a function of its retention factor. Note that the minimum retention time is for $k_B = 2$. Increasing k_B from 2 to 10, for example, approximately doubles solute B's retention time.

> The relationship between retention factor and analysis time in Figure 12.3.1 works to our advantage if a separation produces an acceptable resolution with a large k_B. In this case we may be able to decrease k_B with little loss in resolution and with a significantly shorter analysis time.

To increase k_B without changing selectivity, α, any change to the chromatographic conditions must result in a general, nonselective increase in the retention factor for both solutes. In gas chromatography, we can accomplish this by decreasing the column's temperature. Because a solute's vapor pressure is smaller at lower temperatures, it spends more time in the stationary phase and takes longer to elute. In liquid chromatography, the easiest way to increase a solute's retention factor is to use a mobile phase that is a weaker solvent. When the mobile phase has a lower solvent strength, solutes spend proportionally more time in the stationary phase and take longer to elute.

Adjusting the retention factor to improve the resolution between one pair of solutes may lead to unacceptably long retention times for other solutes. For example, suppose we need to analyze a four-component mixture with baseline resolution and with a run-time of less than 20 min. Our initial choice of conditions gives the chromatogram in Figure 12.3.2 a. Although we successfully separate components 3 and 4 within 15 min, we fail to separate components 1 and 2. Adjusting conditions to improve the resolution for the first two components by increasing k_2 provides a good separation of all four components, but the run-time is too long (Figure 12.3.2 b). This problem of finding a single set of acceptable operating conditions is known as the ***general elution problem***.

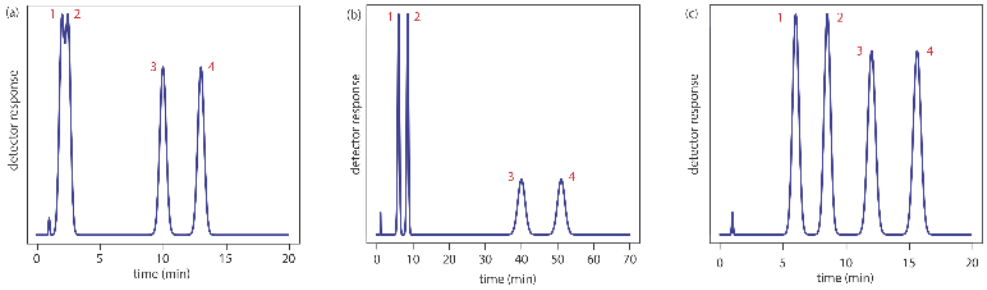


Figure 12.3.2 . Example showing the general elution problem in chromatography. See text for details.

One solution to the general elution problem is to make incremental adjustments to the retention factor as the separation takes place. At the beginning of the separation we set the initial chromatographic conditions to optimize the resolution for early eluting solutes. As the separation progresses, we adjust the chromatographic conditions to decrease the retention factor—and, therefore, to decrease the retention time—for each of the later eluting solutes (Figure 12.3.2 c). In gas chromatography this is accomplished by temperature programming. The column's initial temperature is selected such that the first solutes to elute are resolved fully. The temperature is then increased, either continuously or in steps, to bring off later eluting components with both an acceptable resolution and a reasonable analysis time. In liquid chromatography the same effect is obtained by increasing the solvent's eluting strength. This is known as a gradient elution. We will have more to say about each of these in later sections of this chapter.

USING SELECTIVITY TO OPTIMIZE RESOLUTION

A second approach to improving resolution is to adjust the selectivity, α. In fact, for $\alpha \approx 1$ usually it is not possible to improve resolution by adjusting the solute retention factor, k_B, or the column efficiency, N. A change in α often has a more dramatic effect on resolution than a change in k_B. For example, changing α from 1.1 to 1.5, while holding constant all other terms, improves resolution by 267%. In gas chromatography, we adjust α by changing the stationary phase; in liquid chromatography, we change the composition of the mobile phase to adjust α.

To change α we need to selectively adjust individual solute retention factors. Figure 12.3.3 shows one possible approach for the liquid chromatographic separation of a mixture of substituted benzoic acids. Because the retention time of a compound's weak acid form and its weak base form are different, its retention time will vary with the pH of the mobile phase, as shown in Figure 12.3.3 a. The intersections of the curves in Figure 12.3.3 a show pH values where two solutes co-elute. For example, at a pH of 3.8 terephthalic acid and *p*-hydroxybenzoic acid elute as a single chromatographic peak.

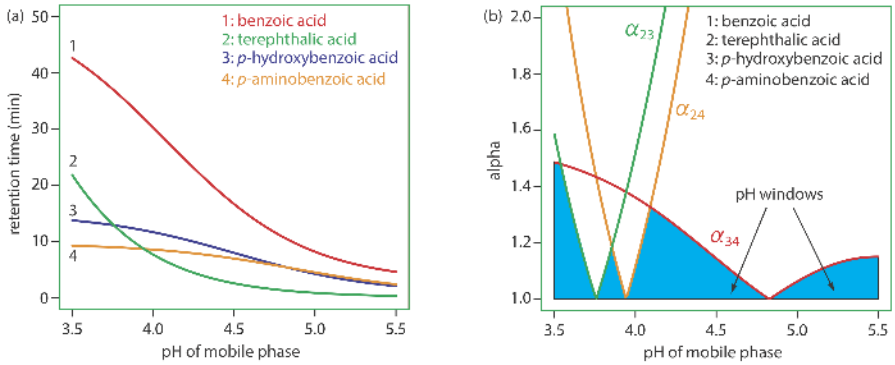


Figure 12.3.3 . Example showing how the mobile phase pH in liquid chromatography affects selectivity: (a) retention times for four substituted benzoic acids as a function of the mobile phase's pH; (b) alpha values for three pairs of solutes that are difficult to separate. See text for details. The mobile phase is an acetic acid/sodium acetate buffer and the stationary phase is a nonpolar hydrocarbon. Data from Harvey, D. T.; Byerly, S.; Bowman, A.; Tomlin, J. "Optimization of HPLC and GC Separations Using Response Surfaces," *J. Chem. Educ.* **1991**, *68*, 162–168.

Figure 12.3.3 a shows that there are many pH values where some separation is possible. To find the optimum separation, we plot a for each pair of solutes. The red, green, and orange curves in Figure 12.3.3 b show the variation in a with pH for the three pairs of solutes that are hardest to separate (for all other pairs of solutes, $\alpha > 2$ at all pH levels). The blue shading shows windows of pH values in which at least a partial separation is possible—this figure is sometimes called a window diagram—and the highest point in each window gives the optimum pH within that range. The best overall separation is the highest point in any window, which, for this example, is a pH of 3.5. Because the analysis time at this pH is more than 40 min (Figure 12.3.3 a), choosing a pH between 4.1–4.4 might produce an acceptable separation with a much shorter analysis time.

Let's use benzoic acid, C_6H_5COOH, to explain why pH can affect a solute's retention time. The separation uses an aqueous mobile phase and a nonpolar stationary phase. At lower pHs, benzoic acid predominately is in its weak acid form, C_6H_5COOH, and partitions easily into the nonpolar stationary phase. At more basic pHs, however, benzoic acid is in its weak base form, $C_6H_5COO^-$. Because it now carries a charge, its solubility in the mobile phase increases and its solubility in the nonpolar stationary phase decreases. As a result, it spends more time in the mobile phase and has a shorter retention time.

Although the usual way to adjust pH is to change the concentration of buffering agents, it also is possible to adjust pH by changing the column's temperature because a solute's pK_a value is pH-dependent; for a review, see Gagliardi, L. G.; Tascon, M.; Castells, C. B. "Effect of Temperature on Acid–Base Equilibria in Separation Techniques: A Review," *Anal. Chim. Acta*, **2015**, *889*, 35–57.

USING COLUMN EFFICIENCY TO OPTIMIZE RESOLUTION

A third approach to improving resolution is to adjust the column's efficiency by increasing the number of theoretical plates, N. If we have values for k_B and α, then we can use Equation 12.7.3 to calculate the number of theoretical plates for any resolution. Table 12.3.1 provides some representative values. For example, if $\alpha = 1.05$ and $k_B = 2.0$, a resolution of 1.25 requires approximately 24 800 theoretical plates. If our column provides only 12 400 plates, half of what is needed, then a separation is not possible. How can we double the number of theoretical plates? The easiest way is to double the length of the column, although this also doubles the analysis time. A better approach is to cut the height of a theoretical plate, H, in half, providing the desired resolution without changing the analysis time. Even better, if we can decrease H by more than 50%, it may be possible to achieve the desired resolution with an even shorter analysis time by also decreasing k_B or α.

Table 12.3.1 . Minimum Number of Theoretical Plates to Achieve Desired Resolution for Selected Values of k_B and α

	R_{AB} = 1.00		R_{AB} = 1.25		R_{AB} = 1.50	
k_B	$\alpha = 1.05$	$\alpha = 1.10$	$\alpha = 1.05$	$\alpha = 1.10$	$\alpha = 1.05$	$\alpha = 1.10$
0.5	63500	17400	99200	27200	143000	39200
1.0	28200	7740	44100	12100	63500	17400
1.5	19600	5380	30600	8400	44100	12100
2.0	15900	4360	24800	6810	35700	9800
3.0	12500	3440	19600	5380	28200	7740
5.0	10200	2790	15900	4360	22900	6270
10.0	8540	2340	13300	3660	19200	5270

To decrease the height of a theoretical plate we need to understand the experimental factors that affect band broadening. There are several theoretical treatments of band broadening. We will consider one approach that considers four contributions: variations in path lengths, longitudinal diffusion, mass transfer in the stationary phase, and mass transfer in the mobile phase.

MULTIPLE PATHS: VARIATIONS IN PATH LENGTH

As solute molecules pass through the column they travel paths that differ in length. Because of this difference in path length, two solute molecules that enter the column at the same time will exit the column at different times. The result, as shown in Figure 12.3.4 , is a broadening of the solute's profile on the column. The contribution of ***multiple paths*** to the height of a theoretical plate, H_p, is

$$H_p = 2\lambda d_p \tag{12.7.5}$$

where d_p is the average diameter of the particulate packing material and λ is a constant that accounts for the consistency of the packing. A smaller range of particle sizes and a more consistent packing produce a smaller value for λ. For a column without packing material, H_p is zero and there is no contribution to band broadening from multiple paths.

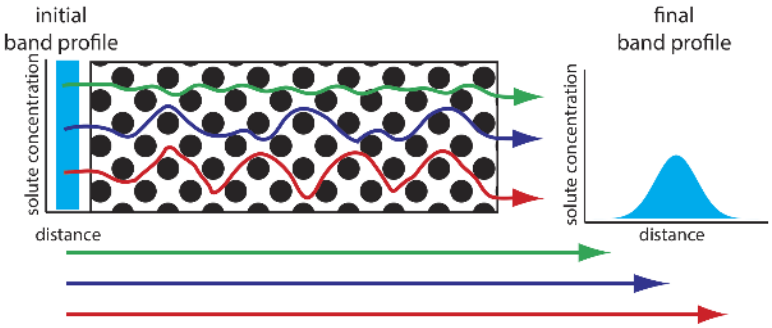


Figure 12.3.4 . The effect of multiple paths on a solute's band broadening. The solute's initial band profile is rectangular. As this band travels through the column, individual solute molecules travel different paths, three of which are shown by the meandering colored paths (the actual lengths of these paths are shown by the straight arrows at the bottom of the figure). Most solute molecules travel paths with lengths similar to that shown in blue, with a few traveling much shorter paths (green) or much longer paths (red). As a result, the solute's band profile at the end of the column is broader and Gaussian in shape.

An inconsistent packing creates channels that allow some solute molecules to travel quickly through the column. It also can creates pockets that temporarily trap some solute molecules, slowing their progress through the column. A more uniform packing minimizes these problems.

LONGITUDINAL DIFFUSION

The second contribution to band broadening is the result of the solute's ***longitudinal diffusion*** in the mobile phase. Solute molecules are in constant motion, diffusing from regions of higher solute concentration to regions where the concentration of solute is smaller. The result is an increase in the solute's band width (Figure 12.3.5). The contribution of longitudinal diffusion to the height of a theoretical plate, H_d, is

$$H_d = \frac{2\gamma D_m}{u} \tag{12.7.6}$$

where D_m is the solute's diffusion coefficient in the mobile phase, u is the mobile phase's velocity, and γ is a constant related to the efficiency of column packing. Note that the effect of H_d on band broadening is inversely proportional to the mobile phase velocity: a higher velocity provides less time for longitudinal diffusion. Because a solute's diffusion coefficient is larger in the gas phase than in a liquid phase, longitudinal diffusion is a more serious problem in gas chromatography.

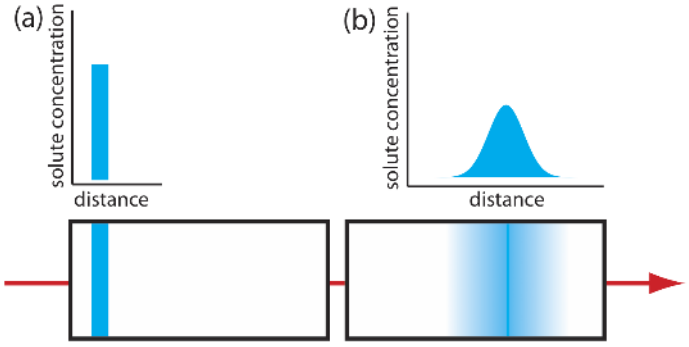


Figure 12.3.5 . The effect of longitudinal diffusion on a solute's band broadening. Two horizontal cross-sections through the column and the corresponding concentration versus distance profiles are shown, with (a) being earlier in time. The red arrow shows the direction in which the mobile phase is moving.

MASS TRANSFER

As the solute passes through the column it moves between the mobile phase and the stationary phase. We call this movement between phases ***mass transfer***. As shown in Figure 12.3.6 , band broadening occurs if the solute's movement within the mobile phase or within the stationary phase is not fast enough to maintain an equilibrium in its concentration between the two phases. On average, a solute molecule in the mobile phase moves down the column before it passes into the stationary phase. A solute molecule in the stationary phase, on the other hand, takes longer than expected to move back into the mobile phase. The contributions of mass transfer in the stationary phase, H_s, and mass transfer in the mobile phase, H_m, are given by the following equations

$$H_s = \frac{qkd_f^2}{(1+k)^2 D_s} u \tag{12.7.7}$$

$$H_m = \frac{fn\left(d_p^2, d_c^2\right)}{D_m} u \tag{12.7.8}$$

where d_f is the thickness of the stationary phase, d_c is the diameter of the column, D_s and D_m are the diffusion coefficients for the solute in the stationary phase and the mobile phase, k is the solute's retention factor, and q is a constant related to the column packing material. Although the exact form of H_m is not known, it is a function of particle size and column diameter. Note that the effect of H_s and H_m on band broadening is directly proportional to the mobile phase velocity because a smaller velocity provides more time for mass transfer.

> The abbreviation *fn* in Equation 12.7.7 means "is a function of."

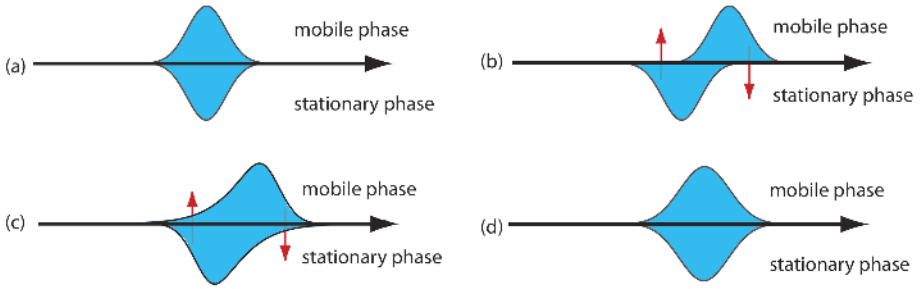


Figure 12.3.6 . Effect of mass transfer on band broadening: (a) Ideal equilibrium Gaussian profiles for the solute in the mobile phase and in the stationary phase. (b, c) If we allow the solute's band to move a small distance down the column, an equilibrium between the two phases no longer exits. The red arrows show the movement of solute—what we call the mass transfer of solute—from the stationary phase to the mobile phase, and from the mobile phase to the stationary phase. (d) Once equilibrium is reestablished, the solute's band is now broader.

PUTTING IT ALL TOGETHER

The height of a theoretical plate is a summation of the contributions from each of the terms affecting band broadening.

$$H = H_p + H_d + H_s + H_m \tag{12.7.9}$$

An alternative form of this equation is the ***van Deemter equation***

$$H = A + \frac{B}{u} + Cu \tag{12.7.10}$$

which emphasizes the importance of the mobile phase's velocity. In the van Deemter equation, *A* accounts for the contribution of multiple paths (H_p), *B*/*u* accounts for the contribution of longitudinal diffusion (H_d), and *Cu* accounts for the combined contribution of mass transfer in the stationary phase and in the mobile phase (H_s and H_m).

There is some disagreement on the best equation for describing the relationship between plate height and mobile phase velocity [Hawkes, S. J. *J. Chem. Educ.* **1983**, *60*, 393–398]. In addition to the van Deemter equation, other equations include

$$H = \frac{B}{u} + (C_s + C_m)\, u$$

where C_s and C_m are the mass transfer terms for the stationary phase and the mobile phase and

$$H = Au^{1/3} + \frac{B}{u} + Cu$$

All three equations, and others, have been used to characterize chromatographic systems, with no single equation providing the best explanation in every case [Kennedy, R. T.; Jorgenson, J. W. *Anal. Chem.* **1989**, *61*, 1128–1135].

To increase the number of theoretical plates without increasing the length of the column, we need to decrease one or more of the terms in Equation 12.7.9. The easiest way to decrease *H* is to adjust the velocity of the mobile phase. For smaller mobile phase velocities, column efficiency is limited by longitudinal diffusion, and for higher mobile phase velocities efficiency is limited by the two mass transfer terms. As shown in Figure 12.3.7 —which uses the van Deemter equation—the optimum mobile phase velocity is the minimum in a plot of *H* as a function of *u*.

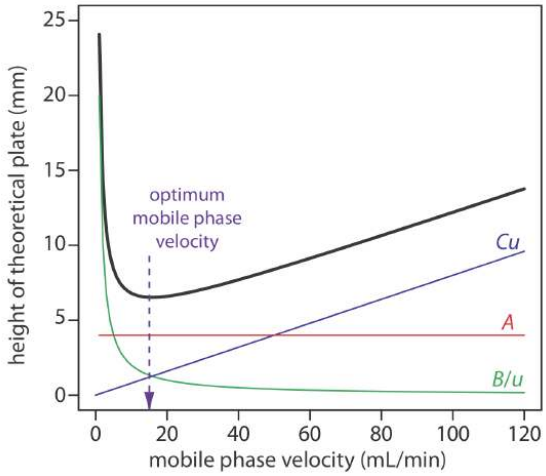


Figure 12.3.7 . Plot showing the relationship between the height of a theoretical plate, *H*, and the mobile phase's velocity, *u*, based on the van Deemter equation.

The remaining parameters that affect the terms in Equation 12.7.9 are functions of the column's properties and suggest other possible approaches to improving column efficiency. For example, both H_p and H_m are a function of the size of the particles used to pack the column. Decreasing particle size, therefore, is another useful method for improving efficiency.

> For a more detailed discussion of ways to assess the quality of a column, see Desmet, G.; Caooter, D.; Broeckhaven, K. "Graphical Data Represenation Methods to Assess the Quality of LC Columns," *Anal. Chem.* **2015**, *87*, 8593–8602.

Perhaps the most important advancement in chromatography columns is the development of open-tubular, or ***capillary columns***. These columns have very small diameters ($d_c \approx$ 50–500 μm) and contain no packing material (d_p = 0). Instead, the capillary column's interior wall is coated with a thin film of the stationary phase. Plate height is reduced because the contribution to *H* from H_p (Equation 12.7.5) disappears and the contribution from H_m (Equation 12.7.8) becomes smaller. Because the column does not contain any solid packing material, it takes less pressure to move the mobile phase through the column, which allows for longer columns. The combination of a longer column and a smaller height for a theoretical plate increases the number of theoretical plates by approximately 100×. Capillary columns are not without disadvantages. Because they are much narrower than packed columns, they require a significantly smaller amount of sample, which may be difficult to inject reproducibly. Another approach to improving resolution is to use thin films of stationary phase, which decreases the contribution to *H* from H_s (Equation 12.7.7).

> The smaller the particles, the more pressure is needed to push the mobile phase through the column. As a result, for any form of chromatography there is a practical limit to particle size.

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12.8: GAS CHROMATOGRAPHY

In ***gas chromatography*** (GC) we inject the sample, which may be a gas or a liquid, into an gaseous mobile phase (often called the carrier gas). The mobile phase carries the sample through a packed or a capillary column that separates the sample's components based on their ability to partition between the mobile phase and the stationary phase. Figure 12.4.1 shows an example of a typical gas chromatograph, which consists of several key components: a supply of compressed gas for the mobile phase; a heated injector, which rapidly volatilizes the components in a liquid sample; a column, which is placed within an oven whose temperature we can control during the separation; and a detector to monitor the eluent as it comes off the column. Let's consider each of these components.



Figure 12.4.1 . Example of a typical gas chromatograph with insets showing the heated injection ports—note the symbol indicating that it is hot—and the oven that houses the column. This particular instrument is equipped with an autosampler for injecting samples, a capillary column, and a mass spectrometer (MS) as the detector. Note that the carrier gas is supplied by a tank of compressed gas.

MOBILE PHASE

The most common mobile phases for gas chromatography are He, Ar, and N_2, which have the advantage of being chemically inert toward both the sample and the stationary phase. The choice of carrier gas often is determined by the needs of instrument's detector. For a packed column the mobile phase velocity usually is 25–150 mL/min. The typical flow rate for a capillary column is 1–25 mL/min.

CHROMATOGRAPHIC COLUMNS

There are two broad classes of chromatographic columns: packed columns and capillary columns. In general, a packed column can handle larger samples and a capillary column can separate more complex mixtures.

PACKED COLUMNS

Packed columns are constructed from glass, stainless steel, copper, or aluminum, and typically are 2–6 m in length with internal diameters of 2–4 mm. The column is filled with a particulate solid support, with particle diameters ranging from 37–44 μm to 250–354 μm. Figure 12.4.2 shows a typical example of a packed column.

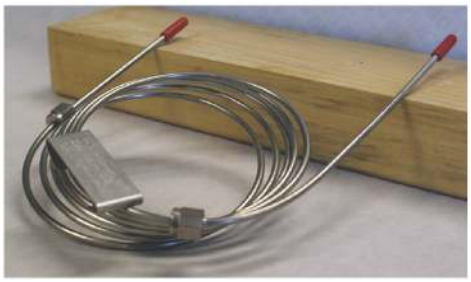


Figure 12.4.2 . Typical example of a packed column for gas chromatography. This column is made from stainless steel and is 2 m long with an internal diameter of 3.2 mm. The packing material in this column has a particle diameter of 149–177 μm. To put this in perspective, beach sand has a typical diameter of 700 μm and the diameter of fine grained sand is 250 μm.

The most widely used particulate support is diatomaceous earth, which is composed of the silica skeletons of diatoms. These particles are very porous, with surface areas ranging from 0.5–7.5 m^2/g, which provides ample contact between the mobile phase and the stationary phase. When hydrolyzed, the surface of a diatomaceous earth contains silanol groups (–SiOH), that serve as active sites for absorbing solute molecules in gas-solid chromatography (GSC).

In ***gas-liquid chromatography*** (GLC), we coat the packing material with a liquid mobile phase. To prevent uncoated packing material from adsorbing solutes, which degrades the quality of the separation, surface silanols are deactivated by reacting them with dimethyldichlorosilane and rinsing with an alcohol—typically methanol—before coating the particles with stationary phase.

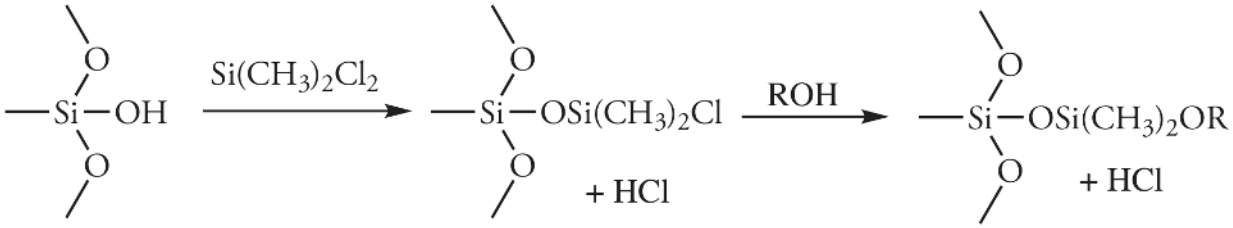


Figure 12.4.2 , for example, has approximately 1800 plates/m, or a total of approximately 3600 theoretical plates. If we assume a V_{max}/V_{min} ≈ 50, then it has a peak capacity (equation 12.2.16) of

$$n_c = 1 + \frac{\sqrt{3600}}{4}\ln(50) \approx 60$$

CAPILLARY COLUMNS

A capillary, or ***open tubular column*** is constructed from fused silica and is coated with a protective polymer coating. Columns range from 15–100 m in length with an internal diameter of approximately 150–300 μm. Figure 12.4.3 shows an example of a typical capillary column.



Figure 12.4.3 . Typical example of a capillary column for gas chromatography. This column is 30 m long with an internal diameter of 247 μm. The interior surface of the capillary has a 0.25 μm coating of the liquid phase.

Capillary columns are of three principal types. In a ***wall-coated open tubular column*** (WCOT) a thin layer of stationary phase, typically 0.25 nm thick, is coated on the capillary's inner wall. In a ***porous-layer open tubular column*** (PLOT), a porous solid support—alumina, silica gel, and molecular sieves are typical examples—is attached to the capillary's inner wall. A ***support-coated open tubular column*** (SCOT) is a PLOT column that includes a liquid stationary phase. Figure 12.4.4 shows the differences between these types of capillary columns.

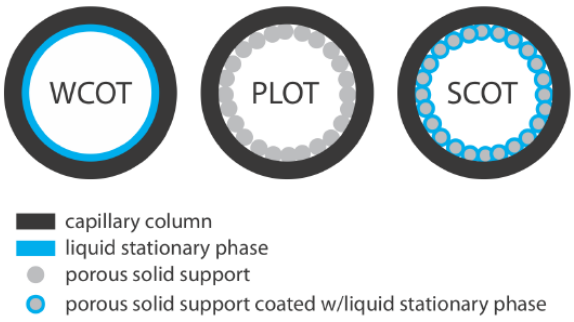


Figure 12.4.4 . Cross sections through the three types of capillary columns.

