Introduction to Algorithms

Third Edition

I Foundations

Introduction

This part will start you thinking about designing and analyzing algorithms. It is intended to be a gentle introduction to how we specify algorithms, some of the design strategies we will use throughout this book, and many of the fundamental ideas used in algorithm analysis. Later parts of this book will build upon this base.

Chapter 1 provides an overview of algorithms and their place in modern computing systems. This chapter defines what an algorithm is and lists some examples. It also makes a case that we should consider algorithms as a technology, alongside technologies such as fast hardware, graphical user interfaces, object-oriented systems, and networks.

In Chapter 2, we see our first algorithms, which solve the problem of sorting a sequence of n numbers. They are written in a pseudocode which, although not directly translatable to any conventional programming language, conveys the structure of the algorithm clearly enough that you should be able to implement it in the language of your choice. The sorting algorithms we examine are insertion sort, which uses an incremental approach, and merge sort, which uses a recursive technique known as "divide-and-conquer." Although the time each requires increases with the value of n, the rate of increase differs between the two algorithms. We determine these running times in Chapter 2, and we develop a useful notation to express them.

Chapter 3 precisely defines this notation, which we call asymptotic notation. It starts by defining several asymptotic notations, which we use for bounding algorithm running times from above and/or below. The rest of Chapter 3 is primarily a presentation of mathematical notation, more to ensure that your use of notation matches that in this book than to teach you new mathematical concepts.

Chapter 4 delves further into the divide-and-conquer method introduced in Chapter 2. It provides additional examples of divide-and-conquer algorithms, including Strassen's surprising method for multiplying two square matrices. Chapter 4 contains methods for solving recurrences, which are useful for describing the running times of recursive algorithms. One powerful technique is the "master method," which we often use to solve recurrences that arise from divide-and-conquer algorithms. Although much of Chapter 4 is devoted to proving the correctness of the master method, you may skip this proof yet still employ the master method.

Chapter 5 introduces probabilistic analysis and randomized algorithms. We typically use probabilistic analysis to determine the running time of an algorithm in cases in which, due to the presence of an inherent probability distribution, the running time may differ on different inputs of the same size. In some cases, we assume that the inputs conform to a known probability distribution, so that we are averaging the running time over all possible inputs. In other cases, the probability distribution comes not from the inputs but from random choices made during the course of the algorithm. An algorithm whose behavior is determined not only by its input but by the values produced by a random-number generator is a randomized algorithm. We can use randomized algorithms to enforce a probability distribution on the inputs—thereby ensuring that no particular input always causes poor performance—or even to bound the error rate of algorithms that are allowed to produce incorrect results on a limited basis.

Appendices A–D contain other mathematical material that you will find helpful as you read this book. You are likely to have seen much of the material in the appendix chapters before having read this book (although the specific definitions and notational conventions we use may differ in some cases from what you have seen in the past), and so you should think of the Appendices as reference material. On the other hand, you probably have not already seen most of the material in Part I. All the chapters in Part I and the Appendices are written with a tutorial flavor.

1 The Role of Algorithms in Computing

What are algorithms? Why is the study of algorithms worthwhile? What is the role of algorithms relative to other technologies used in computers? In this chapter, we will answer these questions.

1.1 Algorithms

Informally, an ***algorithm*** is any well-defined computational procedure that takes some value, or set of values, as ***input*** and produces some value, or set of values, as ***output***. An algorithm is thus a sequence of computational steps that transform the input into the output.

We can also view an algorithm as a tool for solving a well-specified ***computational problem***. The statement of the problem specifies in general terms the desired input/output relationship. The algorithm describes a specific computational procedure for achieving that input/output relationship.

For example, we might need to sort a sequence of numbers into nondecreasing order. This problem arises frequently in practice and provides fertile ground for introducing many standard design techniques and analysis tools. Here is how we formally define the ***sorting problem***:

Input: A sequence of n numbers $\langle a_1, a_2, \ldots, a_n \rangle$.