A capillary column provides a significant improvement in separation efficiency because it has more theoretical plates per meter and is longer than a packed column. For example, the capillary column in Figure 12.4.3 has almost 4300 plates/m, or a total of 129 000 theoretical plates. If we assume a V_{max}/V_{min} ≈ 50, then it has a peak capacity of approximately 350. On the other hand, a packed column can handle a larger sample. Because of its smaller diameter, a capillary column requires a smaller sample, typically less than 10^{-2} μL.

STATIONARY PHASES FOR GAS-LIQUID CHROMATOGRAPHY

Elution order in gas–liquid chromatography depends on two factors: the boiling point of the solutes, and the interaction between the solutes and the stationary phase. If a mixture's components have significantly different boiling points, then the choice of stationary phase is less critical. If two solutes have similar boiling points, then a separation is possible only if the stationary phase selectively interacts with one of the solutes. As a general rule, nonpolar solutes are separated more easily when using a nonpolar stationary phase, and polar solutes are easier to separate when using a polar stationary phase.

There are several important criteria for choosing a stationary phase: it must not react with the solutes, it must be thermally stable, it must have a low volatility, and it must have a polarity that is appropriate for the sample's components. Table 12.4.1 summarizes the properties of several popular stationary phases.

Table 12.4.1 . Selected Examples of Stationary Phases for Gas-Liquid Chromatography

stationary phase	polarity	trade name	temperature limit (°C)	representative applications
squalane	nonpolar	Squalane	150	low-boiling aliphatics hydrocarbons
Apezion L	nonpolar	Apezion L	300	amides, fatty acid methyl esters, terpenoids
polydimethyl siloxane	slightly polar	SE-30	300–350	alkaloids, amino acid derivatives, drugs, pesticides, phenols, steroids
phenylmethyl polysiloxane (50% phenyl, 50% methyl)	moderately polar	OV-17	375	alkaloids, drugs, pesticides, polyaromatic hydrocarbons, polychlorinated biphenyls
trifluoropropylmethyl polysiloxane (50% trifluoropropyl, 50% methyl)	moderately polar	OV-210	275	alkaloids, amino acid derivatives, drugs, halogenated compounds, ketones
cyanopropylphenylmethyl polysiloxane (50%cyanopropyl, 50% phenylmethyl)	polar	OV-225	275	nitriles, pesticides, steroids
polyethylene glycol	polar	Carbowax 20M	225	aldehydes, esters, ethers, phenols

Many stationary phases have the general structure shown in Figure 12.4.5 a. A stationary phase of polydimethyl siloxane, in which all the –R groups are methyl groups, $–CH_3$, is nonpolar and often makes a good first choice for a new separation. The order of elution when using polydimethyl siloxane usually follows the boiling points of the solutes, with lower boiling solutes eluting first. Replacing some of the methyl groups with other substituents increases the stationary phase's polarity and provides greater selectivity. For example, replacing 50% of the $–CH_3$ groups with phenyl groups, $–C_6H_5$, produces a slightly polar stationary phase. Increasing polarity is provided by substituting trifluoropropyl, $–C_3H_6CF$, and cyanopropyl, $–C_3H_6CN$, functional groups, or by using a stationary phase of polyethylene glycol (Figure 12.4.5 b).

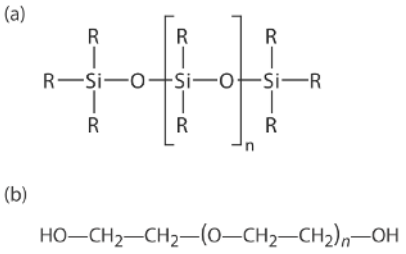


Figure 12.4.5 . General structures of common stationary phases: (a) substituted polysiloxane; (b) polyethylene glycol.

An important problem with all liquid stationary phases is their tendency to elute, or ***bleed*** from the column when it is heated. The temperature limits in Table 12.4.1 minimize this loss of stationary phase. Capillary columns with bonded or cross-linked stationary phases provide superior stability. A bonded stationary phase is attached chemically to the capillary's silica surface. Cross-linking, which is done after the stationary phase is in the capillary column, links together separate polymer chains to provide greater stability.

Another important consideration is the thickness of the stationary phase. From equation 12.3.7 we know that separation efficiency improves with thinner films of stationary phase. The most common thickness is 0.25 μm, although a thicker films is useful for highly volatile solutes, such as gases, because it has a greater capacity for retaining such solutes. Thinner films are used when separating low volatility solutes, such as steroids.

A few stationary phases take advantage of chemical selectivity. The most notable are stationary phases that contain chiral functional groups, which are used to separate enantiomers [Hinshaw, J. V. *LC .GC* **1993**, *11*, 644–648].

SAMPLE INTRODUCTION

Three factors determine how we introduce a sample to the gas chromatograph. First, all of the sample's constituents must be volatile. Second, the analytes must be present at an appropriate concentration. Finally, the physical process of injecting the sample must not degrade the separation. Each of these needs is considered in this section.

PREPARING A VOLATILE SAMPLE

Not every sample can be injected directly into a gas chromatograph. To move through the column, the sample's constituents must be sufficiently volatile. A solute of low volatility, for example, may be retained by the column and continue to elute during the analysis of subsequent samples. A nonvolatile solute will condense at the top of the column, degrading the column's performance.

We can separate a sample's volatile analytes from its nonvolatile components using any of the extraction techniques described in Chapter 7. A liquid–liquid extraction of analytes from an aqueous matrix into methylene chloride or another organic solvent is a common choice. Solid-phase extractions also are used to remove a sample's nonvolatile components.

An attractive approach to isolating analytes is a ***solid-phase microextraction*** (SPME). In one approach, which is illustrated in Figure 12.4.6 , a fused-silica fiber is placed inside a syringe needle. The fiber, which is coated with a thin film of an adsorbent material, such as polydimethyl siloxane, is lowered into the sample by depressing a plunger and is exposed to the sample for a predetermined time. After withdrawing the fiber into the needle, it is transferred to the gas chromatograph for analysis.

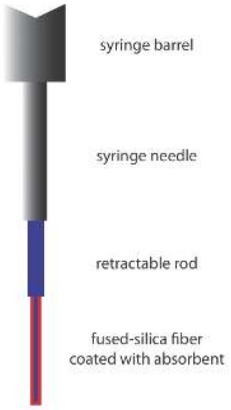


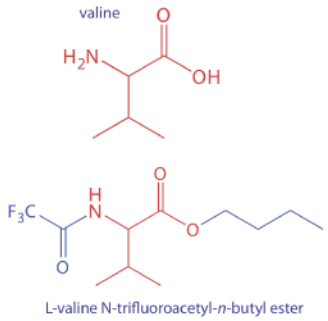
Figure 12.4.6 . Schematic diagram of a solid-phase microextraction device. The absorbent is shown in red.

Two additional methods for isolating volatile analytes are a purge-and-trap and headspace sampling. In a ***purge-and-trap***, we bubble an inert gas, such as He or N_2, through the sample, releasing—or purging—the volatile compounds. These compounds are carried by the purge gas through a trap that contains an absorbent material, such as Tenax, where they are retained. Heating the trap and back-flushing with carrier gas transfers the volatile compounds to the gas chromatograph. In ***headspace sampling*** we place the sample in a closed vial with an overlying air space. After allowing time for the volatile analytes to equilibrate between the sample and the overlying air, we use a syringe to extract a portion of the vapor phase and inject it into the gas chromatograph. Alternatively, we can sample the headspace with an SPME.

Thermal desorption is a useful method for releasing volatile analytes from solids. We place a portion of the solid in a glass-lined, stainless steel tube. After purging with carrier gas to remove any O_2 that might be present, we heat the sample. Volatile analytes are swept from the tube by an inert gas and carried to the GC. Because volatilization is not a rapid process, the volatile analytes often are concentrated at the top of the column by cooling the column inlet below room temperature, a process known as ***cryogenic focusing***. Once volatilization is complete, the column inlet is heated rapidly, releasing the analytes to travel through the column.

> The reason for removing O_2 is to prevent the sample from undergoing an oxidation reaction when it is heated.

To analyze a nonvolatile analyte we must convert it to a volatile form. For example, amino acids are not sufficiently volatile to analyze directly by gas chromatography. Reacting an amino acid, such as valine, with 1-butanol and acetyl chloride produces an esterified amino acid. Subsequent treatment with trifluoroacetic acid gives the amino acid's volatile N-trifluoroacetyl-*n*-butyl ester derivative.



L-valine N-trifluoroacetyl-*n*-butyl ester

ADJUSTING THE ANALYTE'S CONCENTRATION

In an analyte's concentration is too small to give an adequate signal, then we must concentrate the analyte before we inject the sample into the gas chromatograph. A side benefit of many extraction methods is that they often concentrate the analytes. Volatile organic materials isolated from an aqueous sample by a purge-and-trap, for example, are concentrated by as much as 1000×.

If an analyte is too concentrated, it is easy to overload the column, resulting in peak fronting (see Figure 12.2.7) and a poor separation. In addition, the analyte's concentration may exceed the detector's linear response. Injecting less sample or diluting the sample with a volatile solvent, such as methylene chloride, are two possible solutions to this problem.

INJECTING THE SAMPLE

In Chapter 12.3 we examined several explanations for why a solute's band increases in width as it passes through the column, a process we called band broadening. We also introduce an additional source of band broadening if we fail to inject the sample into the minimum possible volume of mobile phase. There are two principal sources of this precolumn band broadening: injecting the sample into a moving stream of mobile phase and injecting a liquid sample instead of a gaseous sample. The design of a gas chromatograph's injector helps minimize these problems.

An example of a simple injection port for a packed column is shown in Figure 12.4.7 . The top of the column fits within a heated injector block, with carrier gas entering from the bottom. The sample is injected through a rubber septum using a microliter syringe, such as the one shown in in Figure 12.4.8 . Injecting the sample directly into the column minimizes band broadening because it mixes the sample with the smallest possible amount of carrier gas. The injector block is heated to a temperature at least 50°C above the boiling point of the least volatile solute, which ensures a rapid vaporization of the sample's components.

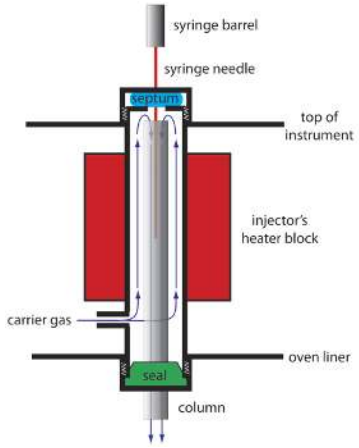


Figure 12.4.7 . Schematic diagram of a heated GC injector port for use with packed columns. The needle pierces a rubber septum and enters into the top of the column, which is located within a heater block.



Figure 12.4.8 . Example of a syringe for injecting samples into a gas chromatograph. This syringe has a maximum capacity of 10 μL with graduations every 0.1 μL.

Because a capillary column's volume is significantly smaller than that for a packed column, it requires a different style of injector to avoid overloading the column with sample. Figure 12.4.9 shows a schematic diagram of a typical split/splitless injector for use with a capillary column.

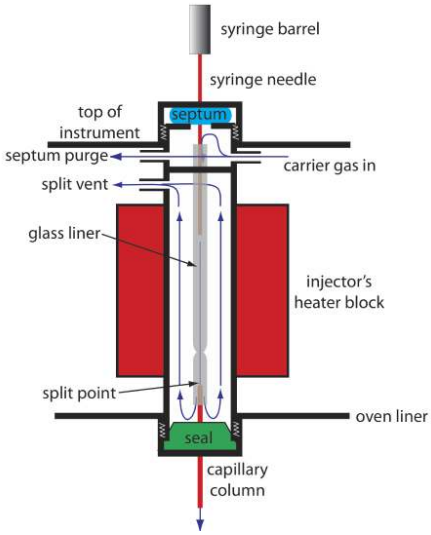


Figure 12.4.9 . Schematic diagram of a split/splitless injection port for use with capillary columns. The needle pierces a rubber septum and enters into a glass liner, which is located within a heater block. In a split injection the split vent is open; the split vent is closed for a splitless injection.

In a ***split injection*** we inject the sample through a rubber septum using a microliter syringe. Instead of injecting the sample directly into the column, it is injected into a glass liner where it mixes with the carrier gas. At the split point, a small fraction of the carrier gas and sample enters the capillary column with the remainder exiting through the split vent. By controlling the flow rate of the carrier gas as it enters the injector, and its flow rate through the septum purge and the split vent, we can control the fraction of sample that enters the capillary column, typically 0.1–10%.

> For example, if the carrier gas flow rate is 50 mL/min, and the flow rates for the septum purge and the split vent are 2 mL/min and 47 mL/min, respectively, then the flow rate through the column is 1 mL/min (= 50 – 2 – 47). The ratio of sample entering the column is 1/50, or 2%.

In a ***splitless injection***, which is useful for trace analysis, we close the split vent and allow all the carrier gas that passes through the glass liner to enter the column—this allows virtually all the sample to enters the column. Because the flow rate through the injector is low, significant precolumn band broadening is a problem. Holding the column's temperature approximately 20–25ºC below the solvent's boiling point allows the solvent to condense at the entry to the capillary column, forming a barrier that traps the solutes. After allowing the solutes to concentrate, the column's temperature is increased and the separation begins.

For samples that decompose easily, an ***on-column injection*** may be necessary. In this method the sample is injected directly into the column without heating. The column temperature is then increased, volatilizing the sample with as low a temperature as is practical.

TEMPERATURE CONTROL

Control of the column's temperature is critical to attaining a good separation when using gas chromatography. For this reason the column is placed inside a thermostated oven (see Figure 12.4.1). In an ***isothermal*** separation we maintain the column at a constant temperature. To increase the interaction between the solutes and the stationary phase, the temperature usually is set slightly below that of the lowest-boiling solute.

One difficulty with an isothermal separation is that a temperature that favors the separation of a low-boiling solute may lead to an unacceptably long retention time for a higher-boiling solute. ***Temperature programming*** provides a solution to this problem. At the beginning of the analysis we set the column's initial temperature below that for the lowest-boiling solute. As the separation progresses, we slowly increase the temperature at either a uniform rate or in a series of steps.

DETECTORS FOR GAS CHROMATOGRAPHY

The final part of a gas chromatograph is the detector. The ideal detector has several desirable features: a low detection limit, a linear response over a wide range of solute concentrations (which makes quantitative work easier), sensitivity for all solutes or selectivity for a specific class of solutes, and an insensitivity to a change in flow rate or temperature.

THERMAL CONDUCTIVITY DETECTOR (TCD)

One of the earliest gas chromatography detectors takes advantage of the mobile phase's thermal conductivity. As the mobile phase exits the column it passes over a tungsten-rhenium wire filament (see Figure 12.4.10 . The filament's electrical resistance depends on its temperature,

which, in turn, depends on the thermal conductivity of the mobile phase. Because of its high thermal conductivity, helium is the mobile phase of choice when using a ***thermal conductivity detector*** (TCD).

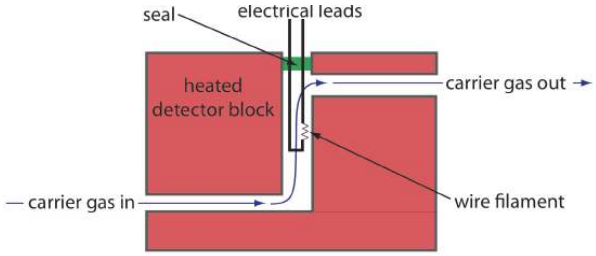


Figure 12.4.10 . Schematic diagram of a thermal conductivity detector showing one cell of a matched pair. The sample cell takes the carrier gas as it elutes from the column. A source of carrier gas that bypasses the column passes through a reference cell.

> Thermal conductivity, as the name suggests, is a measure of how easily a substance conducts heat. A gas with a high thermal conductivity moves heat away from the filament—and, thus, cools the filament—more quickly than does a gas with a low thermal conductivity.

When a solute elutes from the column, the thermal conductivity of the mobile phase in the TCD cell decreases and the temperature of the wire filament, and thus it resistance, increases. A reference cell, through which only the mobile phase passes, corrects for any time-dependent variations in flow rate, pressure, or electrical power, all of which affect the filament's resistance.

Because all solutes affect the mobile phase's thermal conductivity, the thermal conductivity detector is a universal detector. Another advantage is the TCD's linear response over a concentration range spanning 10^4–10^5 orders of magnitude. The detector also is non-destructive, which allows us to recover analytes using a postdetector cold trap. One significant disadvantage of the TCD detector is its poor detection limit for most analytes.

FLAME IONIZATION DETECTOR (FID)

The combustion of an organic compound in an H_2/air flame results in a flame that contains electrons and organic cations, presumably CHO^+. Applying a potential of approximately 300 volts across the flame creates a small current of roughly 10^{-9} to 10^{-12} amps. When amplified, this current provides a useful analytical signal. This is the basis of the popular ***flame ionization detector,*** a schematic diagram of which is shown in Figure 12.4.11 .

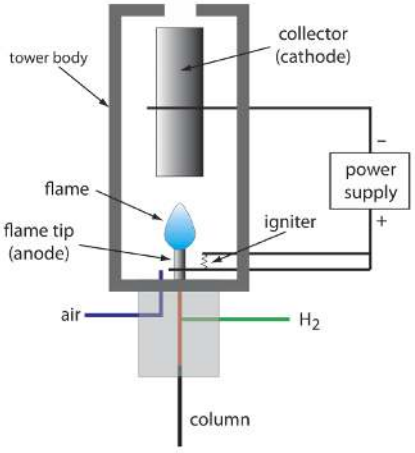


Figure 12.4.11 . Schematic diagram of a flame ionization detector. The eluent from the column mixes with H_2 and is burned in the presence of excess air. Combustion produces a flame that contains electrons and the cation $CHO^{+\cdot}$. Applying a potential between the flame's tip and the collector gives a current that is proportional to the concentration of cations in the flame.

Most carbon atoms—except those in carbonyl and carboxylic groups—generate a signal, which makes the FID an almost universal detector for organic compounds. Most inorganic compounds and many gases, such as H_2O and CO_2, are not detected, which makes the FID detector a useful detector for the analysis of organic analytes in atmospheric and aqueous environmental samples. Advantages of the FID include a detection limit that is approximately two to three orders of magnitude smaller than that for a thermal conductivity detector, and a linear response over 10^6–10^7 orders of magnitude in the amount of analyte injected. The sample, of course, is destroyed when using a flame ionization detector.

ELECTRON CAPTURE DETECTOR (ECD)

The ***electron capture detector*** is an example of a selective detector. As shown in Figure 12.4.12 , the detector consists of a β-emitter, such as ^{63}Ni. The emitted electrons ionize the mobile phase, usually N_2, generating a standing current between a pair of electrodes. When a solute with a high affinity for capturing electrons elutes from the column, the current decreases, which serves as the signal. The ECD is highly selective toward solutes with electronegative functional groups, such as halogens and nitro groups, and is relatively insensitive to amines, alcohols, and hydrocarbons. Although its detection limit is excellent, its linear range extends over only about two orders of magnitude.

> A β-particle is an electron.

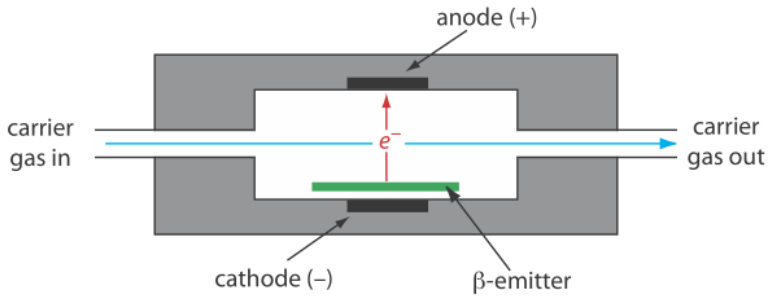


Figure 12.4.12 . Schematic diagram showing an electron capture detector.

MASS SPECTROMETER (MS)

A ***mass spectrometer*** is an instrument that ionizes a gaseous molecule using sufficient energy that the resulting ion breaks apart into smaller ions. Because these ions have different mass-to-charge ratios, it is possible to separate them using a magnetic field or an electrical field. The resulting mass spectrum contains both quantitative and qualitative information about the analyte. Figure 12.4.13 shows a mass spectrum for toluene.

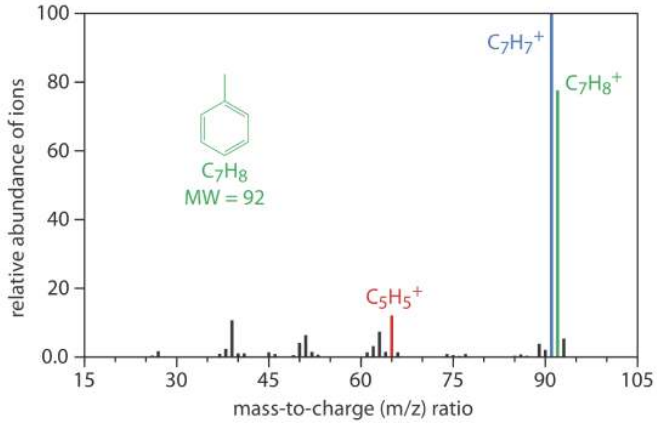


Figure 12.4.13 . Mass spectrum for toluene highlighting the molecular ion in green (m/z=92), and two fragment ions in blue (m/z=91) and in red (m/z= 65). A mass spectrum provides both quantitative and qualitative information: the height of any peak is proportional to the amount of toluene in the mass spectrometer and the fragmentation pattern is unique to toluene.

Figure 12.4.14 shows a block diagram of a typical gas chromatography-mass spectrometer (GC–MS) instrument. The effluent from the column enters the mass spectrometer's ion source in a manner that eliminates the majority of the carrier gas. In the ionization chamber the remaining molecules—a mixture of carrier gas, solvent, and solutes—undergo ionization and fragmentation. The mass spectrometer's mass analyzer separates the ions by their mass-to-charge ratio and a detector counts the ions and displays the mass spectrum.

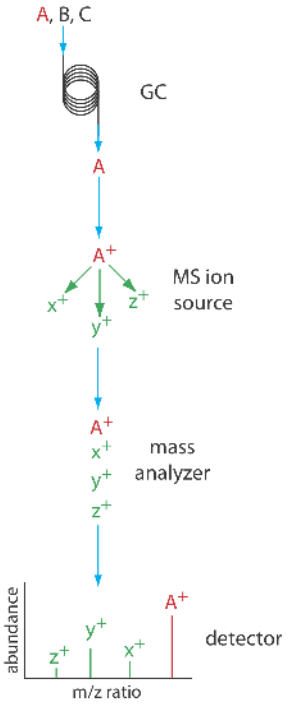


Figure 12.4.14 . Block diagram of GC– MS. A three component mixture enters the GC. When component A elutes from the column, it enters the MS ion source and ionizes to form the parent ion and several fragment ions. The ions enter the mass analyzer, which separates them by their mass-to-charge ratio, providing the mass spectrum shown at the detector.

There are several options for monitoring a chromatogram when using a mass spectrometer as the detector. The most common method is to continuously scan the entire mass spectrum and report the total signal for all ions that reach the detector during each scan. This total ion scan provides universal detection for all analytes. We can achieve some degree of selectivity by monitoring one or more specific mass-to-charge ratios, a process called selective-ion monitoring. A mass spectrometer provides excellent detection limits, typically 25 fg to 100 pg, with a linear range of 10^5 orders of magnitude. Because we continuously record the mass spectrum of the column's eluent, we can go back and examine the mass spectrum for any time increment. This is a distinct advantage for GC–MS because we can use the mass spectrum to help identify a mixture's components.

> For more details on mass spectrometry see Introduction to Mass Spectrometry by Michael Samide and Olujide Akinbo, a resource that is part of the Analytical Sciences Digital Library.

OTHER DETECTORS

Two additional detectors are similar in design to a flame ionization detector. In the flame photometric detector, optical emission from phosphorous and sulfur provides a detector selective for compounds that contain these elements. The thermionic detector responds to compounds that contain nitrogen or phosphorous.

A Fourier transform infrared spectrophotometer (FT–IR) also can serve as a detector. In GC–FT–IR, effluent from the column flows through an optical cell constructed from a 10–40 cm Pyrex tube with an internal diameter of 1–3 mm. The cell's interior surface is coated with a reflecting layer of gold. Multiple reflections of the source radiation as it is transmit- ted through the cell increase the optical path length through the sample. As is the case with GC–MS, an FT–IR detector continuously records the column eluent's spectrum, which allows us to examine the IR spectrum for any time increment.

> See Section 10.3 for a discussion of FT-IR spectroscopy and instrumentation.

QUANTITATIVE APPLICATIONS

Gas chromatography is widely used for the analysis of a diverse array of samples in environmental, clinical, pharmaceutical, biochemical, forensic, food science and petrochemical laboratories. Table 12.4.2 provides some representative examples of applications.

Table 12.4.2 . Representative Applications of Gas Chromatography

area	applications
environmental analysis	green house gases (CO_2, CH_4, NO_x) in air pesticides in water, wastewater, and soil vehicle emissions trihalomethanes in drinking water
clinical analysis	drugs blood alcohols
forensic analysis	analysis of arson accelerants detection of explosives
consumer products	volatile organics in spices and fragrances trace organics in whiskey monomers in latex paint
petrochemical and chemical industry	purity of solvents refinery gas composition of gasoline

QUANTITATIVE CALCULATIONS

In a GC analysis the area under the peak is proportional to the amount of analyte injected onto the column. A peak's area is determined by integration, which usually is handled by the instrument's computer or by an electronic integrating recorder. If two peak are resolved fully, the determination of their respective areas is straightforward.

> Before electronic integrating recorders and computers, two methods were used to find the area under a curve. One method used a manual planimeter; as you use the planimeter to trace an object's perimeter, it records the area. A second approach for finding a peak's area is the cut-and-weigh method. The chromatogram is recorded on a piece of paper and each peak of interest is cut out and weighed. Assuming the paper is uniform in thickness and density of fibers, the ratio of weights for two peaks is the same as the ratio of areas. Of course, this approach destroys your chromatogram.

Overlapping peaks, however, require a choice between one of several options for dividing up the area shared by the two peaks (Figure 12.4.15). Which method we use depends on the relative size of the two peaks and their resolution. In some cases, the use of peak heights provides more accurate results [(a) Bicking, M. K. L. Chromatography Online, April 2006; (b) Bicking, M. K. L. Chromatography Online, June 2006].

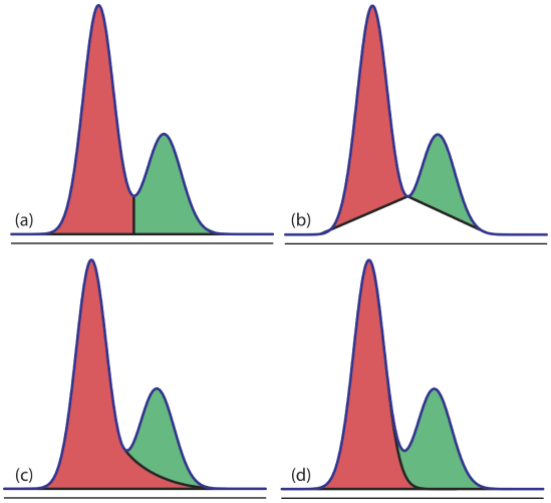


Figure 12.4.15 . Four methods for determining the areas under two overlapping chromatographic peaks: (a) the drop method; (b) the valley method; (c) the exponential skim method; and (d) the Gaussian skim method. Other methods for determining areas also are available.

For quantitative work we need to establish a calibration curve that relates the detector's response to the analyte's concentration. If the injection volume is identical for every standard and sample, then an external standardization provides both accurate and precise results. Unfortunately,even under the best conditions the relative precision for replicate injections may differ by 5%; often it is substantially worse. For quantitative work that requires high accuracy and precision, the use of internal standards is recommended.

> To review the method of internal standards, see Chapter 5.3.

EXAMPLE 12.4.1

Marriott and Carpenter report the following data for five replicate injections of a mixture that contains 1% v/v methyl isobutyl ketone and 1% v/v *p*-xylene in dichloromethane [Marriott, P. J.; Carpenter, P. D. *J. Chem. Educ.* **1996**, *73*, 96–99].

injection	peak	peak area (arb. units)
I	1	48075
	2	78112
II	1	85829
	2	135404
III	1	84136
	2	132332
IV	1	71681
	2	112889
V	1	58054
	2	91287

Assume that *p*-xylene (peak 2) is the analyte, and that methyl isobutyl ketone (peak 1) is the internal standard. Determine the 95% confidence interval for a single-point standardization with and without using the internal standard.

Solution

For a single-point external standardization we ignore the internal standard and determine the relationship between the peak area for *p*-xylene, A_2, and the concentration, C_2, of *p*-xylene.

$$A_2 = kC_2$$

Substituting the known concentration for *p*-xylene (1% v/v) and the appropriate peak areas, gives the following values for the constant *k*.

$$78112 \quad 135404 \quad 132332 \quad 112889 \quad 91287$$

The average value for *k* is 110 000 with a standard deviation of 25 100 (a relative standard deviation of 22.8%). The 95% confidence interval is

$$\mu = \overline{X} \pm \frac{ts}{\sqrt{n}} = 111000 \pm \frac{(2.78)(25100)}{\sqrt{5}} = 111000 \pm 31200$$

For an internal standardization, the relationship between the analyte's peak area, A_2, the internal standard's peak area, A_1, and their respective concentrations, C_2 and C_1, is

$$\frac{A_2}{A_1} = k\frac{C_2}{C_1}$$

Substituting in the known concentrations and the appropriate peak areas gives the following values for the constant *k*.

$$1.5917 \quad 1.5776 \quad 1.5728 \quad 1.5749 \quad 1.5724$$

The average value for *k* is 1.5779 with a standard deviation of 0.0080 (a relative standard deviation of 0.507%). The 95% confidence interval is

$$\mu = \overline{X} \pm \frac{ts}{\sqrt{n}} = 1.5779 \pm \frac{(2.78)(0.0080)}{\sqrt{5}} = 1.5779 \pm 0.0099$$

Although there is a substantial variation in the individual peak areas for this set of replicate injections, the internal standard compensates for these variations, providing a more accurate and precise calibration.

EXERCISE 12.4.1

Figure 12.4.16 shows chromatograms for five standards and for one sample. Each standard and sample contains the same concentration of an internal standard, which is 2.50 mg/mL. For the five standards, the concentrations of analyte are 0.20 mg/mL, 0.40 mg/mL, 0.60 mg/mL, 0.80 mg/mL, and 1.00 mg/mL, respectively. Determine the concentration of analyte in the sample by (a) ignoring the internal standards and creating an external standards calibration curve, and by (b) creating an internal standard calibration curve. For each approach, report the analyte's concentration and the 95% confidence interval. Use peak heights instead of peak areas.

Answer

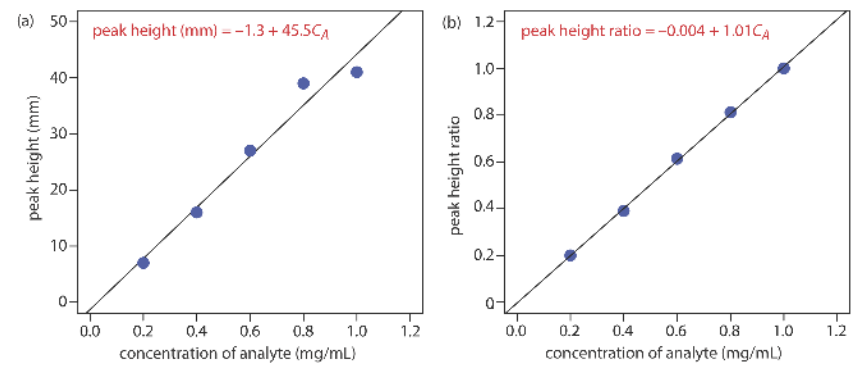
The following table summarizes my measurements of the peak heights for each standard and the sample, and their ratio (although your absolute values for peak heights will differ from mine, depending on the size of your monitor or printout, your relative peak height ratios should be similar to mine).

[standard] (mg/mL)	peak height of standard (mm)	peak height of analyte (mm)	peak height ratio
0.20	35	7	0.20
0.40	41	16	0.39
0.60	44	27	0.61
0.80	48	39	0.81
1.00	41	41	1.00
sample	39	21	0.54

Figure (a) shows the calibration curve and the calibration equation when we ignore the internal standard. Substituting the sample's peak height into the calibration equation gives the analyte's concentration in the sample as 0.49 mg/mL. The 95% confidence interval is ±0.24 mg/mL. The calibration curve shows quite a bit of scatter in the data because of uncertainty in the injection volumes.

Figure (b) shows the calibration curve and the calibration equation when we include the internal standard. Substituting the sample's peak height ratio into the calibration equation gives the analyte's concentration in the sample as 0.54 mg/mL. The 95% confidence interval is ±0.04 mg/mL.

To review the use of Excel or R for regression calculations and confidence intervals, see Chapter 5.5.



The data for this exercise were created so that the analyte's actual concentration is 0.55 mg/mL. Given the resolution of my ruler's scale, my answer is pretty reasonable. Your measurements may be slightly different, but your answers should be close to the actual values.

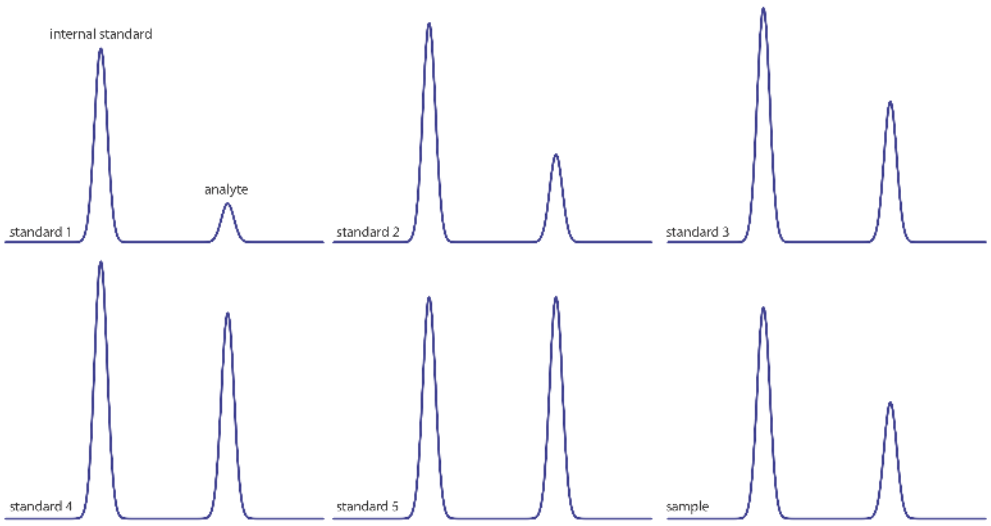


Figure 12.4.16 . Chromatograms for Practice Exercise 12.5.

https://chem.libretexts.org/@go/page/540083

QUALITATIVE APPLICATIONS

In addition to a quantitative analysis, we also can use chromatography to identify the components of a mixture. As noted earlier, when using an FT–IR or a mass spectrometer as the detector we have access to the eluent's full spectrum for any retention time. By interpreting the spectrum or by searching against a library of spectra, we can identify the analyte responsible for each chromatographic peak.

> In addition to identifying the component responsible for a particular chromatographic peak, we also can use the saved spectra to evaluate peak purity. If only one component is responsible for a chromatographic peak, then the spectra should be identical throughout the peak's elution. If a spectrum at the beginning of the peak's elution is different from a spectrum taken near the end of the peak's elution, then at least two components are co-eluting.

When using a nonspectroscopic detector, such as a flame ionization detector, we must find another approach if we wish to identify the components of a mixture. One approach is to spike a sample with the suspected compound and look for an increase in peak height. We also can compare a peak's retention time to the retention time for a known compound if we use identical operating conditions.

Because a compound's retention times on two identical columns are not likely to be the same—differences in packing efficiency, for example, will affect a solute's retention time on a packed column—creating a table of standard retention times is not possible. ***Kovat's retention index*** provides one solution to the problem of matching retention times. Under isothermal conditions, the adjusted retention times for normal alkanes increase logarithmically. Kovat defined the retention index, I, for a normal alkane as 100 times the number of carbon atoms. For example, the retention index is 400 for butane, C_4H_{10}, and 500 for pentane, C_5H_{12}. To determine the a compound's retention index, I_{cpd}, we use the following formula

$$I_{cpd} = 100 \times \frac{\log t'_{r,cpd} - \log t'_{r,x}}{\log t'_{r,x+1} - \log t'_{r,x}} + I_x \tag{12.8.1}$$

where $t'_{r,cpd}$ is the compound's adjusted retention time, $t'_{r,x}$ and $t'_{r,x+1}$ are the adjusted retention times for the normal alkanes that elute immediately before the compound and immediately after the compound, respectively, and I_x is the retention index for the normal alkane that elutes immediately before the compound. A compound's retention index for a particular set of chromatographic conditions—stationary phase, mobile phase, column type, column length, temperature, etc.—is reasonably consistent from day- to-day and between different columns and instruments.

> Tables of Kovat's retention indices are available; see, for example, the NIST Chemistry Webbook. A search for toluene returns 341 values of I for over 20 different stationary phases, and for both packed columns and capillary columns.

✔ EXAMPLE 12.4.2

In a separation of a mixture of hydrocarbons the following adjusted retention times are measured: 2.23 min for propane, 5.71 min for isobutane, and 6.67 min for butane. What is the Kovat's retention index for each of these hydrocarbons?

Solution

Kovat's retention index for a normal alkane is 100 times the number of carbons; thus, for propane, I = 300 and for butane, I = 400. To find Kovat's retention index for isobutane we use Equation 12.8.1.

$$I_{\text{isobutane}} = 100 \times \frac{\log(5.71) - \log(2.23)}{\log(6.67) - \log(2.23)} + 300 = 386$$

? EXERCISE 12.4.2

When using a column with the same stationary phase as in Example 12.4.2 , you find that the retention times for propane and butane are 4.78 min and 6.86 min, respectively. What is the expected retention time for isobutane?

Answer

Because we are using the same column we can assume that isobutane's retention index of 386 remains unchanged. Using Equation 12.8.1, we have

$$386 = 100 \times \frac{\log x - \log(4.78)}{\log(6.86) - \log(4.78)} + 300$$

where x is the retention time for isobutane. Solving for x, we find that

$$0.86 = \frac{\log x - \log(4.78)}{\log(6.86) - \log(4.78)}$$

$$0.135 = \log x - 0.679$$

$$0.814 = \log x$$

$$x = 6.52$$

the retention time for isobutane is 6.5 min.

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of trihalomethanes in drinking water provides an instructive example of a typical procedure. The description here is based on a Method 6232B in *Standard Methods for the Examination of Water and Wastewater*, 20th Ed., American Public Health Association: Washing- ton, DC, 1998.

REPRESENTATIVE METHOD 12.4.1: DETERMINATION OF TRIHALOMETHANES IN DRINKING WATER

Description of Method

Trihalomethanes, such as chloroform, $CHCl_3$, and bromoform, $CHBr_3$, are found in most chlorinated waters. Because chloroform is a suspected carcinogen, the determination of trihalomethanes in public drinking water supplies is of considerable importance. In this method the trihalomethanes $CHCl_3$, $CHBrCl_2$, $CHBr_2Cl$, and $CHBr_3$ are isolated using a liquid–liquid extraction with pentane and determined using a gas chromatograph equipped with an electron capture detector.

Procedure

Collect the sample in a 40-mL glass vial equipped with a screw-cap lined with a TFE-faced septum. Fill the vial until it overflows, ensuring that there are no air bubbles. Add 25 mg of ascorbic acid as a reducing agent to quench the further production of trihalomethanes. Seal the vial and store the sample at 4°C for no longer than 14 days.

Prepare a standard stock solution for each trihalomethane by placing 9.8 mL of methanol in a 10-mL volumetric flask. Let the flask stand for 10 min, or until all surfaces wetted with methanol are dry. Weigh the flask to the nearest ±0.1 mg. Using a 100-µL syringe, add 2 or more drops of trihalomethane to the volumetric flask, allowing each drop to fall directly into the methanol. Reweigh the flask before diluting to volume and mixing. Transfer the solution to a 40-mL glass vial equipped with a TFE-lined screw-top and report the concentration in µg/mL. Store the stock solutions at –10 to –20°C and away from the light.

Prepare a multicomponent working standard from the stock standards by making appropriate dilutions of the stock solution with methanol in a volumetric flask. Choose concentrations so that calibration standards (see below) require no more than 20 µL of working standard per 100 mL of water.

Using the multicomponent working standard, prepare at least three, but preferably 5–7 calibration standards. At least one standard must be near the detection limit and the standards must bracket the expected concentration of trihalomethanes in the samples. Using an appropriate volumetric flask, prepare the standards by injecting at least 10 µL of the working standard below the surface of the water and dilute to volume. Gently mix each standard three times only. Discard the solution in the neck of the volumetric flask and then transfer the remaining solution to a 40-mL glass vial with a TFE-lined screw-top. If the standard has a headspace, it must be analyzed within 1 hr; standards without a headspace may be held for up to 24 hr.

Prepare an internal standard by dissolving 1,2-dibromopentane in hexane. Add a sufficient amount of this solution to pentane to give a final concentration of 30 µg 1,2-dibromopentane/L.

To prepare the calibration standards and samples for analysis, open the screw top vial and remove 5 mL of the solution. Recap the vial and weigh to the nearest ±0.1 mg. Add 2.00 mL of pentane (with the internal standard) to each vial and shake vigorously for 1 min. Allow the two phases to separate for 2 min and then use a glass pipet to transfer at least 1 mL of the pentane (the upper phase) to a 1.8-mL screw top sample vial equipped with a TFE septum, and store at 4°C until you are ready to inject them into the GC. After emptying, rinsing, and drying the sample's original vial, weigh it to the nearest ±0.1 mg and calculate the sample's weight to ±0.1 g. If the density is 1.0 g/mL, then the sample's weight is equivalent to its volume.

Inject a 1–5 µL aliquot of the pentane extracts into a GC equipped with a 2-mm ID, 2-m long glass column packed with a stationary phase of 10% squalane on a packing material of 80/100 mesh Chromosorb WAW. Operate the column at 67°C and a flow rate of 25 mL/min.

A variety of other columns can be used. Another option, for example, is a 30-m fused silica column with an internal diameter of 0.32 mm and a 1 µm coating of the stationary phase DB-1. A linear flow rate of 20 cm/s is used with the following temperature program: hold for 5 min at 35°C; increase to 70°C at 10°C/min; increase to 200°C at 20°C/min.

Questions

1. A simple liquid–liquid extraction rarely extracts 100% of the analyte. How does this method account for incomplete extractions?

Because we use the same extraction procedure for the samples and the standards, we reasonably expect that the extraction efficiency is the same for all samples and standards; thus, the relative amount of analyte in any two samples or standards is unaffected by an incomplete extraction.

2. Water samples are likely to contain trace amounts of other organic compounds, many of which will extract into pentane along with the trihalomethanes. A short, packed column, such as the one used in this method, generally does not do a particularly good job of resolving chromatographic peaks. Why do we not need to worry about these other compounds?

An electron capture detector responds only to compounds, such as the trihalomethanes, that have electronegative functional groups. Because an electron capture detector will not respond to most of the potential interfering compounds, the chromatogram will have relatively few peaks other than those for the trihalomethanes and the internal standard.

3. Predict the order in which the four analytes elute from the GC column.

Retention time should follow the compound's boiling points, eluting from the lowest boiling point to the highest boiling points. The expected elution order is $CHCl_3$ (61.2°C), $CHCl_2Br$ (90°C), $CHClBr_2$ (119°C), and $CHBr_3$ (149.1°C).

4. Although chloroform is an analyte, it also is an interferent because it is present at trace levels in the air. Any chloroform present in the laboratory air, for example, may enter the sample by diffusing through the sample vial's silicon septum. How can we determine whether samples are contaminated in this manner?

A sample blank of trihalomethane-free water is kept with the samples at all times. If the sample blank shows no evidence for chloroform, then we can safely assume that the samples also are free from contamination.

5. Why is it necessary to collect samples without a headspace (a layer of air that overlays the liquid) in the sample vial?

Because trihalomethanes are volatile, the presence of a headspace allows for the loss of analyte from the sample to the headspace, resulting in a negative determinate error.

6. In preparing the stock solution for each trihalomethane, the procedure specifies that we add two or more drops of the pure compound by dropping them into a volumetric flask that contains methanol. When preparing the calibration standards, however, the working standard must be injected below the surface of the methanol. Explain the reason for this difference.

When preparing a stock solution, the potential loss of the volatile trihalomethane is unimportant because we determine its concentration by weight after adding it to the methanol and diluting to volume. When we prepare the calibration standard, however, we must ensure that the addition of trihalomethane is quantitative; thus, we inject it below the surface to avoid the potential loss of analyte.

EVALUATION

SCALE OF OPERATION

Gas chromatography is used to analyze analytes present at levels ranging from major to ultratrace components. Depending on the detector, samples with major and minor analytes may need to be diluted before analysis. The thermal conductivity and flame ionization detectors can handle larger amounts of analyte; other detectors, such as an electron capture detector or a mass spectrometer, require substantially smaller amounts of analyte. Although the injection volume for gas chromatography is quite small—typically about a microliter—the amount of available sample must be sufficient that the injection is a representative subsample. For a trace analyte, the actual amount of injected analyte is often in the picogram range. Using Representative Method 12.4.1 as an example, a 3.0-μL injection of 1 μg/L $CHCl_3$ is equivalent to 15 pg of $CHCl_3$, assuming a 100% extraction efficiency.

ACCURACY

The accuracy of a gas chromatographic method varies substantially from sample-to-sample. For routine samples, accuracies of 1–5% are common. For analytes present at very low concentration levels, for samples with complex matrices, or for samples that require significant processing before analysis, accuracy may be substantially poorer. In the analysis for trihalomethanes described in Representative Method 12.4.1, for example, determinate errors as large as ±25% are possible.

PRECISION

The precision of a gas chromatographic analysis includes contributions from sampling, sample preparation, and the instrument. The relative standard deviation due to the instrument typically is 1–5%, although it can be significantly higher. The principal limitations are detector noise, which affects the determination of peak area, and the reproducibility of injection volumes. In quantitative work, the use of an internal standard compensates for any variability in injection volumes.

SENSITIVITY

In a gas chromatographic analysis, sensitivity is determined by the detector's characteristics. Of particular importance for quantitative work is the detector's linear range; that is, the range of concentrations over which a calibration curve is linear. Detectors with a wide linear range, such as the thermal conductivity detector and the flame ionization detector, can be used to analyze samples over a wide range of concentrations without adjusting operating conditions. Other detectors, such as the electron capture detector, have a much narrower linear range.

SELECTIVITY

Because it combines separation with analysis, chromatographic methods provide excellent selectivity. By adjusting conditions it usually is possible to design a separation so that the analytes elute by themselves, even when the mixture is complex. Additional selectivity is obtained by using a detector, such as the electron capture detector, that does not respond to all compounds.

TIME, COST, AND EQUIPMENT

Analysis time can vary from several minutes for samples that contain only a few constituents, to more than an hour for more complex samples. Preliminary sample preparation may substantially increase the analysis time. Instrumentation for gas chromatography ranges in price from inexpensive (a few thousand dollars) to expensive (>$50,000). The more expensive models are designed for capillary columns, include a variety of injection options, and use more sophisticated detectors, such as a mass spectrometer, or include multiple detectors. Packed columns typically cost <$200, and the cost of a capillary column is typically $300–$1000.

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12.9: HIGH-PERFORMANCE LIQUID CHROMATOGRAPHY

In ***high-performance liquid chromatography*** (HPLC) we inject the sample, which is in solution form, into a liquid mobile phase. The mobile phase carries the sample through a packed or capillary column that separates the sample's components based on their ability to partition between the mobile phase and the stationary phase. Figure 12.5.1 shows an example of a typical HPLC instrument, which has several key components: reservoirs that store the mobile phase; a pump for pushing the mobile phase through the system; an injector for introducing the sample; a column for separating the sample into its component parts; and a detector for monitoring the eluent as it comes off the column. Let's consider each of these components.

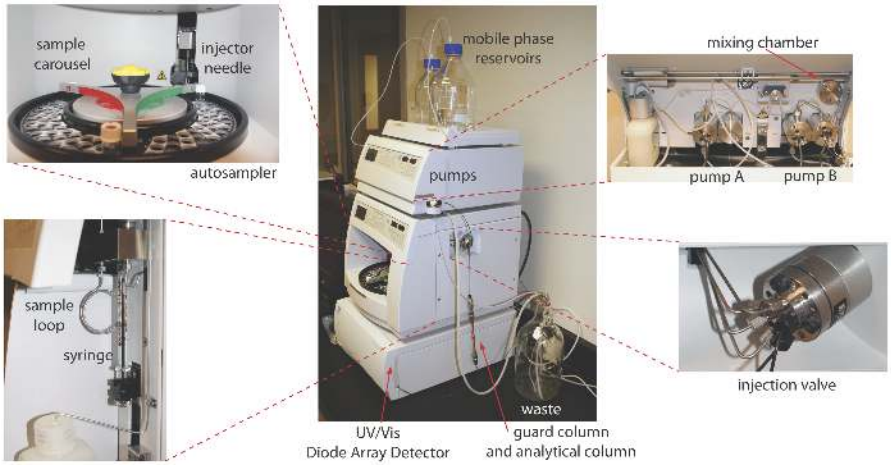


Figure 12.5.1 . Example of a typical high-performance liquid chromatograph with insets showing the pumps that move the mobile phase through the system and the plumbing used to inject the sample into the mobile phase. This particular instrument includes an autosampler. An instrument in which samples are injected manually does not include the features shown in the two left-most insets, and has a different style of loop injection valve.

A solute's retention time in HPLC is determined by its interaction with the stationary phase and the mobile phase. There are several different types of solute/stationary phase interactions, including liquid–solid adsorption, liquid–liquid partitioning, ion-exchange, and size-exclusion. This chapter deals exclusively with HPLC separations based on liquid–liquid partitioning. Other forms of liquid chromatography receive consideration in Chapter 12.6.

HPLC COLUMNS

An HPLC typically includes two columns: an analytical column, which is responsible for the separation, and a guard column that is placed before the analytical column to protect it from contamination.

ANALYTICAL COLUMNS

The most common type of HPLC column is a stainless steel tube with an internal diameter between 2.1 mm and 4.6 mm and a length between 30 mm and 300 mm (Figure 12.5.2). The column is packed with 3–10 µm porous silica particles with either an irregular or a spherical shape. Typical column efficiencies are 40000–60000 theoretical plates/m. Assuming a V_{max}/V_{min} of approximately 50, a 25-cm column with 50 000 plates/m has 12 500 theoretical plates and a peak capacity of 110.



Figure 12.5.2 . Typical packed column for HPLC. This particular column has an internal diameter of 4.6 mm and a length of 150 mm, and is packed with 5 µm particles coated with stationary phase.

Capillary columns use less solvent and, because the sample is diluted to a lesser extent, produce larger signals at the detector. These columns are made from fused silica capillaries with internal diameters from 44–200 µm and lengths of 50–250 mm. Capillary columns packed with 3–5 µm particles have been prepared with column efficiencies of up to 250 000 theoretical plates [Novotony, M. *Science*, **1989**, *246*, 51–57].

One limitation to a packed capillary column is the back pressure that develops when pumping the mobile phase through the small interstitial spaces between the particulate micron-sized packing material (Figure 12.5.3). Because the tubing and fittings that carry the mobile phase have pressure limits, a higher back pressure requires a lower flow rate and a longer analysis time. Monolithic columns, in which the solid

support is a single, porous rod, offer column efficiencies equivalent to a packed capillary column while allowing for faster flow rates. A monolithic column—which usually is similar in size to a conventional packed column, although smaller, capillary columns also are available—is prepared by forming the mono- lithic rod in a mold and covering it with PTFE tubing or a polymer resin. Monolithic rods made of a silica-gel polymer typically have macropores with diameters of approximately 2 μm and mesopores—pores within the macropores—with diameters of approximately 13 nm [Cabrera, K. Chromatography Online, April 1, 2008].

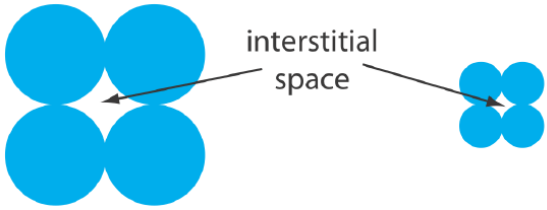


Figure 12.5.3 . The packing of smaller particles creates smaller interstitial spaces than the packing of larger particles. Although reducing particle size by 2× increases efficiency by a factor of 1.4, it also produces a 4-fold increase in back pressure.

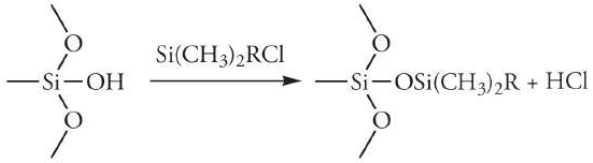
GUARD COLUMNS

Two problems tend to shorten the lifetime of an analytical column. First, solutes that bind irreversibly to the stationary phase degrade the column's performance by decreasing the amount of stationary phase available for effecting a separation. Second, particulate material injected with the sample may clog the analytical column. To minimize these problems we place a guard column before the analytical column. A Guard column usually contains the same particulate packing material and stationary phase as the analytical column, but is significantly shorter and less expensive—a length of 7.5 mm and a cost one-tenth of that for the corresponding analytical column is typical. Because they are intended to be sacrificial, guard columns are replaced regularly.

> If you look closely at Figure 12.5.1 , you will see the small guard column just above the analytical column.

STATIONARY PHASES FOR LIQUID-LIQUID CHROMATOGRAPHY

In liquid–liquid chromatography the stationary phase is a liquid film coated on a packing material, typically 3–10 μm porous silica particles. Because the stationary phase may be partially soluble in the mobile phase, it may elute, or bleed from the column over time. To prevent the loss of stationary phase, which shortens the column's lifetime, it is bound covalently to the silica particles. ***Bonded stationary phases*** are created by reacting the silica particles with an organochlorosilane of the general form $Si(CH_3)_2RCl$, where R is an alkyl or substituted alkyl group.



To prevent unwanted interactions between the solutes and any remaining –SiOH groups, $Si(CH_3)_3Cl$ is used to convert unreacted sites to $-SiOSi(CH_3)_3$; such columns are designated as end-capped.

The properties of a stationary phase depend on the organosilane's alkyl group. If R is a polar functional group, then the stationary phase is polar. Examples of polar stationary phases include those where R contains a cyano ($–C_2H_4CN$), a diol ($–C_3H_6OCH_2CHOHCH_2OH$), or an amino ($–C_3H_6NH_2$) functional group. Because the stationary phase is polar, the mobile phase is a nonpolar or a moderately polar solvent. The combination of a polar stationary phase and a nonpolar mobile phase is called ***normal- phase chromatography***.

In ***reversed-phase chromatography***, which is the more common form of HPLC, the stationary phase is nonpolar and the mobile phase is polar. The most common nonpolar stationary phases use an organochlorosilane where the R group is an *n*-octyl (C_8) or *n*-octyldecyl (C_{18}) hydrocarbon chain. Most reversed-phase separations are carried out using a buffered aqueous solution as a polar mobile phase, or using other polar solvents, such as methanol and acetonitrile. Because the silica substrate may undergo hydrolysis in basic solutions, the pH of the mobile phase must be less than 7.5.

> It seems odd that the more common form of liquid chromatography is identified as reverse-phase instead of normal phase. You might recall that one of the earliest examples of chromatography was Mikhail Tswett's separation of plant pigments using a polar column of calcium carbonate and a nonpolar mobile phase of petroleum ether. The assignment of normal and reversed, therefore, is all about precedence.

MOBILE PHASES

The elution order of solutes in HPLC is governed by polarity. For a normal-phase separation, a solute of lower polarity spends proportionally less time in the polar stationary phase and elutes before a solute that is more polar. Given a particular stationary phase, retention times in normal-phase HPLC are controlled by adjusting the mobile phase's properties. For example, if the resolution between two solutes is poor, switching to a less polar mobile phase keeps the solutes on the column for a longer time and provides more opportunity for their separation. In reversed-phase HPLC the order of elution is the opposite that in a normal-phase separation, with more polar solutes eluting first. Increasing the polarity of the mobile phase leads to longer retention times. Shorter retention times require a mobile phase of lower polarity.

CHOOSING A MOBILE PHASE: USING THE POLARITY INDEX

There are several indices that help in selecting a mobile phase, one of which is the polarity index [Snyder, L. R.; Glajch, J. L.; Kirkland, J. J. *Practical HPLC Method Development*, Wiley-Inter- science: New York, 1988]. Table 12.5.1 provides values of the polarity index, P', for several common mobile phases, where larger values of P' correspond to more polar solvents. Mixing together two or more mobile phases—assuming they are miscible—creates a mobile phase of intermediate polarity. For example, a binary mobile phase made by combining solvent *A* and solvent *B* has a polarity index, P'_{AB}, of

$$P'_{AB} = \Phi_A P'_A + \Phi_B P'_B \tag{12.9.1}$$

where P'_A and P'_B are the polarity indices for solvents *A* and *B*, and Φ_A and Φ_B are the volume fractions for the two solvents.

Table 12.5.1 . Properties of HPLC Mobile Phases

mobile phase	polarity index (P')	UV cutoff (nm)
cyclohexane	0.04	210
n-hexane	0.1	210
carbon tetrachloride	1.6	265
i-propyl ether	2.4	220
toluene	2.4	286
diethyl ether	2.8	218
tetrahydrofuran	4.0	220
ethanol	4.3	210
ethyl acetate	4.4	255
dioxane	4.8	215
methanol	5.1	210
acetonitrile	5.8	190
water	10.2	—

EXAMPLE 12.5.1

A reversed-phase HPLC separation is carried out using a mobile phase of 60% v/v water and 40% v/v methanol. What is the mobile phase's polarity index?

Solution

Using Equation 12.9.1 and the values in Table 12.5.1 , the polarity index for a 60:40 water–methanol mixture is

$$P'_{AB} = \Phi_{\text{water}} P'_{\text{water}} + \Phi_{\text{methanol}} P'_{\text{methanol}}$$

$$P'_{AB} = 0.60 \times 10.2 + 0.40 \times 5.1 = 8.2$$

EXERCISE 12.5.1

Suppose you need a mobile phase with a polarity index of 7.5. Explain how you can prepare this mobile phase using methanol and water.

Answer

If we let *x* be the fraction of water in the mobile phase, then 1 – *x* is the fraction of methanol. Substituting these values into Equation 12.9.1 and solving for *x*

$$7.5 = 10.2x + 5.1(1 - x)$$

$$7.5 = 10.2x + 5.1 - 5.1x$$

$$2.4 = 5.1x$$

gives *x* as 0.47. The mobile phase is 47% v/v water and 53% v/v methanol.

As a general rule, a two unit change in the polarity index corresponds to an approximately 10-fold change in a solute's retention factor. Here is a simple example. If a solute's retention factor, *k*, is 22 when using water as a mobile phase (P' = 10.2), then switching to a mobile phase of 60:40 water–methanol (P' = 8.2) decreases *k* to approximately 2.2. Note that the retention factor becomes smaller because we are switching from a more polar mobile phase to a less polar mobile phase in a reversed-phase separation.

CHOOSING A MOBILE PHASE: ADJUSTING SELECTIVITY

Changing the mobile phase's polarity index changes a solute's retention factor. As we learned in Chapter 12.3, however, a change in *k* is not an effective way to improve resolution when the initial value of *k* is greater than 10. To effect a better separation between two solutes we must improve the selectivity factor, α. There are two common methods for increasing α: adding a reagent to the mobile phase that reacts with the solutes in a secondary equilibrium reaction or switching to a different mobile phase.

Taking advantage of a secondary equilibrium reaction is a useful strategy for improving a separation [(a) Foley, J. P. *Chromatography*, **1987**, *7*, 118–128; (b) Foley, J. P.; May, W. E. Anal. Chem. 1987, 59, 102–109; (c) Foley, J. P.; May, W. E. Anal. Chem. 1987, 59, 110–115]. Figure 12.3.3, which we considered earlier in this chapter, shows the reversed-phase separation of four weak acids—benzoic acid, terephthalic acid, *p*-aminobenzoic acid, and *p*-hydroxybenzoic acid—on a nonpolar C_{18} column using an aqueous buffer of acetic acid and sodium acetate as the mobile phase. The retention times for these weak acids are shorter when using a less acidic mobile phase because each solute is present in an anionic, weak base form that is less soluble in the nonpolar stationary phase. If the mobile phase's pH is sufficiently acidic, the solutes are present as neutral weak acids that are more soluble in the stationary phase and take longer to elute. Because the weak acid solutes do not have identical pK_a values, the pH of the mobile phase has a different effect on each solute's retention time, allowing us to find the optimum pH for effecting a complete separation of the four solutes.

> Acid–base chemistry is not the only example of a secondary equilibrium reaction. Other examples include ion-pairing, complexation, and the interaction of solutes with micelles. We will consider the last of these in Chapter 12.7 when we discuss micellar electrokinetic capillary chromatography.

In Example 12.5.1 we learned how to adjust the mobile phase's polarity by blending together two solvents. A polarity index, however, is just a guide, and binary mobile phase mixtures with identical polarity indices may not resolve equally a pair of solutes. Table 12.5.2 , for example, shows retention times for four weak acids in two mobile phases with nearly identical values for P'. Although the order of elution is the same for both mobile phases, each solute's retention time is affected differently by the choice of organic solvent. If we switch from using acetonitrile to tetrahydrofuran, for example, we find that benzoic acid elutes more quickly and that *p*-hydroxybenzoic acid elutes more slowly. Although we can resolve fully these two solutes using mobile phase that is 16% v/v acetonitrile, we cannot resolve them if the mobile phase is 10% tetrahydrofuran.

Table 12.5.2 . Retention Times for Four Weak Acids in Mobile Phases With Similar Polarity Indexes

retention time (min)	16% acetonitrile (CH_3CN) 84% pH 4.11 aqueous buffer (P' = 9.5)	10% tetrahydrofuran (THF) 90% pH 4.11 aqueous buffer (P' = 9.6)
$t_{r,\,BA}$	5.18	4.01
$t_{r,\,PH}$	1.67	2.91
$t_{r,\,PA}$	1.21	1.05
$t_{r,\,TP}$	0.23	0.54

Key: BA is benzoic acid; PH is *p*-hydroxybenzoic acid; PA is *p*-aminobenzoic acid; TP is terephthalic acid
Source: Harvey, D. T.; Byerly, S.; Bowman, A.; Tomlin, J. "Optimization of HPLC and GC Separations Using Re- sponse Surfaces," *J. Chem. Educ.* **1991**, *68*, 162–168.

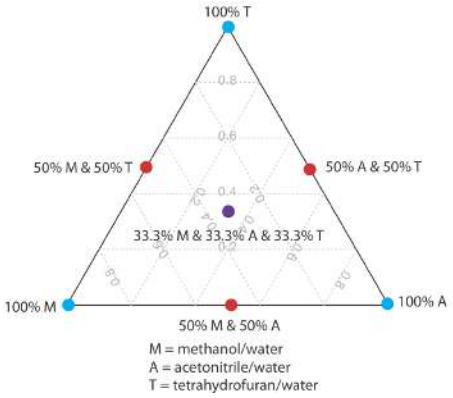


Figure 12.5.4 . Solvent triangle for optimizing a reversed-phase HPLC separation. The three blue circles show mobile phases consisting of an organic solvent and water. The three red circles are binary mobile phases created by combining equal volumes of the pure mobile phases. The ternary mobile phase shown by the purple circle contains all three of the pure mobile phases.

One strategy for finding the best mobile phase is to use the solvent triangle shown in Figure 12.5.4 , which allows us to explore a broad range of mobile phases with only seven experiments. We begin by adjusting the amount of acetonitrile in the mobile phase to produce the best possible separation within the desired analysis time. Next, we use Table 12.5.3 to estimate the composition of methanol/H_2O and tetrahydrofuran/H_2O mobile phases that will produce similar analysis times. Four additional mobile phases are prepared using the binary and ternary mobile phases shown in Figure 12.5.4 . When we examine the chromatograms from these seven mobile phases we may find that one or more provides an adequate separation, or we may identify a region within the solvent triangle where a separation is feasible. Figure 12.5.5 shows a resolution map for the reversed-phase separation of benzoic acid, terephthalic acid, *p*-aminobenzoic acid, and *p*-hydroxybenzoic acid on a nonpolar C_{18} column in which the maximum desired analysis time is set to 6 min [Harvey, D. T.; Byerly, S.; Bowman, A.; Tomlin, J. *J. Chem. Educ.* **1991**, *68*, 162–168]. The areas in blue, green, and red show mobile phase compositions that do not provide baseline resolution. The unshaded area represents mobile phase compositions where a separation is possible.

> The choice to start with acetonitrile is arbitrary—we can just as easily choose to begin with methanol or with tetrahydrofuran.

Table 12.5.3 . Composition of Mobile Phases With Approximately Equal Solvent Strengths

%v/v CH_3OH	% v/v CH_3CN	%v/v THF
0	0	0
10	6	4
20	14	10
30	22	16
40	32	24
50	40	30
6	50	36
70	60	44
80	72	52
90	87	62
100	99	71

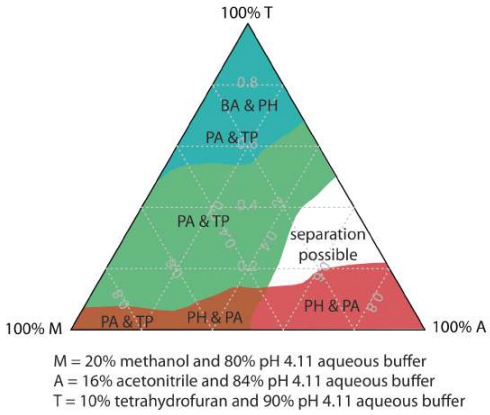


Figure 12.5.5 . Resolution map for the separation of benzoic acid (BA), terephthalic acid (TP), *p*-aminobenzoic acid (PA), and *p*-hydroxybenzoic acid (PH) on a nonpolar C_{18} column subject to a maximum analysis time of 6 min. The shaded areas represent regions where a separation is not possible, with the unresolved solutes identified. A separation is possible in the unshaded area. See Harvey, D. T.; Byerly, S.; Bowman, A.; Tomlin, J. "Optimization of HPLC and GC Separations Using Response Surfaces," *J. Chem. Educ.* **1991**, *68*, 162–168 for details on the mathematical model used to generate the resolution map.

CHOOSING A MOBILE PHASE: ISOCRATIC AND GRADIENT ELUTIONS

A separation using a mobile phase that has a fixed composition is an ***isocratic elution***. One difficulty with an isocratic elution is that an appropriate mobile phase strength for resolving early-eluting solutes may lead to unacceptably long retention times for late-eluting solutes. Optimizing the mobile phase for late-eluting solutes, on the other hand, may provide an inadequate separation of early-eluting solutes. Changing the mobile phase's composition as the separation progresses is one solution to this problem. For a reversed-phase separation we use an initial mobile phase that is more polar. As the separation progresses, we adjust the composition of mobile phase so that it becomes less polar (see Figure 12.5.6). Such separations are called ***gradient elutions***.

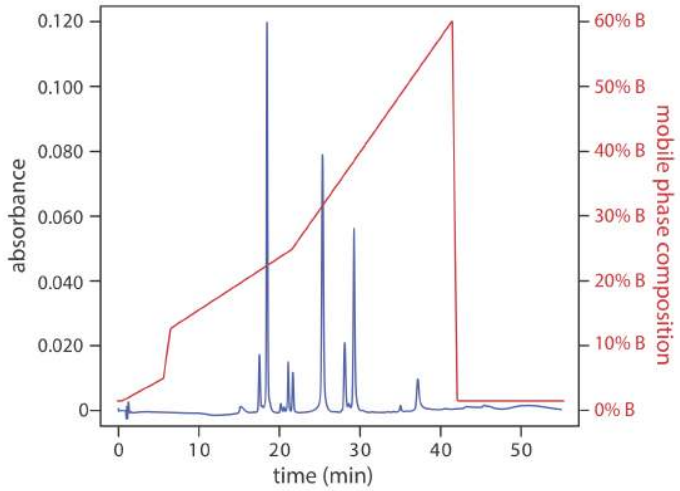


Figure 12.5.6 . Gradient elution separation of a mixture of flavonoids. Mobile phase A is an aqueous solution of 0.1% formic acid and mobile phase B is 0.1% formic acid in acetonitrile. The initial mobile phase is 98% A and 2% B. The percentage of mobile phase B increases in four steps: from 2% to 5% over 5 min, beginning at 0.5 min; from 5% to 12% over 1 min, beginning at 5.5 min; from 12% to 25% over 15 min, beginning at 6.5 min; and from 25% to 60% over 20 min, beginning at 21.5 min. Data provided by Christopher Schardon, Kyle Meinhardt, and Michelle Bushey, Department of Chemistry, Trinty University.

HPLC PLUMBING

In a gas chromatograph the pressure from a compressed gas cylinder is sufficient to push the mobile phase through the column. Pushing a liquid mobile phase through a column, however, takes a great deal more effort, generating pressures in excess of several hundred atmospheres. In this section we consider the basic plumbing needed to move the mobile phase through the column and to inject the sample into the mobile phase.

MOVING THE MOBILE PHASE

A typical HPLC includes between 1–4 reservoirs for storing mobile phase solvents. The instrument in Figure 12.5.1 , for example, has two mobile phase reservoirs that are used for an isocratic elution or a gradient elution by drawing solvents from one or both reservoirs.

Before using a mobile phase solvent we must remove dissolved gases, such as N_2 and O_2, and small particulate matter, such as dust. Because there is a large drop in pressure across the column—the pressure at the column's entrance is as much as several hundred atmospheres, but it is atmospheric pressure at the column's exit—gases dissolved in the mobile phase are released as gas bubbles that may interfere with the detector's response. Degassing is accomplished in several ways, but the most common are the use of a vacuum pump or sparging with an inert gas, such as He, which has a low solubility in the mobile phase. Particulate materials, which may clog the HPLC tubing or column, are removed by filtering the solvents.

> Bubbling an inert gas through the mobile phase releases volatile dissolved gases. This process is called sparging.

The mobile phase solvents are pulled from their reservoirs by the action of one or more pumps. Figure 12.5.7 shows a close-up view of the pumps for the instrument in Figure 12.5.1 . The working pump and the equilibrating pump each have a piston whose back and forth movement maintains a constant flow rate of up to several mL/min and provides the high output pressure needed to push the mobile phase through the chromatographic column. In this particular instrument, each pump sends its mobile phase to a mixing chamber where they combine to form the final mobile phase. The relative speed of the two pumps determines the mobile phase's final composition.

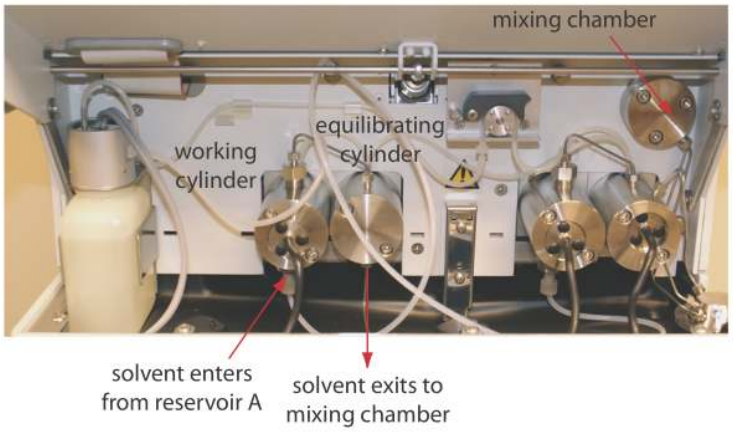


Figure 12.5.7 . Close-up view of the pumps for the instrument shown in Figure 12.5.1 . The working cylinder and the equilibrating cylinder for the pump on the left take solvent from reservoir A and send it to the mixing chamber. The pump on the right moves solvent from reservoir B to the mixing chamber. The mobile phase's flow rate is determined by the combined speeds of the two pumps. By changing the relative speeds of the two pumps, different binary mobile phases can be prepared.

The back and forth movement of a reciprocating pump creates a pulsed flow that contributes noise to the chromatogram. To minimize these pulses, each pump in Figure 12.5.7 has two cylinders. During the working cylinder's forward stoke it fills the equilibrating cylinder and establishes flow through the column. When the working cylinder is on its reverse stroke, the flow is maintained by the piston in the equilibrating cylinder. The result is a pulse-free flow.

> There are other possible ways to control the mobile phase's composition and flow rate. For example, instead of the two pumps in Figure 12.5.7 , we can place a solvent proportioning valve before a single pump. The solvent proportioning value connects two or more solvent reservoirs to the pump and determines how much of each solvent is pulled during each of the pump's cycles. Another approach for eliminating a pulsed flow is to include a pulse damper between the pump and the column. A pulse damper is a chamber filled with an easily compressed fluid and a flexible diaphragm. During the piston's forward stroke the fluid in the pulse damper is compressed. When the piston withdraws to refill the pump, pressure from the expanding fluid in the pulse damper maintains the flow rate.

INJECTING THE SAMPLE

The operating pressure within an HPLC is sufficiently high that we cannot inject the sample into the mobile phase by inserting a syringe through a septum, as is possible in gas chromatography. Instead, we inject the sample using a ***loop injector***, a diagram of which is shown in Figure 12.5.8 . In the load position a sample loop—which is available in a variety of sizes ranging from 0.5 µL to 5 mL—is isolated from the mobile phase and open to the atmosphere. The sample loop is filled using a syringe with a capacity several times that of the sample loop, with excess sample exiting through the waste line. After loading the sample, the injector is turned to the inject position, which redirects the mobile phase through the sample loop and onto the column.

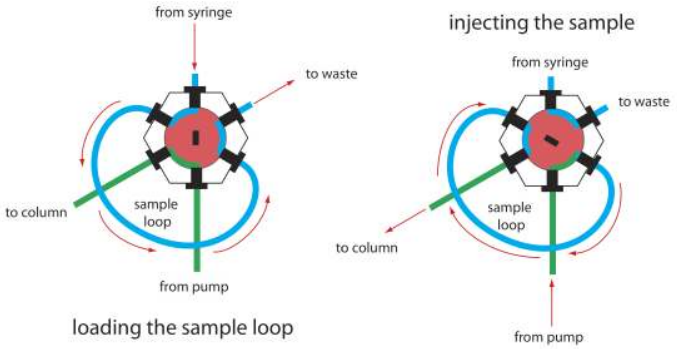


Figure 12.5.8 . Schematic diagram of a manual loop injector. In the load position the flow of mobile phase from the pump to the column (shown in green) is isolated from the sample loop, which is filled using a syringe (shown in blue). Rotating the inner valve (shown in red) to the inject position directs the mobile phase through the sample loop and onto the column.

The instrument in Figure 12.5.1 uses an autosampler to inject samples. Instead of using a syringe to push the sample into the sample loop, the syringe draws sample into the sample loop.

DETECTORS FOR HPLC

Many different types of detectors have been use to monitor HPLC separations, most of which use the spectroscopic techniques from Chapter 10 or the electrochemical techniques from Chapter 11.

SPECTROSCOPIC DETECTORS

The most popular HPLC detectors take advantage of an analyte's UV/Vis absorption spectrum. These detectors range from simple designs, in which the analytical wavelength is selected using appropriate filters, to a modified spectrophotometer in which the sample compartment includes a flow cell. Figure 12.5.9 shows the design of a typical flow cell when using a diode array spectrometer as the detector. The flow cell has a volume of 1–10 μL and a path length of 0.2–1 cm.

To review the details of how we measure absorbance, see Chapter 10.2. More information about different types of instruments, including the diode array spectrometer, is in Chapter 10.3.

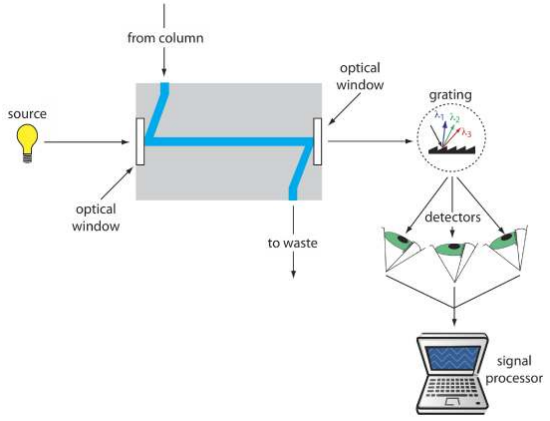


Figure 12.5.9 . Schematic diagram of a flow cell for a detector equipped with a diode array spectrometer.

When using a UV/Vis detector the resulting chromatogram is a plot of absorbance as a function of elution time (see Figure 12.5.10). If the detector is a diode array spectrometer, then we also can display the result as a three-dimensional chromatogram that shows absorbance as a function of wavelength and elution time. One limitation to using absorbance is that the mobile phase cannot absorb at the wavelengths we wish to monitor. Table 12.5.1 lists the minimum useful UV wavelength for several common HPLC solvents. Absorbance detectors provide detection limits of as little as 100 pg–1 ng of injected analyte.

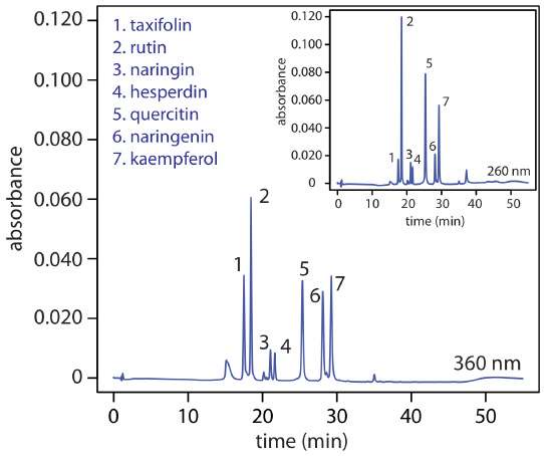


Figure 12.5.10 . HPLC separation of a mixture of flavonoids with UV/Vis detection at 360 nm and, in the inset, at 260 nm. The choice of wavelength affects each analyte's signal. By carefully choosing the wavelength, we can enhance the signal for the analytes of greatest interest. Data provided by Christopher Schardon, Kyle Meinhardt, and Michelle Bushey, Department of Chemistry, Trinty University.

If an analyte is fluorescent, we can place the flow cell in a spectrofluorimeter. As shown in Figure 12.5.11 , a fluorescence detector provides additional selectivity because only a few of a sample's components are fluorescent. Detection limits are as little as 1–10 pg of injected analyte.

> See Chapter 10.6 for a review of fluorescence spectroscopy and spectrofluorimeters.

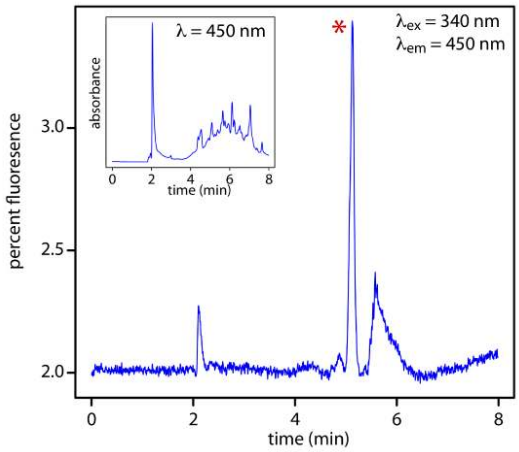


Figure 12.5.11 . HPLC chromatogram for the determination of riboflavin in urine using fluorescence detection with exci-tation at a wavelength of 340 nm and detection at 450 nm. The peak corresponding to riboflavin is marked with a red asterisk (*). The inset shows the same chromatogram when using a less-selective UV/Vis detector at a wavelength of 450 nm. Data provided by Jason Schultz, Jonna Berry, Kaelene Lundstrom, and Dwight Stoll, Department of Chemistry, Gustavus Adolphus College.

ELECTROCHEMICAL DETECTORS

Another common group of HPLC detectors are those based on electrochemical measurements such as amperometry, voltammetry, coulometry, and conductivity. Figure 12.5.12 , for example, shows an amperometric flow cell. Effluent from the column passes over the working electrode—held at a constant potential relative to a downstream reference electrode—that completely oxidizes or reduces the analytes. The current flowing between the working electrode and the auxiliary electrode serves as the analytical signal. Detection limits for amperometric electrochemical detection are from 10 pg–1 ng of injected analyte.

> See Chapter 11.4 for a review of amperometry.

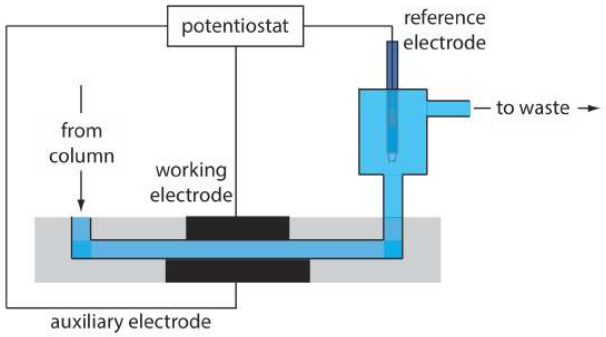


Figure 12.5.12 . Schematic diagram showing a flow cell for an amperometric electrochemical detector.

OTHER DETECTORS

Several other detectors have been used in HPLC. Measuring a change in the mobile phase's refractive index is analogous to monitoring the mobile phase's thermal conductivity in gas chromatography. A refractive index detector is nearly universal, responding to almost all compounds, but has a relatively poor detection limit of 0.1–1 μg of injected analyte. An additional limitation of a refractive index detector is that it cannot be used for a gradient elution unless the mobile phase components have identical refractive indexes.

Another useful detector is a mass spectrometer. Figure 12.5.13 shows a block diagram of a typical HPLC–MS instrument. The effluent from the column enters the mass spectrometer's ion source using an interface the removes most of the mobile phase, an essential need because of the incompatibility between the liquid mobile phase and the mass spectrometer's high vacuum environment. In the ionization chamber the remaining molecules—a mixture of the mobile phase components and solutes—undergo ionization and fragmentation. The mass spectrometer's mass analyzer separates the ions by their mass-to-charge ratio (m/z). A detector counts the ions and displays the mass spectrum.

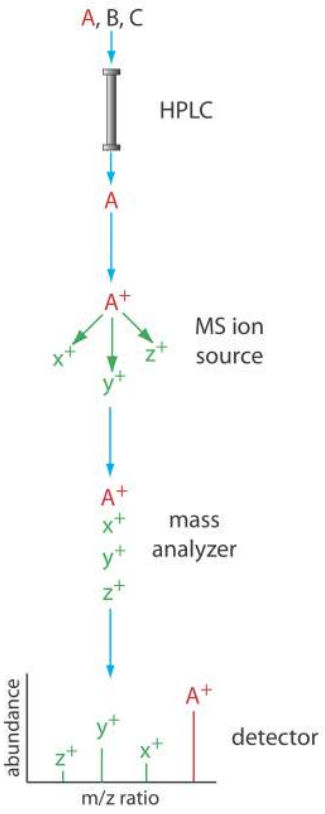


Figure 12.5.13 . Block diagram of an HPLC–MS. A three component mixture enters the HPLC. When component A elutes from the column, it enters the MS ion source and ionizes to form the parent ion and several fragment ions. The ions enter the mass analyzer, which separates them by their mass-to-charge ratio, providing the mass spectrum shown at the detector.

There are several options for monitoring the chromatogram when using a mass spectrometer as the detector. The most common method is to continuously scan the entire mass spectrum and report the total signal for all ions reaching the detector during each scan. This total ion scan

provides universal detection for all analytes. As seen in Figure 12.5.14 , we can achieve some degree of selectivity by monitoring only specific mass-to-charge ratios, a process called selective-ion monitoring.

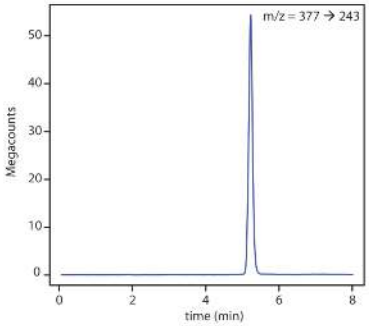


Figure 12.5.14 . HPLC–MS/MS chromatogram for the determination of riboflavin in urine. An initial parent ion with an m/z ratio of 377 enters a second mass spectrometer where it undergoes additional 20 ionization; the fragment ion with an m/z ratio of 243 provides the signal. The selectivity of this detector is evident when you compare this chromatogram to the one in Figure 12.5.11 , which uses fluoresence deterction. Data provided by Jason Schultz, Jonna Berry, Kaelene Lundstrom, and Dwight Stoll, Department of Chemistry, Gustavus Adolphus College.

The advantages of using a mass spectrometer in HPLC are the same as for gas chromatography. Detection limits are very good, typically 0.1–1 ng of injected analyte, with values as low as 1–10 pg for some samples. In addition, a mass spectrometer provides qualitative, structural information that can help to identify the analytes. The interface between the HPLC and the mass spectrometer is technically more difficult than that in a GC–MS because of the incompatibility of a liquid mobile phase with the mass spectrometer's high vacuum requirement.

> For more details on mass spectrometry see Introduction to Mass Spectrometry by Michael Samide and Olujide Akinbo, a resource that is part of the Analytical Sciences Digital Library.

QUANTITATIVE APPLICATIONS

High-performance liquid chromatography is used routinely for both qualitative and quantitative analyses of environmental, pharmaceutical, industrial, forensic, clinical, and consumer product samples.

PREPARING SAMPLES FOR ANALYSIS

Samples in liquid form are injected into the HPLC after a suitable clean-up to remove any particulate materials, or after a suitable extraction to remove matrix interferents. In determining polyaromatic hydrocarbons (PAH) in wastewater, for example, an extraction with CH_2Cl_2 serves the dual purpose of concentrating the analytes and isolating them from matrix interferents. Solid samples are first dissolved in a suitable solvent or the analytes of interest brought into solution by extraction. For example, an HPLC analysis for the active ingredients and the degradation products in a pharmaceutical tablet often begins by extracting the powdered tablet with a portion of mobile phase. Gas samples are collected by bubbling them through a trap that contains a suitable solvent. Organic isocyanates in industrial atmospheres are collected by bubbling the air through a solution of 1-(2-methoxyphenyl)piperazine in toluene. The reaction between the isocyanates and 1-(2-methoxyphenyl)piperazine both stabilizes them against degradation before the HPLC analysis and converts them to a chemical form that can be monitored by UV absorption.

QUANTITATIVE CALCULATIONS

A quantitative HPLC analysis is often easier than a quantitative GC analysis because a fixed volume sample loop provides a more precise and accurate injection. As a result, most quantitative HPLC methods do not need an internal standard and, instead, use external standards and a normal calibration curve.

> An internal standard is necessary when using HPLC–MS because the interface between the HPLC and the mass spectrometer does not allow for a reproducible transfer of the column's eluent into the MS's ionization chamber.

✔ EXAMPLE 12.5.2

The concentration of polynuclear aromatic hydrocarbons (PAH) in soil is determined by first extracting the PAHs with methylene chloride. The extract is diluted, if necessary, and the PAHs separated by HPLC using a UV/Vis or fluorescence detector. Calibration is achieved using one or more external standards. In a typical analysis a 2.013-g sample of dried soil is extracted with 20.00 mL of methylene chloride. After filtering to remove the soil, a 1.00-mL portion of the extract is removed and diluted to 10.00 mL with acetonitrile. Injecting 5 µL of the diluted extract into an HPLC gives a signal of 0.217 (arbitrary units) for the PAH fluoranthene. When

5 µL of a 20.0-ppm fluoranthene standard is analyzed using the same conditions, a signal of 0.258 is measured. Report the parts per million of fluoranthene in the soil.

Solution

For a single-point external standard, the relationship between the signal, *S*, and the concentration, *C*, of fluoranthene is

$$S = kC$$

Substituting in values for the standard's signal and concentration gives the value of *k* as

$$k = \frac{S}{C} = \frac{0.258}{20.0 \text{ ppm}} = 0.0129 \text{ ppm}^{-1}$$

Using this value for *k* and the sample's HPLC signal gives a fluoranthene concentration of

$$C = \frac{S}{k} = \frac{0.217}{0.0129 \text{ ppm}^{-1}} = 16.8 \text{ ppm}$$

for the extracted and diluted soil sample. The concentration of fluoranthene in the soil is

$$\frac{16.8 \text{ g/mL} \times \frac{10.00 \text{ mL}}{1.00 \text{ mL}} \times 20.00 \text{ mL}}{2.013 \text{ g sample}} = 1670 \text{ ppm fluoranthene}$$

EXERCISE 12.5.2

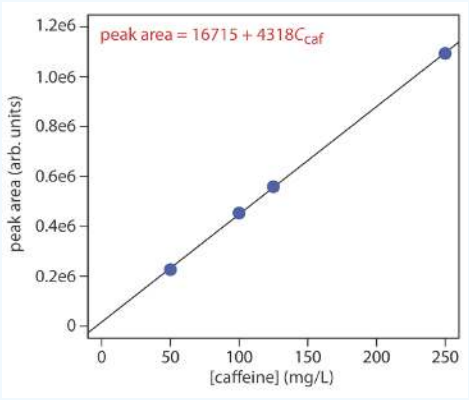
The concentration of caffeine in beverages is determined by a reversed-phase HPLC separation using a mobile phase of 20% acetonitrile and 80% water, and using a nonpolar C_8 column. Results for a series of 10-µL injections of caffeine standards are in the following table.

[caffeine] (mg/L)	peak area (arb. units)
50.0	226724
100.0	453762
125.0	559443
250.0	1093637

What is the concentration of caffeine in a sample if a 10-µL injection gives a peak area of 424195? The data in this problem comes from Kusch, P.; Knupp, G. "Simultaneous Determination of Caffeine in Cola Drinks and Other Beverages by Reversed-Phase HPTLC and Reversed-Phase HPLC," *Chem. Educator*, **2003**, *8*, 201–205.

Answer

The figure below shows the calibration curve and calibration equation for the set of external standards. Substituting the sample's peak area into the calibration equation gives the concentration of caffeine in the sample as 94.4 mg/L.



The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of fluoxetine in serum provides an instructive example of a typical procedure. The description here is based on Smyth, W. F. *Analytical Chemistry of Complex Matricies*, Wiley Teubner: Chichester, England, 1996, pp. 187–189.

REPRESENTATIVE METHOD 12.5.1: DETERMINATION OF FLUOXETINE IN SERUM

Description of Method

Fluoxetine is another name for the antidepressant drug Prozac. The determination of fluoxetine in serum is an important part of monitoring its therapeutic use. The analysis is complicated by the complex matrix of serum samples. A solid-phase extraction followed by an HPLC analysis using a fluorescence detector provides the necessary selectivity and detection limits.

Procedure

Add a known amount of the antidepressant protriptyline, which serves as an internal standard, to each serum sample and to each external standard. To remove matrix interferents, pass a 0.5-mL aliquot of each serum sample or standard through a C_{18} solid-phase extraction cartridge. After washing the cartridge to remove the interferents, elute the remaining constituents, including the analyte and the internal standard, by washing the cartridge with 0.25 mL of a 25:75 v/v mixture of 0.1 M $HClO_4$ and acetonitrile. Inject a 20-µL aliquot onto a 15-cm × 4.6-mm column packed with a 5 µm C_8-bonded stationary phase. The isocratic mobile phase is 37.5:62.5 v/v acetonitrile and water (that contains 1.5 g of tetramethylammonium perchlorate and 0.1 mL of 70% v/v $HClO_4$). Monitor the chromatogram using a fluorescence detector set to an excitation wave- length of 235 nm and an emission wavelength of 310 nm.

Questions

1. The solid-phase extraction is important because it removes constitutions in the serum that might interfere with the analysis. What types of interferences are possible?

Blood serum, which is a complex mixture of compounds, is approximately 92% water, 6–8% soluble proteins, and less than 1% each of various salts, lipids, and glucose. A direct injection of serum is not advisable for three reasons. First, any particulate materials in the serum will clog the column and restrict the flow of mobile phase. Second, some of the compounds in the serum may absorb too strongly to the stationary phase, degrading the column's performance. Finally, although an HPLC can separate and analyze complex mixtures, an analysis is difficult if the number of constituents exceeds the column's peak capacity.

2. One advantage of an HPLC analysis is that a loop injector often eliminates the need for an internal standard. Why is an internal standard used in this analysis? What assumption(s) must we make when using the internal standard?

An internal standard is necessary because of uncertainties introduced during the solid-phase extraction. For example, the volume of serum transferred to the solid-phase extraction cartridge, 0.5 mL, and the volume of solvent used to remove the analyte and internal standard, 0.25 mL, are very small. The precision and accuracy with which we can measure these volumes is not as good as when we use larger volumes. For example, if we extract the analyte into a volume of 0.24 mL instead of a volume of 0.25 mL, then the analyte's concentration increases by slightly more than 4%. In addition, the concentration of eluted analytes may vary from trial-to-trial due to variations in the amount of solution held up by the cartridge. Using an internal standard compensates for these variation. To be useful we must assume that the analyte and the internal standard are retained completely during the initial loading, that they are not lost when the cartridge is washed, and that they are extracted completely during the final elution.

3. Why does the procedure monitor fluorescence instead of monitoring UV absorption?

Fluorescence is a more selective technique for detecting analytes. Many other commonly prescribed antidepressants (and their metabolites) elute with retention times similar to that of fluoxetine. These compounds, however, either do not fluoresce or are only weakly fluorescent.

4. If the peaks for fluoxetine and protriptyline are resolved insufficiently, how might you alter the mobile phase to improve their separation?

Decreasing the amount of acetonitrile and increasing the amount of water in the mobile will increase retention times, providing more time to effect a separation.

EVALUATION

With a few exceptions, the scale of operation, accuracy, precision, sensitivity, selectivity, analysis time, and cost for an HPLC method are similar to GC methods. Injection volumes for an HPLC method usually are larger than for a GC method because HPLC columns have a greater capacity. Because it uses a loop injection, the precision of an HPLC method often is better than a GC method. HPLC is not limited to volatile analytes, which means we can analyze a broader range of compounds. Capillary GC columns, on the other hand, have more theoretical plates, and can separate more complex mixtures.

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12.10: OTHER FORMS OF CHROMATOGRAPHY

At the beginning of Section 12.5, we noted that there are several different types of solute/stationary phase interactions in liquid chromatography, but limited our discussion to liquid–liquid chromatography. In this section we turn our attention to liquid chromatography techniques in which partitioning occurs by liquid–solid adsorption, ion-exchange, and size exclusion.

LIQUID-SOLID CHROMATOGRAPHY

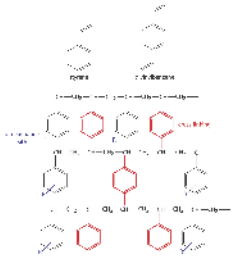
In ***liquid–solid adsorption chromatography*** (LSC) the column packing also serves as the stationary phase. In Tswett's original work the stationary phase was finely divided $CaCO_3$, but modern columns employ porous 3–10 μm particles of silica or alumina. Because the stationary phase is polar, the mobile phase usually is a nonpolar or a moderately polar solvent. Typical mobile phases include hexane, isooctane, and methylene chloride. The usual order of elution—from shorter to longer retention times—is

olefins < aromatic hydrocarbons < ethers < esters, aldehydes, ketones < alcohols, amines < amide < carboxylic acids

Nonpolar stationary phases, such as charcoal-based absorbents, also are used. For most samples, liquid–solid chromatography does not offer any special advantages over liquid–liquid chromatography. One exception is the analysis of isomers, where LSC excels.

ION-EXCHANGE CHROMATOGRAPHY

In ***ion-exchange chromatography*** (IEC) the stationary phase is a cross-linked polymer resin, usually divinylbenzene cross-linked polystyrene, with covalently attached ionic functional groups (see Figure 12.6.1 and Table 12.6.1). The counterions to these fixed charges are mobile and are displaced by ions that compete more favorably for the exchange sites. Ion-exchange resins are divided into four categories: strong acid cation exchangers; weak acid cation exchangers; strong base anion exchangers; and weak base anion exchangers.



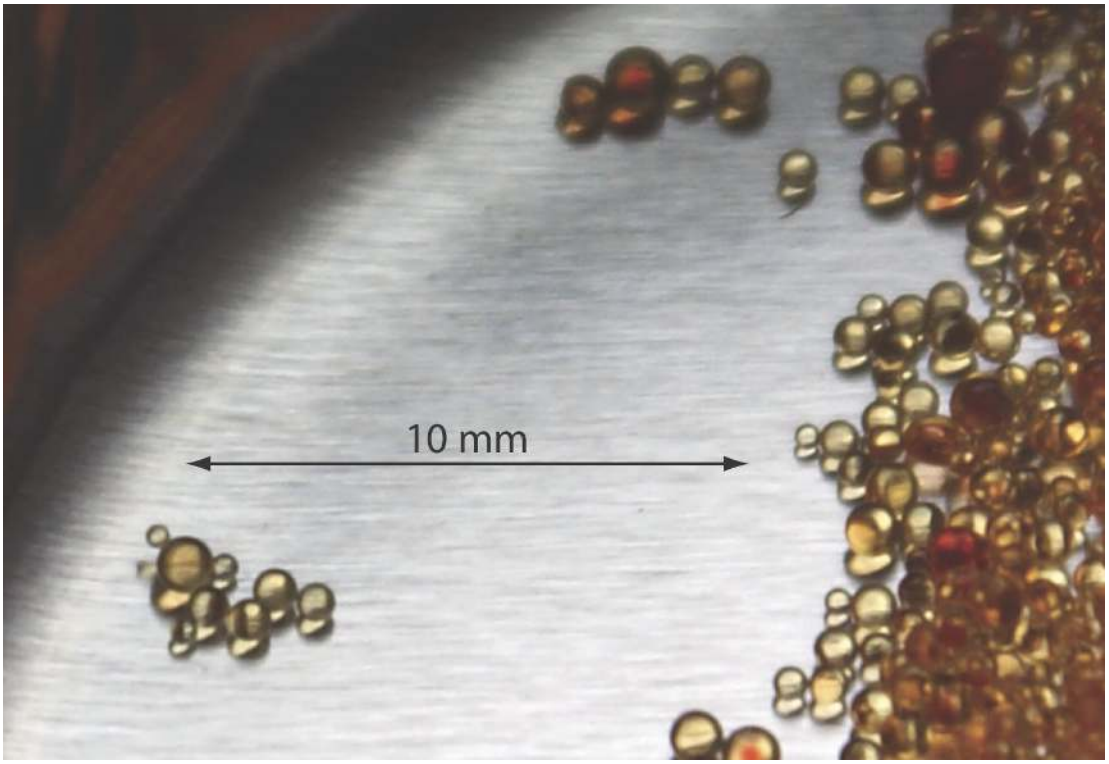


Figure 12.6.1 . Structures of styrene, divinylbenzene, and a styrene–divinylbenzene co-polymer modified for use as an ion-exchange resin are shown on the left. The ion-exchange sites, indicated by R and shown in blue, are mostly in the *para* position and are not necessarily bound to all styrene units. The cross-linking is shown in red. The photo on the right shows an example of the polymer beads. These beads are approximately 0.30–0.85 mm in diameter. Resins for use in ion-exchange chromatography typically are 5–11 μm in diameter.

Table 12.6.1 . Examples of Common Ion-Exchange Resins

type	functional group	examples
strong acid cation exchanger	sulfonic acid	$-SO_3^-$ $-CH_2CH_2SO_3^-$
weak acid cation exchanger	carboxylic acid	$-COO^-$ $-CH_2COO^-$
strong base anion exchanger	quaternary amine	$-CH_2N(CH_3)_3^+$ $-CH_2CH_2N(CH_2CH_3)_3^+$
weak base anion exchanger	amine	$-NH_4^+$ $-CH_2CH_2NH(CH_2CH_3)_3^+$

Strong acid cation exchangers include a sulfonic acid functional group that retains it anionic form—and thus its capacity for ion-exchange—in strongly acidic solutions. The functional groups for a weak acid cation exchanger, on the other hand, are fully protonated at pH levels less then 4 and lose their exchange capacity. The strong base anion exchangers include a quaternary amine, which retains a positive charge even in strongly basic solutions. Weak base anion exchangers remain protonated only at pH levels that are moderately basic. Under more basic conditions a weak base anion exchanger loses a proton and its exchange capacity.

The ion-exchange reaction of a monovalent cation, M^+, exchange site is

$$-SO_3^-H^+(s) + M^+(aq) \rightleftharpoons -SO_3^-M^+(s) + H^+(aq)$$

The equilibrium constant for this ion-exchange reaction, which we call the selectivity coefficient, *K*, is

$$K = \frac{\{-SO_3^-M^+\}\left[H^+\right]}{\{-SO_3^-H^+\}\left[M^+\right]} \tag{12.10.1}$$

where we use curly brackets, { }, to indicate a surface concentration instead of a solution concentration.

> We don't usually think about a solid's concentration. There is a good reason for this. In most cases, a solid's concentration is a constant. If you break a piece of chalk into two parts, for example, the mass and the volume of each piece retains the same proportional relationship as in the original piece of chalk. When we consider an ion binding to a reactive site on the solid's surface, however, the fraction of sites that are bound, and thus the concentration of bound sites, can take on any value between 0 and some maximum value that is proportional to the density of reactive sites.

Rearranging Equation 12.10.1 shows us that the distribution ratio, *D*, for the exchange reaction

$$D = \frac{\text{amount of } M^+ \text{ in the stationary phase}}{\text{amount of } M^+ \text{ in the mobile phase}}$$

$$D = \frac{\{-SO_3^-M^+\}}{\left[M^+\right]} = K \times \frac{\{-SO_3^-H^+\}}{\left[H^+\right]} \tag{12.10.2}$$

is a function of the concentration of H^+ and, therefore, the pH of the mobile phase.

An ion-exchange resin's selectivity is somewhat dependent on whether it includes strong or weak exchange sites and on the extent of cross-linking. The latter is particularly important as it controls the resin's permeability, and, therefore, the accessibility of exchange sites. An approximate order of selectivity for a typical strong acid cation exchange resin, in order of decreasing *D*, is

$$Al^{3+} > Ba^{2+} > Pb^{2+} > Ca^{2+} > Ni^{2+} > Cd^{2+} > Cu^{2+} > Co^{2+} > Zn^{2+} > Mg^{2+} > Ag^+ > K^+ > NH_4^+ > Na^+ > H^+ > Li^+$$

Note that highly charged cations bind more strongly than cations of lower charge, and that for cations of similar charge, those with a smaller hydrated radius (see Table 6.9.1 in Chapter 6), or that are more polarizable, bind more strongly. For a strong base anion exchanger the general elution order is

$$SO_4^{2-} > I^- > HSO_4^- > NO_3^- > Br^- > NO_2^- > Cl^- > HCO_3^- > CH3COO^- > OH^- > F^-$$

Anions of higher charge and of smaller hydrated radius bind more strongly than anions with a lower charge and a larger hydrated radius.

The mobile phase in IEC usually is an aqueous buffer, the pH and ionic composition of which determines a solute's retention time. Gradient elutions are possible in which the mobile phase's ionic strength or pH is changed with time. For example, an IEC separation of cations might use a dilute solution of HCl as the mobile phase. Increasing the concentration of HCl speeds the elution rate for more strongly retained cations because the higher concentration of H^+ allows it to compete more successfully for the ion-exchange sites.

> From Equation 12.10.2, a cation's distribution ratio, *D*, becomes smaller when the concentration of H^+ in the mobile phase increases.

An ion-exchange resin is incorporated into an HPLC column either as 5–11 μm porous polymer beads or by coating the resin on porous silica particles. Columns typically are 250 mm in length with internal diameters ranging from 2–5 mm.

Measuring the conductivity of the mobile phase as it elutes from the column serves as a universal detector for cationic and anionic analytes. Because the mobile phase contains a high concentration of ions—a mobile phase of dilute HCl, for example, contains significant concentrations of H^+ and Cl^-—we need a method for detecting the analytes in the presence of a significant background conductivity.

To minimize the mobile phase's contribution to conductivity, an ***ion-suppressor column*** is placed between the analytical column and the detector. This column selectively removes mobile phase ions without removing solute ions. For example, in cation-exchange chromatography using a dilute solution of HCl as the mobile phase, the suppressor column contains a strong base anion-exchange resin. The exchange reaction

$$H^+(aq) + Cl^-(aq) + \text{Resin}^+OH^-(s) \rightleftharpoons \text{Resin}^+\,Cl^-(s) + H_2O(l)$$

replaces the mobile phase ions H^+ and Cl^- with H_2O. A similar process is used in anion-exchange chromatography where the suppressor column contains a cation-exchange resin. If the mobile phase is a solution of Na_2CO_3, the exchange reaction

$$2Na^+(aq) + CO_3^{2-}(aq) + 2\,\text{Resin}^-\,H^+(s) \rightleftharpoons 2\,\text{Resin}^-\,Na^+(s) + H_2CO_3(aq)$$

replaces a strong electrolyte, Na_2CO_3, with a weak electrolyte, H_2CO_3.

Ion-suppression is necessary when the mobile phase contains a high concentration of ions. ***Single-column ion chromatography***, in which an ion-suppressor column is not needed, is possible if the concentration of ions in the mobile phase is small. Typically the stationary phase is a resin with a low capacity for ion-exchange and the mobile phase is a very dilute solution of methane sulfonic acid for cationic analytes, or potassium benzoate or potassium hydrogen phthalate for anionic analytes. Because the background conductivity is sufficiently small, it is possible to monitor a change in conductivity as the analytes elute from the column.

A UV/Vis absorbance detector can be used if the analytes absorb ultraviolet or visible radiation. Alternatively, we can detect indirectly analytes that do not absorb in the UV/Vis if the mobile phase contains a UV/Vis absorbing species. In this case, when a solute band passes through the detector, a decrease in absorbance is measured at the detector.

Ion-exchange chromatography is an important technique for the analysis of anions and cations in water. For example, an ion-exchange chromatographic analysis for the anions F^-, Cl^-, Br^-, NO_2^-, NO_3^-, PO_4^{3-}, and SO_4^{2-} takes approximately 15 minutes (Figure 12.6.2). A complete analysis of the same set of anions by a combination of potentiometry and spectrophotometry requires 1–2 days. Ion-exchange chromatography also is used for the analysis of proteins, amino acids, sugars, nucleotides, pharmaceuticals, consumer products, and clinical samples.

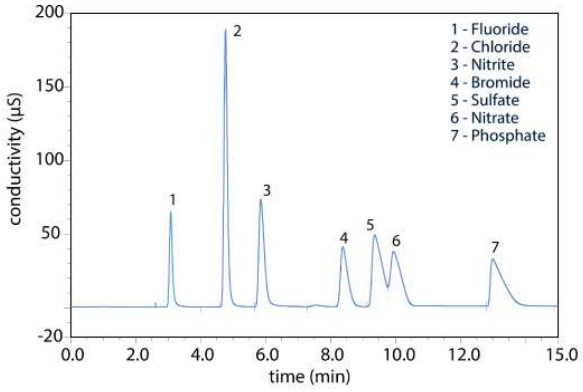


Figure 12.6.2 . Ion-exchange chromatographic analysis of water from Big Walnut Creek in Putnam County, Indiana. Data provided by Jeanette Pope, Department of Geosciences, DePauw University.

SIZE-EXCLUSION CHROMATOGRAPHY

We have considered two classes of micron-sized stationary phases in this section: silica particles and cross-linked polymer resin beads. Both materials are porous, with pore sizes ranging from approximately 5–400 nm for silica particles, and from 5 nm to 100 μm for divinylbenzene cross-linked polystyrene resins. In ***size-exclusion chromatography***—which also is known by the terms molecular-exclusion or gel permeation chromatography—the separation of solutes depends upon their ability to enter into the pores of the stationary phase. Smaller solutes spend proportionally more time within the pores and take longer to elute from the column.

A stationary phase's size selectivity extends over a finite range. All solutes significantly smaller than the pores move through the column's entire volume and elute simultaneously, with a retention volume, V_r, of

$$V_r = V_i + V_o \tag{12.10.3}$$

where V_i is the volume of mobile phase occupying the stationary phase's pore space and V_o is volume of mobile phase in the remainder of the column. The largest solute for which Equation 12.10.3 holds is the column's inclusion limit, or permeation limit. Those solutes too large to enter the pores elute simultaneously with an retention volume of

$$V_r = V_o \tag{12.10.4}$$

Equation 12.10.4 defines the column's ***exclusion limit***.

For a solute whose size is between the inclusion limit and the exclusion limit, the amount of time it spends in the stationary phase's pores is proportional to its size. The retention volume for these solutes is

$$V_r = DV_i + V_o \tag{12.10.5}$$

where D is the solute's distribution ratio, which ranges from 0 at the exclusion limit to 1 at the inclusion limit. Equation 12.10.5 assumes that size-exclusion is the only interaction between the solute and the stationary phase that affects the separation. For this reason, stationary phases using silica particles are deactivated as described earlier, and polymer resins are synthesized without exchange sites.

Size-exclusion chromatography provides a rapid means for separating larger molecules, including polymers and biomolecules. A stationary phase for proteins that consists of particles with 30 nm pores has an inclusion limit of 7500 g/mol and an exclusion limit of 1.2×10^6 g/mol. Mixtures of proteins that span a wider range of molecular weights are separated by joining together in series several columns with different inclusion and exclusion limits.

Another important application of size-exclusion chromatography is the estimation of a solute's molecular weight (MW). Calibration curves are prepared using a series of standards of known molecular weight and measuring each standard's retention volume. As shown in Figure 12.6.3 , a plot of log(MW) versus V_r is roughly linear between the exclusion limit and the inclusion limit. Because a solute's retention volume is influenced by both its size and its shape, a reasonably accurate estimation of molecular weight is possible only if the standards are chosen carefully to minimize the effect of shape.

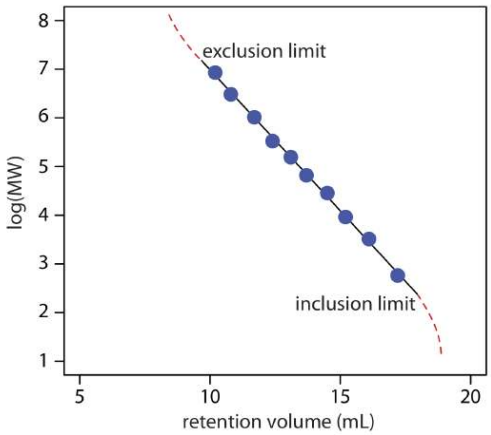


Figure 12.6.3 . Calibration curve for the determination of molecular weight by size-exclusion chromatography. The data shown here are adapted from Rouessac, F.; Rouessac, A. *Chemical Analysis: Modern Instrumentation Methods and Techniques*, Wiley: Chichester, England, 2004, p 141.

Size-exclusion chromatography is carried out using conventional HPLC instrumentation, replacing the HPLC column with an appropriate size-exclusion column. A UV/Vis detector is the most common means for obtaining the chromatogram.

SUPERCRITICAL FLUID CHROMATOGRAPHY

Although there are many analytical applications of gas chromatography and liquid chromatography, they can not separate and analyze all types of samples. Capillary column GC separates complex mixtures with excellent resolution and short analysis times. Its application is limited, however, to volatile analytes or to analytes made volatile by a suitable derivatization reaction. Liquid chromatography separates a wider range of solutes than GC, but the most common detectors—UV, fluorescence, and electrochemical— have poorer detection limits and smaller linear ranges than GC detectors, and are not as universal in their selectivity.

For some samples, ***supercritical fluid chromatography*** (SFC) provides a useful alternative to gas chromatography and liquid chromatography. The mobile phase in supercritical fluid chromatography is a gas held at a temperature and pressure that exceeds its critical point (Figure 12.6.4). Under these conditions the mobile phase is neither a gas nor a liquid. Instead, the mobile phase is a supercritical fluid.

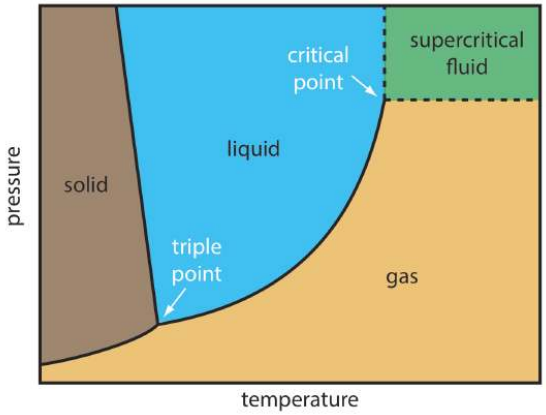


Figure 12.6.4 . Phase diagram showing the combinations of temperature and pres- sure for which a compound is in its solid state, its liquid state, and its gas state. For pressures and temperatures above the critical point, the compound is a supercritical fluid with properties intermediate between a gas and a liquid. Click here to see an interesting video demonstration of supercritical fluids from Nottingham Science City at the University of Nottingham.

Some properties of a supercritical fluid, as shown in Table 12.6.2 , are similar to a gas; other properties, however, are similar to a liquid. The viscosity of a supercritical fluid, for example, is similar to a gas, which means we can move a supercritical fluid through a capillary column or a packed column without the high pressures needed in HPLC. Analysis time and resolution, although not as good as in GC, usually are better than in conventional HPLC. The density of a supercritical fluid, on the other hand, is much closer to that of a liquid, which explains why supercritical fluids are good solvents. In terms of its separation power, a mobile phase in SFC behaves more like the liquid mobile phase in HPLC than the gaseous mobile phase in GC.

Table 12.6.2 . Typical Properties of Gases, Liquids, and Supercritical Fluids

phase	density (g/cm^3)	viscosity ($g\ cm^{-1}\ s^{-1}$)	diffusion coefficient ($cm^2\ s^{-1}$)
gas	$\approx 10^{-3}$	$\approx 10^{-4}$	≈ 0.1
supercritical fluid	$\approx 0.1 - 1$	$\approx 10^{-4} - 10^{-3}$	$\approx 10^{-4} - 10^{-3}$
liquid	≈ 1	$\approx 10^{-2}$	$\approx 10^{-3}$

The most common mobile phase for supercritical fluid chromatography is CO_2. Its low critical temperature of 31.1ºC and its low critical pressure of 72.9 atm are relatively easy to achieve and maintain. Although supercritical CO_2 is a good solvent for nonpolar organics, it is less useful for polar solutes. The addition of an organic modifier, such as methanol, improves the mobile phase's elution strength. Other common mobile phases and their critical temperatures and pressures are listed in Table 12.6.3 .

Table 12.6.3 . Critical Points for Selected Supercritical Fluids

compound	critical temperature (ºC)	critical pressure (atm)
carbon dioxide	31.3	72.9
ethane	32.4	48.3
nitrous oxide	36.5	71.4
ammonia	132.3	111.3
diethyl ether	193.6	36.3
isopropanol	235.3	47.0
methanol	240.5	78.9
ethanol	243.4	63.0
water	374.4	226.8

The instrumentation for supercritical fluid chromatography essentially is the same as that for a standard HPLC. The only important additions are a heated oven for the column and a pressure restrictor downstream from the column to maintain the critical pressure. Gradient elutions are accomplished by changing the applied pressure over time. The resulting change in the mobile phase's density affects its solvent strength. Detection is accomplished using standard GC detectors or HPLC detectors. Supercritical fluid chromatography has many applications in the analysis of polymers, fossil fuels, waxes, drugs, and food products.

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12.11: ELECTROPHORESIS

Electrophoresis is a class of separation techniques in which we separate analytes by their ability to move through a conductive medium—usually an aqueous buffer—in response to an applied electric field. In the absence of other effects, cations migrate toward the electric field's negatively charged cathode. Cations with larger charge-to-size ratios—which favors ions of greater charge and of smaller size—migrate at a faster rate than larger cat- ions with smaller charges. Anions migrate toward the positively charged anode and neutral species do not experience the electrical field and remain stationary.

> As we will see shortly, under normal conditions even neutral species and anions migrate toward the cathode.

There are several forms of electrophoresis. In slab gel electrophoresis the conducting buffer is retained within a porous gel of agarose or polyacrylamide. Slabs are formed by pouring the gel between two glass plates separated by spacers. Typical thicknesses are 0.25–1 mm. Gel electrophoresis is an important technique in biochemistry where it frequently is used to separate DNA fragments and proteins. Although it is a powerful tool for the qualitative analysis of complex mixtures, it is less useful for quantitative work.

In ***capillary electrophoresis*** the conducting buffer is retained within a capillary tube with an inner diameter that typically is 25–75 μm. The sample is injected into one end of the capillary tube, and as it migrates through the capillary the sample's components separate and elute from the column at different times. The resulting ***electropherogram*** looks similar to a GC or an HPLC chromatogram, and provides both qualitative and quantitative information. Only capillary electrophoretic methods receive further consideration in this section.

THEORY OF ELECTROPHORESIS

In capillary electrophoresis we inject the sample into a buffered solution retained within a capillary tube. When an electric field is applied across the capillary tube, the sample's components migrate as the result of two types of actions: electrophoretic mobility and electroosmotic mobility. ***Electrophoretic mobility*** is the solute's response to the applied electrical field in which cations move toward the negatively charged cathode, anions move toward the positively charged anode, and neutral species remain stationary. The other contribution to a solute's migration is ***electroosmotic flow***, which occurs when the buffer moves through the capillary in response to the applied electrical field. Under normal conditions the buffer moves toward the cathode, sweeping most solutes, including the anions and neutral species, toward the negatively charged cathode.

ELECTROPHORETIC MOBILITY

The velocity with which a solute moves in response to the applied electric field is called its ***electrophoretic velocity***, ν_{ep}; it is defined as

$$\nu_{ep} = \mu_{ep} E \tag{12.11.1}$$

where μ_{ep} is the solute's electrophoretic mobility, and E is the magnitude of the applied electrical field. A solute's electrophoretic mobility is defined as

$$\mu_{ep} = \frac{q}{6\pi\eta r} \tag{12.11.2}$$

where q is the solute's charge, η is the buffer's viscosity, and r is the solute's radius. Using Equation 12.11.1 and Equation 12.11.2 we can make several important conclusions about a solute's electrophoretic velocity. Electrophoretic mobility and, therefore, electrophoretic velocity, increases for more highly charged solutes and for solutes of smaller size. Because q is positive for a cation and negative for an anion, these species migrate in opposite directions. A neutral species, for which q is zero, has an electrophoretic velocity of zero.

ELECTROOSMOTIC MOBILITY

When an electric field is applied to a capillary filled with an aqueous buffer we expect the buffer's ions to migrate in response to their electrophoretic mobility. Because the solvent, H_2O, is neutral we might reasonably expect it to remain stationary. What we observe under normal conditions, however, is that the buffer moves toward the cathode. This phenomenon is called the electroosmotic flow.

Electroosmotic flow occurs because the walls of the capillary tubing carry a charge. The surface of a silica capillary contains large numbers of silanol groups (–SiOH). At a pH level greater than approximately 2 or 3, the silanol groups ionize to form negatively charged silanate ions ($–SiO^-$). Cations from the buffer are attracted to the silanate ions. As shown in Figure 12.7.1 , some of these cations bind tightly to the silanate ions, forming a fixed layer. Because the cations in the fixed layer only partially neutralize the negative charge on the capillary walls, the solution adjacent to the fixed layer—which is called the diffuse layer—contains more cations than anions. Together these two layers are known as the double layer. Cations in the diffuse layer migrate toward the cathode. Because these cations are solvated, the solution also is pulled along, producing the electroosmotic flow.

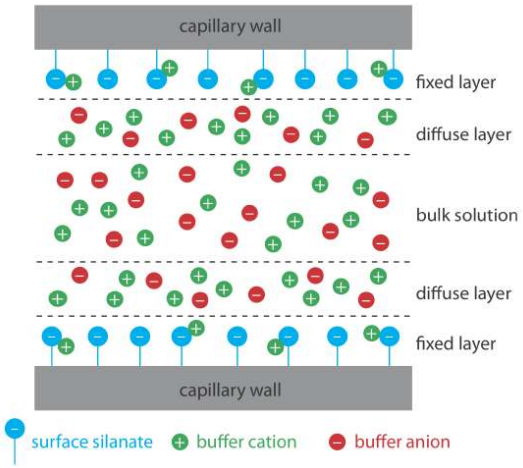


Figure 12.7.1 . Schematic diagram showing the origin of the double layer within a capillary tube. Although the net charge within the capillary is zero, the distribution of charge is not. The walls of the capillary have an excess of negative charge, which decreases across the fixed layer and the diffuse layer, reaching a value of zero in bulk solution.

> The anions in the diffuse layer, which also are solvated, try to move toward the anode. Because there are more cations than anions, however, the cations win out and the electroosmotic flow moves in the direction of the cathode.

The rate at which the buffer moves through the capillary, what we call its ***electroosmotic flow velocity***, ν_{eof}, is a function of the applied electric field, E, and the buffer's electroosmotic mobility, μ_{eof}.

$$\nu_{eof} = \mu_{eof} E \tag{12.11.3}$$

Electroosmotic mobility is defined as

$$\mu_{eof} = \frac{\varepsilon \zeta}{4\pi\eta} \tag{12.11.4}$$

where ϵ is the buffer dielectric constant, ζ is the zeta potential, and η is the buffer's viscosity.

The ***zeta potential***—the potential of the diffuse layer at a finite distance from the capillary wall—plays an important role in determining the electroosmotic flow velocity. Two factors determine the zeta potential's value. First, the zeta potential is directly proportional to the charge on the capillary walls, with a greater density of silanate ions corresponding to a larger zeta potential. Below a pH of 2 there are few silanate ions and the zeta potential and the electroosmotic flow velocity approach zero. As the pH increases, both the zeta potential and the electroosmotic flow velocity increase. Second, the zeta potential is directly proportional to the thickness of the double layer. Increasing the buffer's ionic strength provides a higher concentration of cations, which decreases the thickness of the double layer and decreases the electroosmotic flow.

> The definition of zeta potential given here admittedly is a bit fuzzy. For a more detailed explanation see Delgado, A. V.; González-Caballero, F.; Hunter, R. J.; Koopal, L. K.; Lyklema, J. "Measurement and Interpretation of Electrokinetic Phenomena," *Pure. Appl. Chem.* **2005**, *77*, 1753–1805. Although this is a very technical report, Sections 1.3–1.5 provide a good introduction to the difficulty of defining the zeta potential and of measuring its value.

The electroosmotic flow profile is very different from that of a fluid moving under forced pressure. Figure 12.7.2 compares the electroosmotic flow profile with the hydrodynamic flow profile in gas chromatography and liquid chromatography. The uniform, flat profile for electroosmosis helps minimize band broadening in capillary electrophoresis, improving separation efficiency.

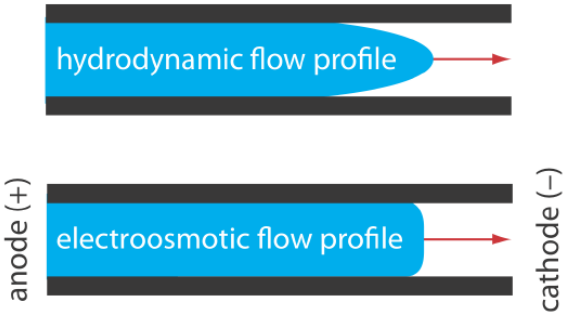


Figure 12.7.2 . Comparison of hydrodynamic flow and electroosmotic flow. The nearly uniform electroosmotic flow profile means that the electroosmotic flow velocity is nearly constant across the capillary.

TOTAL MOBILITY

A solute's total velocity, ν_{tot}, as it moves through the capillary is the sum of its electrophoretic velocity and the electroosmotic flow velocity.

$$\nu_{tot} = \nu_{ep} + \nu_{eof}$$

As shown in Figure 12.7.3 , under normal conditions the following general relationships hold true.

$$(\nu_{tot})_{cations} > \nu_{eof}$$

$$(\nu_{tot})_{neutrals} = \nu_{eof}$$

$$(\nu_{tot})_{anions} < \nu_{eof}$$

Cations elute first in an order that corresponds to their electrophoretic mobilities, with small, highly charged cations eluting before larger cations of lower charge. Neutral species elute as a single band with an elution rate equal to the electroosmotic flow velocity. Finally, anions are the last components to elute, with smaller, highly charged anions having the longest elution time.

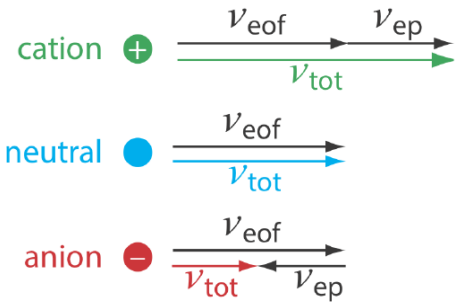


Figure 12.7.3 . Visual explanation for the general elution order in capillary electrophoresis. Each species has the same electroosmotic flow, ν_{eof}. Cations elute first because they have a positive electrophoretic velocity, ν_{ep}. Anions elute last because their negative electrophoretic velocity partially offsets the electroosmotic flow velocity. Neutrals elute with a velocity equal to the electroosmotic flow.

MIGRATION TIME

Another way to express a solute's velocity is to divide the distance it travels by the elapsed time

$$\nu_{tot} = \frac{l}{t_m} \tag{12.11.5}$$

where l is the distance between the point of injection and the detector, and t_m is the solute's migration time. To understand the experimental variables that affect migration time, we begin by noting that

$$\nu_{tot} = \mu_{tot} E = (\mu_{ep} + \mu_{eof}) E \tag{12.11.6}$$

Combining Equation 12.11.5 and Equation 12.11.6 and solving for t_m leaves us with

$$t_m = \frac{l}{(\mu_{ep} + \mu_{eof}) E} \tag{12.11.7}$$

The magnitude of the electrical field is

$$E = \frac{V}{L} \tag{12.11.8}$$

where V is the applied potential and L is the length of the capillary tube. Finally, substituting Equation 12.11.8 into Equation 12.11.7 leaves us with the following equation for a solute's migration time.

$$t_{\mathrm{m}} = \frac{lL}{(\mu_{ep} + \mu_{eof})\,V} \tag{12.11.9}$$

To decrease a solute's migration time—which shortens the analysis time—we can apply a higher voltage or use a shorter capillary tube. We can also shorten the migration time by increasing the electroosmotic flow, although this decreases resolution.

EFFICIENCY

As we learned in Chapter 12.2, the efficiency of a separation is given by the number of theoretical plates, N. In capillary electrophoresis the number of theoretic plates is

$$N = \frac{l^2}{2Dt_m} = \frac{(\mu_{ep} + \mu_{eof})\,El}{2DL} \tag{12.11.10}$$

where D is the solute's diffusion coefficient. From Equation 12.11.10, the efficiency of a capillary electrophoretic separation increases with higher voltages. Increasing the electroosmotic flow velocity improves efficiency, but at the expense of resolution. Two additional observations deserve comment. First, solutes with larger electrophoretic mobilities—in the same direction as the electroosmotic flow—have greater efficiencies; thus, smaller, more highly charged cations are not only the first solutes to elute, but do so with greater efficiency. Second, efficiency in capillary electrophoresis is independent of the capillary's length. Theoretical plate counts of approximately 100 000–200 000 are not unusual.

> It is possible to design an electrophoretic experiment so that anions elute before cations—more about this later—in which smaller, more highly charged anions elute with greater efficiencies.

SELECTIVITY

In chromatography we defined the selectivity between two solutes as the ratio of their retention factors. In capillary electrophoresis the analogous expression for selectivity is

$$\alpha = \frac{\mu_{ep,1}}{\mu_{ep,2}}$$

where $\mu_{ep,1}$ and $\mu_{ep,2}$ are the electrophoretic mobilities for the two solutes, chosen such that $\alpha \geq 1$. We can often improve selectivity by adjusting the pH of the buffer solution. For example, NH_4^+ is a weak acid with a pK_a of 9.75. At a pH of 9.75 the concentrations of NH_4^+ and NH_3 are equal. Decreasing the pH below 9.75 increases its electrophoretic mobility because a greater fraction of the solute is present as the cation NH_4^+. On the other hand, raising the pH above 9.75 increases the proportion of neutral NH_3, decreasing its electrophoretic mobility.

RESOLUTION

The resolution between two solutes is

$$R = \frac{0.177(\mu_{ep,2} - \mu_{ep,1})\sqrt{V}}{\sqrt{D(\mu_{avg} + \mu_{eof}}} \tag{12.11.11}$$

where μ_{avg} is the average electrophoretic mobility for the two solutes. Increasing the applied voltage and decreasing the electroosmotic flow velocity improves resolution. The latter effect is particularly important. Although increasing electroosmotic flow improves analysis time and efficiency, it de- creases resolution.

INSTRUMENTATION

The basic instrumentation for capillary electrophoresis is shown in Figure 12.7.4 and includes a power supply for applying the electric field, anode and cathode compartments that contain reservoirs of the buffer solution, a sample vial that contains the sample, the capillary tube, and a detector. Each part of the instrument receives further consideration in this section.

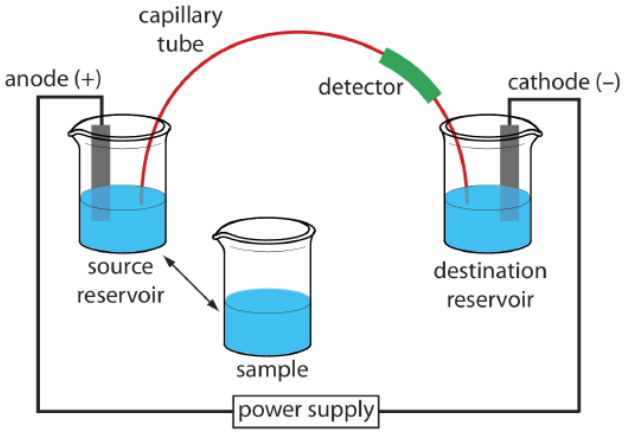


Figure 12.7.4 . Schematic diagram of the basic instrumentation for capillary electrophoresis. The sample and the source reservoir are switched when making injections.

CAPILLARY TUBES

Figure 12.7.5 shows a cross-section of a typical capillary tube. Most capillary tubes are made from fused silica coated with a 15–35 μm layer of polyimide to give it mechanical strength. The inner diameter is typically 25–75 μm, which is smaller than the internal diameter of a capillary GC column, with an outer diameter of 200–375 μm.

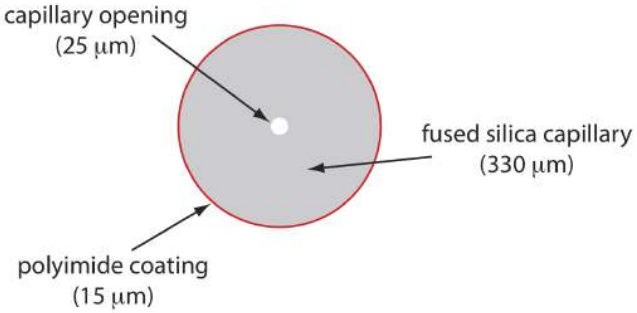


Figure 12.7.5 . Cross section of a capillary column for capillary electrophoresis. The dimensions shown here are typical and are scaled proportionally in this figure.

The capillary column's narrow opening and the thickness of its walls are important. When an electric field is applied to the buffer solution, current flows through the capillary. This current leads to the release of heat, which we call ***Joule heating***. The amount of heat released is proportional to the capillary's radius and to the magnitude of the electrical field. Joule heating is a problem because it changes the buffer's viscosity, with the solution at the center of the capillary being less viscous than that near the capillary walls. Because a solute's electrophoretic mobility depends on its viscosity (see Equation 12.11.2), solute species in the center of the capillary migrate at a faster rate than those near the capillary walls. The result is an additional source of band broadening that degrades the separation. Capillaries with smaller inner diameters generate less Joule heating, and capillaries with larger outer diameters are more effective at dissipating the heat. Placing the capillary tube inside a thermostated jacket is another method for minimizing the effect of Joule heating; in this case a smaller outer diameter allows for a more rapid dissipation of thermal energy.

INJECTING THE SAMPLE

There are two common methods for injecting a sample into a capillary electrophoresis column: hydrodynamic injection and electrokinetic injection. In both methods the capillary tube is filled with the buffer solution. One end of the capillary tube is placed in the destination reservoir and the other end is placed in the sample vial.

Hydrodynamic injection uses pressure to force a small portion of sample into the capillary tubing. A difference in pressure is applied across the capillary either by pressurizing the sample vial or by applying a vacuum to the destination reservoir. The volume of sample injected, in liters, is given by the following equation

$$V_{\text{inj}} = \frac{\Delta P d^4 \pi t}{128 \eta L} \times 10^3 \tag{12.11.12}$$

where ΔP is the difference in pressure across the capillary in pascals, d is the capillary's inner diameter in meters, t is the amount of time the pressure is applied in seconds, η is the buffer's viscosity in kg m^{-1} s^{-1}, and L is the length of the capillary tubing in meters. The factor of

10^3 changes the units from cubic meters to liters.

For a hydrodynamic injection we move the capillary from the source reservoir to the sample. The anode remains in the source reservoir. A hydrodynamic injection also is possible if we raise the sample vial above the destination reservoir and briefly insert the filled capillary.

EXAMPLE 12.7.1

In a hydrodynamic injection we apply a pressure difference of 2.5×10^3 Pa (a $\Delta P \approx 0.02$ atm) for 2 s to a 75-cm long capillary tube with an internal diameter of 50 μm. Assuming the buffer's viscosity is 10^{-3} kg m^{-1} s^{-1}, what volume and length of sample did we inject?

Solution

Making appropriate substitutions into Equation 12.11.12 gives the sample's volume as

$$V_{inj} = \frac{\left(2.5 \times 10^3 \text{ kg m}^{-1} \text{ s}^{-2}\right)\left(50 \times 10^{-6} \text{ m}\right)^4 (3.14)(2 \text{ s})}{(128)\left(0.001 \text{ kg m}^{-1} \text{ s}^{-1}\right)(0.75 \text{ m})} \times 10^3 \text{L/m}^3$$

$$V_{inj} = 1 \times 10^{-9} \text{ L} = 1 \text{ nL}$$

Because the interior of the capillary is cylindrical, the length of the sample, *l*, is easy to calculate using the equation for the volume of a cylinder; thus

$$l = \frac{V_{\text{inj}}}{\pi r^2} = \frac{\left(1 \times 10^{-9} \text{ L}\right)\left(10^{-3} \text{ m}^3\text{/L}\right)}{(3.14)\left(25 \times 10^{-6} \text{ m}\right)^2} = 5 \times 10^{-4} \text{ m} = 0.5 \text{ mm}$$

EXERCISE 12.7.1

Suppose you need to limit your injection to less than 0.20% of the capillary's length. Using the information from Example 12.7.1 , what is the maximum injection time for a hydrodynamic injection?

Answer

The capillary is 75 cm long, which means that 0.20% of that sample's maximum length is 0.15 cm. To convert this to the maximum volume of sample we use the equation for the volume of a cylinder.

$$V_{inj} = l\pi r^2 = (0.15 \text{ cm})(3.14)\left(25 \times 10^{-4} \text{ cm}\right)^2 = 2.94 \times 10^{-6} \text{ cm}^3$$

Given that 1 cm^3 is equivalent to 1 mL, the maximum volume is 2.94×10^{-6} mL or 2.94×10^{-9} L. To find the maximum injection time, we first solve Equation 12.11.12 for *t*

$$t = \frac{128 V_{inj} \eta L}{P d^4 \pi} \times 10^{-3} \text{ m}^3\text{/L}$$

and then make appropriate substitutions.

$$t = \frac{(128)\left(2.94 \times 10^{-9} \text{ L}\right)\left(0.001 \text{ kg } \text{ m}^{-1} \text{ s}^{-1}\right)(0.75 \text{ m})}{\left(2.5 \times 10^3 \text{ kg m}^{-1} \text{ s}^{-2}\right)\left(50 \times 10^{-6} \text{ m}\right)^4 (3.14)} \times \frac{10^{-3} \text{ m}^3}{\text{L}} = 5.8 \text{ s}$$

The maximum injection time, therefore, is 5.8 s.

In an ***electrokinetic injection*** we place both the capillary and the anode into the sample and briefly apply an potential. The volume of injected sample is the product of the capillary's cross sectional area and the length of the capillary occupied by the sample. In turn, this length is the product of the solute's velocity (see Equation 12.11.6) and time; thus

$$V_{inj} = \pi r^2 L = \pi r^2 (\mu_{ep} + \mu_{eof}) E' t \tag{12.11.13}$$

where *r* is the capillary's radius, *L* is the capillary's length, and E' is the effective electric field in the sample. An important consequence of Equation 12.11.13 is that an electrokinetic injection is biased toward solutes with larger electrophoretic mobilities. If two solutes have equal concentrations in a sample, we inject a larger volume—and thus more moles—of the solute with the larger μ_{ep}.

The electric field in the sample is different that the electric field in the rest of the capillary because the sample and the buffer have different ionic compositions. In general, the sample's ionic strength is smaller, which makes its conductivity smaller. The effective electric field is

$$E' = E \times \frac{\chi_{\text{buffer}}}{\chi_{\text{sample}}}$$

where χ_{buffer} and χ_{sample} are the conductivities of the buffer and the sample, respectively.

When an analyte's concentration is too small to detect reliably, it maybe possible to inject it in a manner that increases its concentration. This method of injection is called ***stacking***. Stacking is accomplished by placing the sample in a solution whose ionic strength is significantly less than that of the buffer in the capillary tube. Because the sample plug has a lower concentration of buffer ions, the effective field strength across the sample plug, E', is larger than that in the rest of the capillary.

We know from Equation 12.11.1 that electrophoretic velocity is directly proportional to the electrical field. As a result, the cations in the sample plug migrate toward the cathode with a greater velocity, and the anions migrate more slowly—neutral species are unaffected and move with the electroosmotic flow. When the ions reach their respective boundaries between the sample plug and the buffer, the electrical field decreases and the electrophoretic velocity of the cations decreases and that for the anions increases. As shown in Figure 12.7.6 , the result is a stacking of cations and anions into separate, smaller sampling zones. Over time, the buffer within the capillary becomes more homogeneous and the separation proceeds without additional stacking.

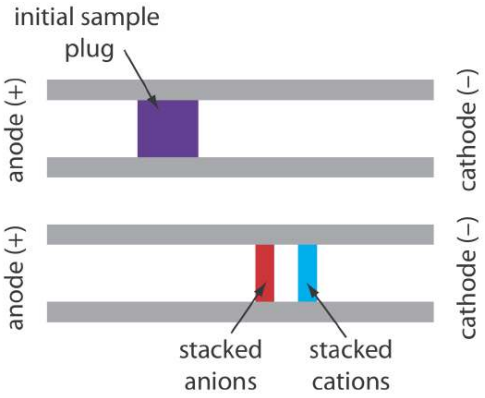


Figure 12.7.6 . The stacking of cations and anions. The top diagram shows the initial sample plug and the bottom diagram shows how the cations and anions are concentrated at opposite sides of the sample plug.

APPLYING THE ELECTRICAL FIELD

Migration in electrophoresis occurs in response to an applied electric field. The ability to apply a large electric field is important because higher voltages lead to shorter analysis times (Equation 12.11.9), more efficient separations (Equation 12.11.10), and better resolution (Equation 12.11.11). Because narrow bored capillary tubes dissipate Joule heating so efficiently, voltages of up to 40 kV are possible.

Because of the high voltages, be sure to follow your instrument's safety guidelines.

DETECTORS

Most of the detectors used in HPLC also find use in capillary electrophoresis. Among the more common detectors are those based on the absorption of UV/Vis radiation, fluorescence, conductivity, amperometry, and mass spectrometry. Whenever possible, detection is done "on-column" before the solutes elute from the capillary tube and additional band broadening occurs.

UV/Vis detectors are among the most popular. Because absorbance is directly proportional to path length, the capillary tubing's small diameter leads to signals that are smaller than those obtained in HPLC. Several approaches have been used to increase the pathlength, including a Z-shaped sample cell and multiple reflections (see Figure 12.7.7). Detection limits are about 10^{-7} M.

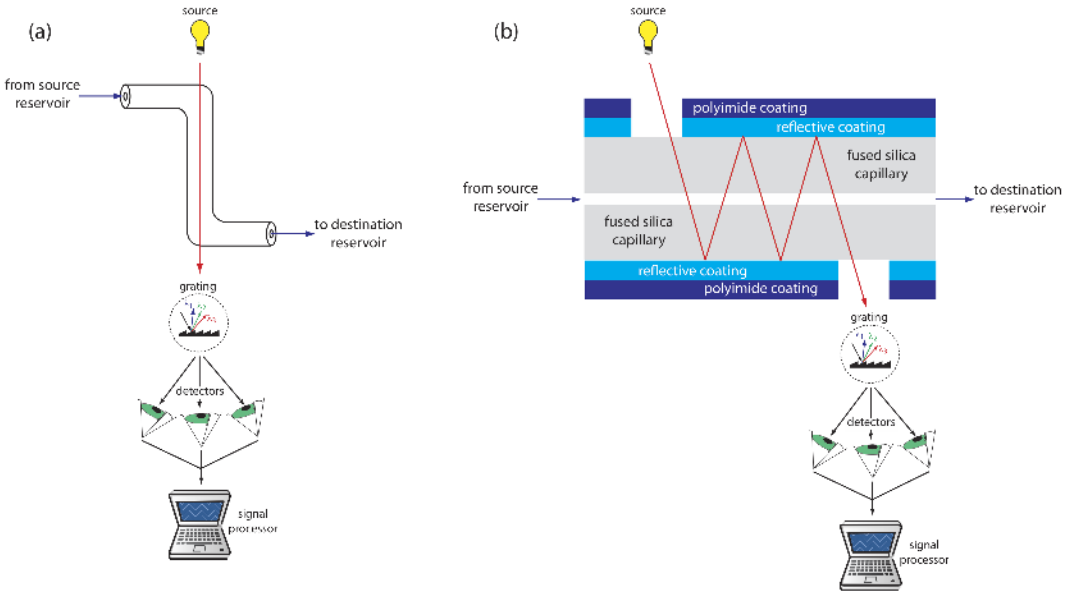


Figure 12.7.7 . Two approaches to on-column detection in capillary electrophoresis using a UV/Vis diode array spectrometer: (a) Z-shaped bend in capillary, and (b) multiple reflections.

Better detection limits are obtained using fluorescence, particularly when using a laser as an excitation source. When using fluorescence detection a small portion of the capillary's protective coating is removed and the laser beam is focused on the inner portion of the capillary tubing. Emission is measured at an angle of 90º to the laser. Because the laser provides an intense source of radiation that can be focused to a narrow spot, detection limits are as low as 10^{-16} M.

Solutes that do not absorb UV/Vis radiation or that do not undergo fluorescence can be detected by other detectors. Table 12.7.1 provides a list of detectors for capillary electrophoresis along with some of their important characteristics.

Table 12.7.1 . Characteristics of Detectors for Capillary Electrophoresis

detector	selectivity (universal or analyte must ...)	detection limited (moles injected)	detection limit (molarity)	on-column detection?
UV/Vis absorbance	have a UV/Vis chromophore	$10^{-13} - 10^{-16}$	$10^{-5} - 10^{-7}$	yes
indirect absorbancd	universal	$10^{-12} - 10^{-15}$	$10^{-4} - 10^{-6}$	yes
fluoresence	have a favorable quantum yield	$10^{-13} - 10^{-17}$	$10^{-7} - 10^{-9}$	yes
laser fluorescence	have a favorable quantum yield	$10^{-18} - 10^{-20}$	$10^{-13} - 10^{-16}$	yes
mass spectrometer	universal (total ion) selective (single ion)	$10^{-16} - 10^{-17}$	$10^{-8} - 10^{-10}$	no
amperometry	undergo oxidation or reduction	$10^{-18} - 10^{-19}$	$10^{-7} - 10^{-10}$	no
conductivity	universal	$10^{-15} - 10^{-16}$	$10^{-7} - 10^{-9}$	no
radiometric	be radioactive	$10^{-17} - 10^{-19}$	$10^{-10} - 10^{-12}$	yes

CAPILLARY ELECTROPHORESIS METHODS

There are several different forms of capillary electrophoresis, each of which has its particular advantages. Four of these methods are described briefly in this section.

CAPILLARY ZONE ELECTROPHORESIS (CZE)

The simplest form of capillary electrophoresis is ***capillary zone electrophoresis***. In CZE we fill the capillary tube with a buffer and, after loading the sample, place the ends of the capillary tube in reservoirs that contain additional buffer. Usually the end of the capillary containing the sample is the anode and solutes migrate toward the cathode at a velocity determined by their respective electrophoretic mobilities and the electroosmotic flow. Cations elute first, with smaller, more highly charged cations eluting before larger cations with smaller charges. Neutral species elute as a single band. Anions are the last species to elute, with smaller, more negatively charged anions being the last to elute.

We can reverse the direction of electroosmotic flow by adding an alkylammonium salt to the buffer solution. As shown in Figure 12.7.8 , the positively charged end of the alkyl ammonium ions bind to the negatively charged silanate ions on the capillary's walls. The tail of the alkyl ammonium ion is hydrophobic and associates with the tail of another alkyl ammonium ion. The result is a layer of positive charges that attract anions in the buffer. The migration of these solvated anions toward the anode reverses the electroosmotic flow's direction. The order of elution is exactly opposite that observed under normal conditions.

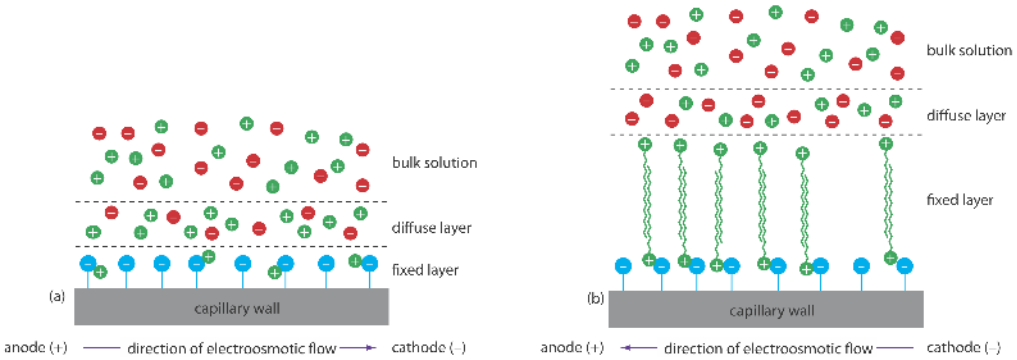


Figure 12.7.8 . Two modes of capillary zone electrophoresis showing (a) normal migration with electroosmotic flow toward the cathode and (b) reversed migration in which the electroosmotic flow is toward the anode.

Coating the capillary's walls with a nonionic reagent eliminates the electroosmotic flow. In this form of CZE the cations migrate from the anode to the cathode. Anions elute into the source reservoir and neutral species remain stationary.

Capillary zone electrophoresis provides effective separations of charged species, including inorganic anions and cations, organic acids and amines, and large biomolecules such as proteins. For example, CZE was used to separate a mixture of 36 inorganic and organic ions in less than three minutes [Jones, W. R.; Jandik, P. *J. Chromatog*. **1992**, *608*, 385–393]. A mixture of neutral species, of course, can not be resolved.

MICELLAR ELECTROKINETIC CAPILLARY CHROMATOGRAPHY (MEKC)

One limitation to CZE is its inability to separate neutral species. ***Micellar electrokinetic capillary chromatography*** overcomes this limitation by adding a surfactant, such as sodium dodecylsulfate (Figure 12.7.9 a) to the buffer solution. Sodium dodecylsulfate, or SDS, consists of a long-chain hydrophobic tail and a negatively charged ionic functional group at its head. When the concentration of SDS is sufficiently large a micelle forms. A micelle consists of a spherical agglomeration of 40–100 surfactant molecules in which the hydrocarbon tails point inward and the negatively charged heads point outward (Figure 12.7.9 b).

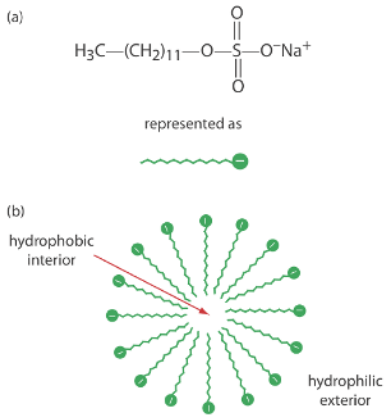


Figure 12.7.9 . (a) Structure of sodium dodecylsulfate and (b) cross section through a micelle showing its hydrophobic interior and its hydrophilic exterior.

Because micelles have a negative charge, they migrate toward the cathode with a velocity less than the electroosmotic flow velocity. Neutral species partition themselves between the micelles and the buffer solution in a manner similar to the partitioning of solutes between the two liquid phases in HPLC. Because there is a partitioning between two phases, we include the descriptive term chromatography in the techniques name. Note that in MEKC both phases are mobile.

The elution order for neutral species in MEKC depends on the extent to which each species partitions into the micelles. Hydrophilic neutrals are insoluble in the micelle's hydrophobic inner environment and elute as a single band, as they would in CZE. Neutral solutes that are extremely hy- drophobic are completely soluble in the micelle, eluting with the micelles as a single band. Those neutral species that exist in a partition equilibrium between the buffer and the micelles elute between the completely hydro- philic and completely hydrophobic neutral species. Those neutral species that favor the buffer elute before those favoring the micelles. Micellar electrokinetic chromatography is used to separate a wide variety of samples, including mixtures of pharmaceutical compounds, vitamins, and explosives.

CAPILLARY GEL ELECTROPHORESIS (CGE)

In ***capillary gel electrophoresis*** the capillary tubing is filled with a polymeric gel. Because the gel is porous, a solute migrates through the gel with a velocity determined both by its electrophoretic mobility and by its size. The ability to effect a separation using size is helpful

when the solutes have similar electrophoretic mobilities. For example, fragments of DNA of varying length have similar charge-to-size ratios, making their separation by CZE difficult. Because the DNA fragments are of different size, a CGE separation is possible.

The capillary used for CGE usually is treated to eliminate electroosmotic flow to prevent the gel from extruding from the capillary tubing. Samples are injected electrokinetically because the gel provides too much resistance for hydrodynamic sampling. The primary application of CGE is the separation of large biomolecules, including DNA fragments, proteins, and oligonucleotides.

CAPILLARY ELECTROCHROMATOGRAPHY (CEC)

Another approach to separating neutral species is ***capillary electrochromatography***. In CEC the capillary tubing is packed with 1.5–3 μm particles coated with a bonded stationary phase. Neutral species separate based on their ability to partition between the stationary phase and the buffer, which is moving as a result of the electroosmotic flow; Figure 12.7.10 provides a representative example for the separation of a mixture of hydrocarbons. A CEC separation is similar to the analogous HPLC separation, but without the need for high pressure pumps. Efficiency in CEC is better than in HPLC, and analysis times are shorter.

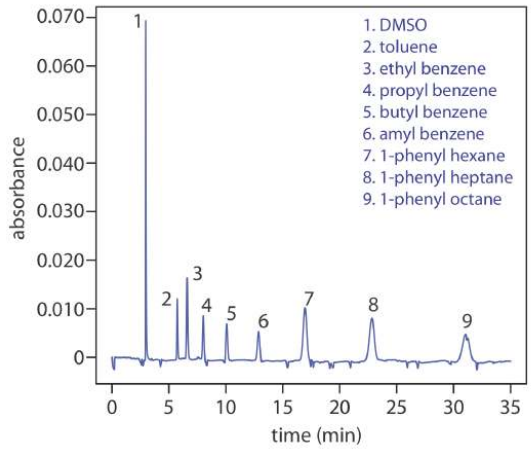


Figure 12.7.10 . Capillary electrochromatographic separation of a mixture of hydrocarbons in DMSO. The column contains a porous polymer of butyl methacrylate and lauryl acrylate (25%:75% mol:mol) with butane dioldacrylate as a crosslinker. Data provided by Zoe LaPier and Michelle Bushey, Department of Chemistry, Trinity University.

The best way to appreciate the theoretical and the practical details discussed in this section is to carefully examine a typical analytical method. Although each method is unique, the following description of the determination of a vitamin B complex by capillary zone electrophoresis or by micellar electrokinetic capillary chromatography provides an instructive example of a typical procedure. The description here is based on Smyth, W. F. *Analytical Chemistry of Complex Matrices*, Wiley Teubner: Chichester, England, 1996, pp. 154–156.

REPRESENTATIVE METHOD 12.7.1: DETERMINATION OF VITAMIN B COMPLEX BY CZE OR MEKC

Description of Method

The water soluble vitamins B_1 (thiamine hydrochloride), B_2 (riboflavin), B_3 (niacinamide), and B_6 (pyridoxine hydrochloride) are determined by CZE using a pH 9 sodium tetraborate-sodium dihydrogen phosphate buffer, or by MEKC using the same buffer with the addition of sodium dodecyl sulfate. Detection is by UV absorption at 200 nm. An internal standard of *o*-ethoxybenzamide is used to standardize the method.

Procedure

Crush a vitamin B complex tablet and place it in a beaker with 20.00 mL of a 50 % v/v methanol solution that is 20 mM in sodium tetraborate and 100.0 ppm in *o*-ethoxybenzamide. After mixing for 2 min to ensure that the B vitamins are dissolved, pass a 5.00-mL portion through a 0.45-μm filter to remove insoluble binders. Load an approximately 4 nL sample into a capillary column with an inner diameter of a 50 μm. For CZE the capillary column contains a 20 mM pH 9 sodium tetraborate-sodium dihydrogen phosphate buffer. For MEKC the buffer is also 150 mM in sodium dodecyl sulfate. Apply a 40 kV/m electrical field to effect both the CZE and MEKC separations.

Questions

1. Methanol, which elutes at 4.69 min, is included as a neutral species to indicate the electroosmotic flow. When using standard solutions of each vitamin, CZE peaks are found at 3.41 min, 4.69 min, 6.31 min, and 8.31 min. Examine the structures and pK_a information in Figure 12.7.11 and identify the order in which the four B vitamins elute.

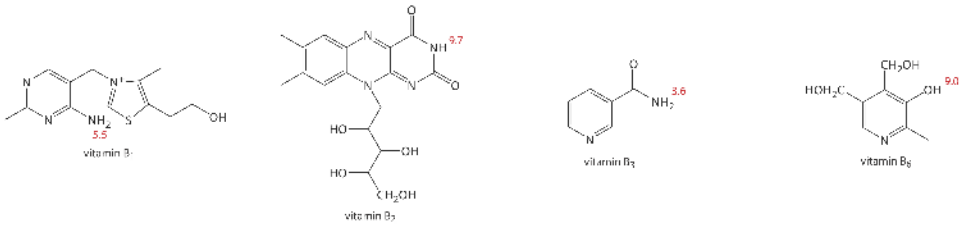


Figure 12.7.11 . Structures of the four water soluble B vitamins in their predominate forms at a pH of 9; pK_a values are shown in red.

At a pH of 9, vitamin B_1 is a cation and elutes before the neutral species methanol; thus it is the compound that elutes at 3.41 min. Vitamin B_3 is a neutral species at a pH of 9 and elutes with methanol at 4.69 min. The remaining two B vitamins are weak acids that partially ionize to weak base anions at a pH of 9. Of the two, vitamin B_6 is the stronger acid (a pK_a of 9.0 versus a pK_a of 9.7) and is present to a greater extent in its anionic form. Vitamin B_6, therefore, is the last of the vitamins to elute.

2. The order of elution when using MEKC is vitamin B_3 (5.58 min), vitamin B_6 (6.59 min), vitamin B_2 (8.81 min), and vitamin B_1 (11.21 min). What conclusions can you make about the solubility of the B vitamins in the sodium dodecylsulfate micelles? The micelles elute at 17.7 min.

The elution time for vitamin B_1 shows the greatest change, increasing from 3.41 min to 11.21 minutes. Clearly vitamin B_1 has the greatest solubility in the micelles. Vitamin B_2 and vitamin B3 have a more limited solubility in the micelles, and show only slightly longer elution times in the presence of the micelles. Interestingly, the elution time for vitamin B_6 decreases in the presence of the micelles.

3. For quantitative work an internal standard of *o*-ethoxybenzamide is added to all samples and standards. Why is an internal standard necessary?

Although the method of injection is not specified, neither a hydrodynamic injection nor an electrokinetic injection is particularly reproducible. The use of an internal standard compensates for this limitation.

EVALUATION

When compared to GC and HPLC, capillary electrophoresis provides similar levels of accuracy, precision, and sensitivity, and it provides a comparable degree of selectivity. The amount of material injected into a capillary electrophoretic column is significantly smaller than that for GC and HPLC—typically 1 nL versus 0.1 µL for capillary GC and 1–100 µL for HPLC. Detection limits for capillary electrophoresis, however, are 100–1000 times poorer than that for GC and HPLC. The most significant advantages of capillary electrophoresis are improvements in separation efficiency, time, and cost. Capillary electrophoretic columns contain substantially more theoretical plates ($\approx 10^6$ plates/m) than that found in HPLC ($\approx 10^5$ plates/m) and capillary GC columns ($\approx 10^3$ plates/m), providing unparalleled resolution and peak capacity. Separations in capillary electrophoresis are fast and efficient. Furthermore, the capillary column's small volume means that a capillary electrophoresis separation requires only a few microliters of buffer, compared to 20–30 mL of mobile phase for a typical HPLC separation.

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12.12: PROBLEMS

1. The following data were obtained for four compounds separated on a 20-m capillary column.

compound	t_r (min)	w (min)
A	8.04	0.15
B	8.26	0.15
C	8.43	0.16

(a) Calculate the number of theoretical plates for each compound and the average number of theoretical plates for the column, in mm.

(b) Calculate the average height of a theoretical plate.

(c) Explain why it is possible for each compound to have a different number of theoretical plates.

2. Using the data from Problem 1, calculate the resolution and the selectivity factors for each pair of adjacent compounds. For resolution, use both equation 12.2.1 and equation 12.3.3, and compare your results. Discuss how you might improve the resolution between compounds B and C. The retention time for an nonretained solute is 1.19 min.

3. Use the chromatogram in Figure 12.8.1 , obtained using a 2-m column, to determine values for t_r, w, t'_r, k, N, and H.

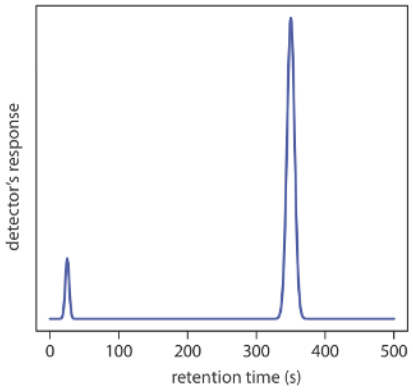


Figure 12.8.1 . Chromatogram for Problem 3.

4. Use the partial chromatogram in Figure 12.8.2 to determine the resolution between the two solute bands.

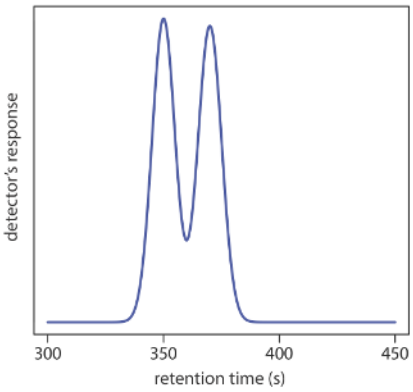


Figure 12.8.2 . Chromatogram for Problem 4.

5. The chromatogram in Problem 4 was obtained on a 2-m column with a column dead time of 50 s. Suppose you want to increase the resolution between the two components to 1.5. Without changing the height of a theoretical plate, what length column do you need? What height of a theoretical plate do you need to achieve a resolution of 1.5 without increasing the column's length?

6. Complete the following table.

N_B	α	k_B	R
100000	1.05	0.50	
10000	1.10		1.50
10000		4.0	1.00
	1.05	3.0	1.75

7. Moody studied the efficiency of a GC separation of 2-butanone on a dinonyl phthalate packed column [Moody, H. W. *J. Chem. Educ.* **1982**, *59*, 218–219]. Evaluating plate height as a function of flow rate gave a van Deemter equation for which *A* is 1.65 mm, *B* is 25.8 mm•mL min^{-1}, and *C* is 0.0236 mm•min mL^{-1}.

(a) Prepare a graph of *H* versus *u* for flow rates between 5 –120 mL/min.

(b) For what range of flow rates does each term in the Van Deemter equation have the greatest effect?

(c) What is the optimum flow rate and the corresponding height of a theoretical plate?

(d) For open-tubular columns the *A* term no longer is needed. If the *B* and *C* terms remain unchanged, what is the optimum flow rate and the corresponding height of a theoretical plate?

(e) Compared to the packed column, how many more theoretical plates are in the open-tubular column?

8. Hsieh and Jorgenson prepared 12–33 µm inner diameter HPLC columns packed with 5.44-µm spherical stationary phase particles [Hsieh, S.; Jorgenson, J. W. *Anal. Chem.* **1996**, *68*, 1212–1217]. To evaluate these columns they measured reduced plate height, *h*, as a function of reduced flow rate, *v*,

$$b = \frac{H}{d_p} \quad v = \frac{ud_p}{D_m}$$

where d_p is the particle diameter and D_m is the solute's diffusion coefficient in the mobile phase. The data were analyzed using van Deemter plots. The following table contains a portion of their results for norepinephrine.

internal diameter (µm)	A	B	C
33	0.63	1.32	0.10
33	0.67	1.30	0.08
23	0.40	1.34	0.09
23	0.58	1.11	0.09
17	0.31	1.47	0.11
17	0.40	1.41	0.11
12	0.22	1.53	0.11
12	0.19	1.27	0.12

(a) Construct separate van Deemter plots using the data in the first row and in the last row for reduced flow rates in the range 0.7–15. Determine the optimum flow rate and plate height for each case given d_p = 5.44 µm and $D_m = 6.23 \times 10^{-6}$ $cm^2\ s^{-1}$.

(b) The *A* term in the van Deemter equation is strongly correlated with the column's inner diameter, with smaller diameter columns providing smaller values of *A*. Offer an explanation for this observation. *Hint: consider how many particles can fit across a capillary of each diameter.*

> When comparing columns, chromatographers often use dimensionless, reduced parameters. By including particle size and the solute's diffusion coefficient, the reduced plate height and reduced flow rate correct for differences between the packing material, the solute, and the mobile phase.

9. A mixture of *n*-heptane, tetrahydrofuran, 2-butanone, and *n*-propanol elutes in this order when using a polar stationary phase such as Carbowax. The elution order is exactly the opposite when using a nonpolar stationary phase such as polydimethyl siloxane. Explain the order of elution in each case.

10. The analysis of trihalomethanes in drinking water is described in Representative Method 12.4.1. A single standard that contains all four trihalomethanes gives the following results.

compound	concentration (ppb)	peak area
$CHCl_3$	1.30	1.35×10^4
$CHCl_2Br$	0.90	6.12×10^4
$CHClBr_2$	4.00	1.71×10^4
$CHBr_3$	1.20	1.52×10^4

Analysis of water collected from a drinking fountain gives areas of 1.56×10^4, 5.13×10^4, 1.49×10^4, and 1.76×10^4 for, respectively, $CHCl_3$, $CHCl_2Br$, $CHClBr_2$, and $CHBr_3$. All peak areas were corrected for variations in injection volumes using an internal standard of 1,2-dibromopentane. Determine the concentration of each of the trihalomethanes in the sample of water.

11. Zhou and colleagues determined the %w/w H_2O in methanol by capillary column GC using a polar stationary phase and a thermal conductivity detector [Zhou, X.; Hines, P. A.; White, K. C.; Borer, M. W. *Anal. Chem.* **1998**, *70*, 390–394]. A series of calibration standards

gave the following results.

%w/w H_2O	peak height (arb. units)
0.00	1.15
0.0145	2.74
0.0472	6.33
0.0951	11.58
0.1757	20.43
0.2901	32.97

(a) What is the %w/w H_2O in a sample that has a peak height of 8.63?

(b) The %w/w H_2O in a freeze-dried antibiotic is determined in the following manner. A 0.175-g sample is placed in a vial along with 4.489 g of methanol. Water in the vial extracts into the methanol. Analysis of the sample gave a peak height of 13.66. What is the %w/w H_2O in the antibiotic?

12. Loconto and co-workers describe a method for determining trace levels of water in soil [Loconto, P. R.; Pan, Y. L.; Voice, T. C. *LC•GC* **1996**, *14*, 128–132]. The method takes advantage of the reaction of water with calcium carbide, CaC_2, to produce acetylene gas, C_2H_2. By carrying out the reaction in a sealed vial, the amount of acetylene produced is determined by sampling the headspace. In a typical analysis a sample of soil is placed in a sealed vial with CaC_2. Analysis of the headspace gives a blank corrected signal of 2.70×10^5. A second sample is prepared in the same manner except that a standard addition of 5.0 mg H_2O/g soil is added, giving a blank-corrected signal of 1.06×10^6. Determine the milligrams H_2O/g soil in the soil sample.

13. Van Atta and Van Atta used gas chromatography to determine the %v/v methyl salicylate in rubbing alcohol [Van Atta, R. E.; Van Atta, R. L. *J. Chem. Educ.* **1980**, *57*, 230–231]. A set of standard additions was prepared by transferring 20.00 mL of rubbing alcohol to separate 25-mL volumetric flasks and pipeting 0.00 mL, 0.20 mL, and 0.50 mL of methyl salicylate to the flasks. All three flasks were diluted to volume using isopropanol. Analysis of the three samples gave peak heights for methyl salicylate of 57.00 mm, 88.5 mm, and 132.5 mm, respectively. Determine the %v/v methyl salicylate in the rubbing alcohol.

14. The amount of camphor in an analgesic ointment is determined by GC using the method of internal standards [Pant, S. K.; Gupta, P. N.; Thomas, K. M.; Maitin, B. K.; Jain, C. L. *LC•GC* **1990**, *8*, 322–325]. A standard sample is prepared by placing 45.2 mg of camphor and 2.00 mL of a 6.00 mg/mL internal standard solution of terpene hydrate in a 25-mL volumetric flask and diluting to volume with CCl_4. When an approximately 2-µL sample of the standard is injected, the FID signals for the two components are measured (in arbitrary units) as 67.3 for camphor and 19.8 for terpene hydrate. A 53.6-mg sample of an analgesic ointment is prepared for analysis by placing it in a 50-mL Erlenmeyer flask along with 10 mL of CCl_4. After heating to 50°C in a water bath, the sample is cooled to below room temperature and filtered. The residue is washed with two 5-mL portions of CCl_4 and the combined filtrates are collected in a 25-mL volumetric flask. After adding 2.00 mL of the internal standard solution, the contents of the flask are diluted to volume with CCl_4. Analysis of an approximately 2-µL sample gives FID signals of 13.5 for the terpene hydrate and 24.9 for the camphor. Report the %w/w camphor in the analgesic ointment.

15. The concentration of pesticide residues on agricultural products, such as oranges, is determined by GC-MS [Feigel, C. *Varian GC/MS Application Note*, Number 52]. Pesticide residues are extracted from the sample using methylene chloride and concentrated by evaporating the methylene chloride to a smaller volume. Calibration is accomplished using anthracene-d_{10} as an internal standard. In a study to determine the parts per billion heptachlor epoxide on oranges, a 50.0-g sample of orange rinds is chopped and extracted with 50.00 mL of methylene chloride. After removing any insoluble material by filtration, the methylene chloride is reduced in volume, spiked with a known amount of the internal standard and diluted to 10 mL in a volumetric flask. Analysis of the sample gives a peak–area ratio ($A_{analyte}/A_{intstd}$) of 0.108. A series of calibration standards, each containing the same amount of anthracene-d_{10} as the sample, gives the following results.

ppb heptachlor epoxide	$A_{analyte}/A_{intstd}$
20.0	0.065
60.0	0.153
200.0	0.637
500.0	1.554
1000.0	3.198

Report the nanograms per gram of heptachlor epoxide residue on the oranges.

16. The adjusted retention times for octane, toluene, and nonane on a particular GC column are 15.98 min, 17.73 min, and 20.42 min, respectively. What is the retention index for each compound?

17. The following data were collected for a series of normal alkanes using a stationary phase of Carbowax 20M.

alkane	t'_r (min)
pentane	0.79
hexane	1.99
heptane	4.47
octane	14.12
nonane	33.11

What is the retention index for a compound whose adjusted retention time is 9.36 min?

18. The following data were reported for the gas chromatographic analysis of *p*-xylene and methylisobutylketone (MIBK) on a capillary column [Marriott, P. J.; Carpenter, P. D. *J. Chem. Educ.* **1996**, *73*, 96–99].

injection mode	compound	t_r (min)	peak area (arb. units)	peak width (min)
split	MIBK	1.878	54285	0.028
	p-xylene	5.234	123483	0.044
splitless	MIBK	3.420	2493005	1.057
	p-xylene	5.795	3396656	1.051

Explain the difference in the retention times, the peak areas, and the peak widths when switching from a split injection to a splitless injection.

19. Otto and Wegscheider report the following retention factors for the reversed-phase separation of 2-aminobenzoic acid on a C_{18} column when using 10% v/v methanol as a mobile phase [Otto, M.; Wegscheider, W. *J. Chromatog.* **1983**, *258*, 11–22].

pH	*k*
2.0	10.5
3.0	16.7
4.0	15.8
5.0	8.0
6.0	2.2
7.0	1.8

Explain the effect of pH on the retention factor for 2-aminobenzene.

20. Haddad and associates report the following retention factors for the reversed-phase separation of salicylamide and caffeine [Haddad, P.; Hutchins, S.; Tuffy, M. *J. Chem. Educ.* **1983**, *60*, 166-168].

%v/v methanol	30%	35%	40%	45%	50%	55%
k_{sal}	2.4	1.6	1.6	1.0	0.7	0.7
k_{caff}	4.3	2.8	2.3	1.4	1.1	0.9

(a) Explain the trends in the retention factors for these compounds.

(b) What is the advantage of using a mobile phase with a smaller %v/v methanol? Are there any disadvantages?

21. Suppose you need to separate a mixture of benzoic acid, aspartame, and caffeine in a diet soda. The following information is available.

	t_r in aqueous mobile phase of pH			
compound	3.0	3.5	4.0	4.5
benzoic acid	7.4	7.0	6.9	4.4
aspartame	5.9	6.0	7.1	8.1
caffeine	3.6	3.7	4.1	4.4

(a) Explain the change in each compound's retention time.

(b) Prepare a single graph that shows retention time versus pH for each compound. Using your plot, identify a pH level that will yield an acceptable separation.

22. The composition of a multivitamin tablet is determined using an HPLC with a diode array UV/Vis detector. A 5-µL standard sample that contains 170 ppm vitamin C, 130 ppm niacin, 120 ppm niacinamide, 150 ppm pyridoxine, 60 ppm thiamine, 15 ppm folic acid, and 10 ppm riboflavin is injected into the HPLC, giving signals (in arbitrary units) of, respectively, 0.22, 1.35, 0.90, 1.37, 0.82, 0.36, and 0.29. The multivitamin tablet is prepared for analysis by grinding into a powder and transferring to a 125-mL Erlenmeyer flask that contains 10 mL of 1% v/v NH_3 in dimethyl sulfoxide. After sonicating in an ultrasonic bath for 2 min, 90 mL of 2% acetic acid is added and the mixture is stirred for 1 min and sonicated at 40°C for 5 min. The extract is then filtered through a 0.45-µm membrane filter. Injection of a 5-µL sample

into the HPLC gives signals of 0.87 for vitamin C, 0.00 for niacin, 1.40 for niacinamide, 0.22 for pyridoxine, 0.19 for thiamine, 0.11 for folic acid, and 0.44 for riboflavin. Report the milligrams of each vitamin present in the tablet.

23. The amount of caffeine in an analgesic tablet was determined by HPLC using a normal calibration curve. Standard solutions of caffeine were prepared and analyzed using a 10-μL fixed-volume injection loop. Results for the standards are summarized in the following table.

concentration (ppm)	signal (arb. units)
50.0	8.354
100.0	16925
150.0	25218
200.0	33584
250.0	42002

The sample is prepared by placing a single analgesic tablet in a small beaker and adding 10 mL of methanol. After allowing the sample to dissolve, the contents of the beaker, including the insoluble binder, are quantitatively transferred to a 25-mL volumetric flask and diluted to volume with methanol. The sample is then filtered, and a 1.00-mL aliquot transferred to a 10-mL volumetric flask and diluted to volume with methanol. When analyzed by HPLC, the signal for caffeine is found to be 21 469. Report the milligrams of caffeine in the analgesic tablet.

24. Kagel and Farwell report a reversed-phase HPLC method for determining the concentration of acetylsalicylic acid (ASA) and caffeine (CAF) in analgesic tablets using salicylic acid (SA) as an internal standard [Kagel, R. A.; Farwell, S. O. *J. Chem. Educ.* **1983**, *60*, 163–166]. A series of standards was prepared by adding known amounts of ace- tylsalicylic acid and caffeine to 250-mL Erlenmeyer flasks and adding 100 mL of methanol. A 10.00-mL aliquot of a standard solution of salicylic acid was then added to each. The following results were obtained for a typical set of standard solutions.

	milligrams of		peak height ratios for	
standard	ASA	CAF	ASA/SA	CAF/SA
1	200.0	20.0	20.5	10.6
2	250.0	40.0	25.1	23.0
3	300.0	60.0	30.9	36.8

A sample of an analgesic tablet was placed in a 250-mL Erlenmeyer flask and dissolved in 100 mL of methanol. After adding a 10.00-mL portion of the internal standard, the solution was filtered. Analysis of the sample gave a peak height ratio of 23.2 for ASA and of 17.9 for CAF.

(a) Determine the milligrams of ASA and CAF in the tablet.

(b) Why is it necessary to filter the sample?

(c) The directions indicate that approximately 100 mL of methanol is used to dissolve the standards and samples. Why is it not necessary to measure this volume more precisely?

(d) In the presence of moisture, ASA decomposes to SA and acetic acid. What complication might this present for this analysis? How might you evaluate whether this is a problem?

25. Bohman and colleagues described a reversed-phase HPLC method for the quantitative analysis of vitamin A in food using the method of standard additions Bohman, O.; Engdahl, K. A.; Johnsson, H. *J. Chem. Educ.* **1982**, *59*, 251–252]. In a typical example, a 10.067-g sample of cereal is placed in a 250-mL Erlenmeyer flask along with 1 g of sodium ascorbate, 40 mL of ethanol, and 10 mL of 50% w/v KOH. After refluxing for 30 min, 60 mL of ethanol is added and the solution cooled to room temperature. Vitamin A is extracted using three 100-mL portions of hexane. The combined portions of hexane are evaporated and the residue containing vitamin A transferred to a 5-mL volumetric flask and diluted to volume with methanol. A standard addition is prepared in a similar manner using a 10.093-g sample of the cereal and spiking with 0.0200 mg of vitamin A. Injecting the sample and standard addition into the HPLC gives peak areas of, respectively, 6.77×10^3 and 1.32×10^4. Report the vitamin A content of the sample in milligrams/100 g cereal.

26. Ohta and Tanaka reported on an ion-exchange chromatographic method for the simultaneous analysis of several inorganic anions and the cations Mg^{2+} and Ca^{2+} in water [Ohta, K.; Tanaka, K. *Anal. Chim. Acta* **1998**, *373*, 189–195]. The mobile phase includes the ligand 1,2,4-benzenetricarboxylate, which absorbs strongly at 270 nm. Indirect detection of the analytes is possible because its absorbance decreases when complexed with an anion.

(a) The procedure also calls for adding the ligand EDTA to the mobile phase. What role does the EDTA play in this analysis?

(b) A standard solution of 1.0 mM $NaHCO_3$, 0.20 mM $NaNO_2$, 0.20 mM $MgSO_4$, 0.10 mM $CaCl_2$, and 0.10 mM $Ca(NO_3)_2$ gives the following peak areas (arbitrary units).

ion	HCO_3^-	Cl^-	NO_2^-	NO_3^-
peak area	373.5	322.5	264.8	262.7
ion	Ca^{2+}	Mg^{2+}	SO_4^{2-}	
peak area	458.9	352.0	341.3	

Analysis of a river water sample (pH of 7.49) gives the following results.

ion	HCO_3^-	Cl^-	NO_2^-	NO_3^-
peak area	310.0	403.1	3.97	157.6
ion	Ca^{2+}	Mg^{2+}	SO_4^{2-}	
peak area	734.3	193.6	324.3	

Determine the concentration of each ion in the sample.

(c) The detection of HCO_3^- actually gives the total concentration of carbonate in solution ($[CO_3^{2-}]+[HCO_3^-]+[H_2CO_3]$). Given that the pH of the water is 7.49, what is the actual concentration of HCO_3^-?

(d) An independent analysis gives the following additional concentrations for ions in the sample: $[Na^+]$ = 0.60 mM; $[NH_4^+]$ = 0.014 mM; and $[K^+]$ = 0.046 mM. A solution's ion balance is defined as the ratio of the total cation charge to the total anion charge. Determine the charge balance for this sample of water and comment on whether the result is reasonable.

27. The concentrations of Cl^-, NO_2^-, and SO_4^{2-} are determined by ion chromatography. A 50-µL standard sample of 10.0 ppm Cl^-, 2.00 ppm NO_2^-, and 5.00 ppm SO_4^{2-} gave signals (in arbitrary units) of 59.3, 16.1, and 6.08 respectively. A sample of effluent from a wastewater treatment plant is diluted tenfold and a 50-µL portion gives signals of 44.2 for Cl^-, 2.73 for NO_2^-, and 5.04 for SO_4^{2-}. Report the parts per million for each anion in the effluent sample.

28. A series of polyvinylpyridine standards of different molecular weight was analyzed by size-exclusion chromatography, yielding the following results.

formula weight	retention volume (mL)
600000	6.42
100000	7.98
30000	9.30
3000	10.94

When a preparation of polyvinylpyridine of unknown formula weight is analyzed, the retention volume is 8.45 mL. Report the average formula weight for the preparation.

29. Diet soft drinks contain appreciable quantities of aspartame, benzoic acid, and caffeine. What is the expected order of elution for these compounds in a capillary zone electrophoresis separation using a pH 9.4 buffer given that aspartame has pK_a values of 2.964 and 7.37, benzoic acid has a pK_a of 4.2, and the pK_a for caffeine is less than 0. Figure 12.8.3 provides the structures of these compounds.

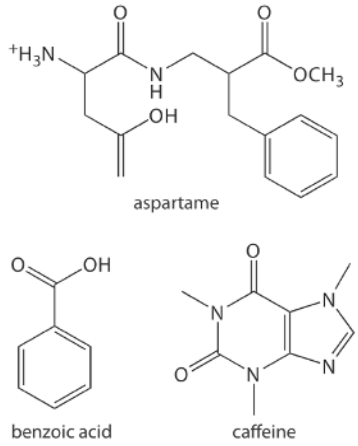


Figure 12.8.3
. Structures for the compounds in Problem 29.

30. Janusa and coworkers describe the determination of chloride by CZE [Janusa, M. A.; Andermann, L. J.; Kliebert, N. M.; Nannie, M. H. *J. Chem. Educ.* **1998**, *75*, 1463–1465]. Analysis of a series of external standards gives the following calibration curve.

$$\text{area} = -883 + 5590 \times \text{ppm } Cl^-$$

A standard sample of 57.22% w/w Cl^- is analyzed by placing 0.1011-g portions in separate 100-mL volumetric flasks and diluting to volume. Three unknowns are prepared by pipeting 0.250 mL, 0.500 mL, an 0.750 mL of the bulk unknown in separate 50-mL volumetric flasks and diluting to volume. Analysis of the three unknowns gives areas of 15 310, 31 546, and 47 582, respectively. Evaluate the accuracy of this analysis.

31. The analysis of NO_3^- in aquarium water is carried out by CZE using IO_4^- as an internal standard. A standard solution of 15.0 ppm NO_3^- and 10.0 ppm IO_4^- gives peak heights (arbitrary units) of 95.0 and 100.1, respectively. A sample of water from an aquarium is diluted 1:100 and sufficient internal standard added to make its concentration 10.0 ppm in IO_4^-. Analysis gives signals of 29.2 and 105.8 for NO_3^- and IO_4^-, respectively. Report the ppm NO_3^- in the sample of aquarium water.

32. Suggest conditions to separate a mixture of 2-aminobenzoic acid (pK_{a1} = 2.08, pK_{a2} = 4.96), benzylamine (pK_a = 9.35), and 4-methylphenol (pK_{a2} = 10.26) by capillary zone electrophoresis. Figure $PageIndex4$ provides the structures of these compounds.

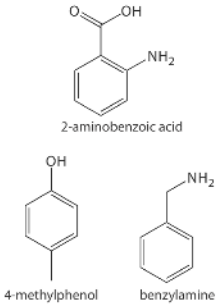


Figure 12.8.4 . Structures for the compounds in Problem 32.

33. McKillop and associates examined the electrophoretic separation of some alkylpyridines by CZE [McKillop, A. G.; Smith, R. M.; Rowe, R. C.; Wren, S. A. C. *Anal. Chem.* **1999**, *71*, 497–503]. Separations were carried out using either 50-µm or 75-µm inner diameter capillaries, with a total length of 57 cm and a length of 50 cm from the point of injection to the detector. The run buffer was a pH 2.5 lithium phosphate buffer. Separations were achieved using an applied voltage of 15 kV. The electroosmotic mobility, μ_{eof}, as measured using a neutral marker, was found to be 6.398×10^{-5} $cm^2\ V^{-1}\ s^{-1}$. The diffusion coefficient for alkylpyridines is 1.0×10^{-5} $cm^2\ s^{-1}$.

(a) Calculate the electrophoretic mobility for 2-ethylpyridine given that its elution time is 8.20 min.

(b) How many theoretical plates are there for 2-ethylpyridine?

(c) The electrophoretic mobilities for 3-ethylpyridine and 4-ethylpyridine are 3.366×10^{-4} $cm^2\ V^{-1}\ s^{-1}$ and 3.397×10^{-4} $cm^2\ V^{-1}\ s^{-1}$, respectively. What is the expected resolution between these two alkylpyridines?

(d) Explain the trends in electrophoretic mobility shown in the following table.

alkylpyridine	μ_{ep} ($cm^2\ V^{-1}\ s^{-1}$)
2-methylpyridine	3.581×10^{-4}
2-ethylpyridine	3.222×10^{-4}
2-propylpyridine	2.923×10^{-4}
2-pentylpyridine	2.534×10^{-4}
2-hexylpyridine	2.391×10^{-4}

(e) Explain the trends in electrophoretic mobility shown in the following table.

alkylpyridine	μ_{ep} ($cm^2\ V^{-1}\ s^{-1}$)
2-ethylpyridine	3.222×10^{-4}
3-ethylpyridine	3.366×10^{-4}
4-ethylpyridine	3.397×10^{-4}

(f) The pK_a for pyridine is 5.229. At a pH of 2.5 the electrophoretic mobility of pyridine is 4.176×10^{-4} $cm^2\ V^{-1}\ s^{-1}$. What is the expected electrophoretic mobility if the run buffer's pH is 7.5?

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12.13: ADDITIONAL RESOURCES

The following set of experiments introduce students to the applications of chromatography and electrophoresis. Experiments are grouped into five categories: gas chromatography, high-performance liquid chromatography, ion-exchange chromatography, size-exclusion chromatography, and electrophoresis.

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12.14: CHAPTER SUMMARY AND KEY TERMS

CHAPTER SUMMARY

Chromatography and electrophoresis are powerful analytical techniques that both separate a sample into its components and provide a means for determining each component's concentration. Chromatographic separations utilize the selective partitioning of the sample's components between a stationary phase that is immobilized within a column and a mobile phase that passes through the column.

The effectiveness of a chromatographic separation is described by the resolution between two chromatographic bands and is a function of each component's retention factor, the column's efficiency, and the column's selectivity. A solute's retention factor is a measure of its partitioning into the stationary phase, with larger retention factors corresponding to more strongly retained solutes. The column's selectivity for two solutes is the ratio of their retention factors, providing a relative measure of the column's ability to retain the two solutes. Column efficiency accounts for those factors that cause a solute's chromatographic band to increase in width during the separation. Column efficiency is defined in terms of the number of theoretical plates and the height of a theoretical plate, the later of which is a function of a number of parameters, most notably the mobile phase's flow rate. Chromatographic separations are optimized by increasing the number of theoretical plates, by increasing the column's selectivity, or by increasing the solute retention factor.

In gas chromatography the mobile phase is an inert gas and the stationary phase is a nonpolar or polar organic liquid that either is coated on a particulate material and packed into a wide-bore column, or coated on the walls of a narrow-bore capillary column. Gas chromatography is useful for the analysis of volatile components.

In high-performance liquid chromatography the mobile phase is either a nonpolar solvent (normal phase) or a polar solvent (reversed-phase). A stationary phase of opposite polarity, which is bonded to a particulate material, is packed into a wide-bore column. HPLC is applied to a wider range of samples than GC; however, the separation efficiency for HPLC is not as good as that for capillary GC.

Together, GC and HPLC account for the largest number of chromatographic separations. Other separation techniques, however, find specialized applications: of particular importance are ion-exchange chromatography for separating anions and cations; size-exclusion chromatography for separating large molecules; and supercritical fluid chromatography for the analysis of samples that are not easily analyzed by GC or HPLC.

In capillary zone electrophoresis a sample's components are separated based on their ability to move through a conductive medium under the influence of an applied electric field. Positively charged solutes elute first, with smaller, more highly charged cations eluting before larger cations of lower charge. Neutral species elute without undergoing further separation. Finally, anions elute last, with smaller, more negatively charged anions being the last to elute. By adding a surfactant, neutral species can be separated by micellar electrokinetic capillary chromatography. Electrophoretic separations also can take advantage of the ability of polymeric gels to separate solutes by size (capillary gel electrophoresis), and the ability of solutes to partition into a stationary phase (capillary electrochromatography). In comparison to GC and HPLC, capillary electrophoresis provides faster and more efficient separations.

KEY TERMS

adjusted retention time
adsorption chromatography
band broadening
baseline width
bleed
bonded stationary phase
capillary column
capillary electrochromatography
capillary electrophoresis
capillary gel electrophoresis
capillary zone electrophoresis
chromatogram
chromatography
column chromatography
counter-current extraction
cryogenic focusing
electrokinetic injection
electroosmotic flow
electroosmotic flow velocity
electron capture detector
electropherogram
electrophoresis
electrophoretic mobility
electrophoretic velocity
exclusion limit
flame ionization detector
fronting
gas chromatography
gas–liquid chromatography
gas–solid chromatography
general elution problem
guard column
gradient elution
headspace sampling
high-performance liquid chromatography
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inclusion limit
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isothermal
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Kovat's retention index
liquid–solid adsorption chromatography
longitudinal diffusion
loop injector
mass spectrometer
mass spectrum
mass transfer
micelle
micellar electrokinetic capillary chromatography
mobile phase
monolithic column
multiple paths
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on-column injection
open tubular column
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retention time
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selectivity factor
single-column ion chromatography
solid-phase microextraction
split injection
splitless injection
stacking
stationary phase
supercritical fluid chromatography
support-coated open tubular column
tailing
temperature programming
theoretical plate
thermal conductivity detector
van Deemter equation
void time
wall-coated open-tubular column
zeta potential

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