Output: A permutation (reordering) $\langle a'_1, a'_2, \ldots, a'_n \rangle$ of the input sequence such that $a'_1 \leq a'_2 \leq \cdots \leq a'_n$.

For example, given the input sequence $\langle 31, 41, 59, 26, 41, 58 \rangle$, a sorting algorithm returns as output the sequence $\langle 26, 31, 41, 41, 58, 59 \rangle$. Such an input sequence is called an ***instance*** of the sorting problem. In general, an ***instance of a problem*** consists of the input (satisfying whatever constraints are imposed in the problem statement) needed to compute a solution to the problem.

Because many programs use it as an intermediate step, sorting is a fundamental operation in computer science. As a result, we have a large number of good sorting algorithms at our disposal. Which algorithm is best for a given application depends on—among other factors—the number of items to be sorted, the extent to which the items are already somewhat sorted, possible restrictions on the item values, the architecture of the computer, and the kind of storage devices to be used: main memory, disks, or even tapes.

An algorithm is said to be ***correct*** if, for every input instance, it halts with the correct output. We say that a correct algorithm ***solves*** the given computational problem. An incorrect algorithm might not halt at all on some input instances, or it might halt with an incorrect answer. Contrary to what you might expect, incorrect algorithms can sometimes be useful, if we can control their error rate. We shall see an example of an algorithm with a controllable error rate in Chapter 31 when we study algorithms for finding large prime numbers. Ordinarily, however, we shall be concerned only with correct algorithms.

An algorithm can be specified in English, as a computer program, or even as a hardware design. The only requirement is that the specification must provide a precise description of the computational procedure to be followed.

What kinds of problems are solved by algorithms?

Sorting is by no means the only computational problem for which algorithms have been developed. (You probably suspected as much when you saw the size of this book.) Practical applications of algorithms are ubiquitous and include the following examples:

- The Human Genome Project has made great progress toward the goals of identifying all the 100,000 genes in human DNA, determining the sequences of the 3 billion chemical base pairs that make up human DNA, storing this information in databases, and developing tools for data analysis. Each of these steps requires sophisticated algorithms. Although the solutions to the various problems involved are beyond the scope of this book, many methods to solve these biological problems use ideas from several of the chapters in this book, thereby enabling scientists to accomplish tasks while using resources efficiently. The savings are in time, both human and machine, and in money, as more information can be extracted from laboratory techniques.
- The Internet enables people all around the world to quickly access and retrieve large amounts of information. With the aid of clever algorithms, sites on the Internet are able to manage and manipulate this large volume of data. Examples of problems that make essential use of algorithms include finding good routes on which the data will travel (techniques for solving such problems appear in

Chapter 24), and using a search engine to quickly find pages on which particular information resides (related techniques are in Chapters 11 and 32).

- Electronic commerce enables goods and services to be negotiated and exchanged electronically, and it depends on the privacy of personal information such as credit card numbers, passwords, and bank statements. The core technologies used in electronic commerce include public-key cryptography and digital signatures (covered in Chapter 31), which are based on numerical algorithms and number theory.
- Manufacturing and other commercial enterprises often need to allocate scarce resources in the most beneficial way. An oil company may wish to know where to place its wells in order to maximize its expected profit. A political candidate may want to determine where to spend money buying campaign advertising in order to maximize the chances of winning an election. An airline may wish to assign crews to flights in the least expensive way possible, making sure that each flight is covered and that government regulations regarding crew scheduling are met. An Internet service provider may wish to determine where to place additional resources in order to serve its customers more effectively. All of these are examples of problems that can be solved using linear programming, which we shall study in Chapter 29.

Although some of the details of these examples are beyond the scope of this book, we do give underlying techniques that apply to these problems and problem areas. We also show how to solve many specific problems, including the following:

- We are given a road map on which the distance between each pair of adjacent intersections is marked, and we wish to determine the shortest route from one intersection to another. The number of possible routes can be huge, even if we disallow routes that cross over themselves. How do we choose which of all possible routes is the shortest? Here, we model the road map (which is itself a model of the actual roads) as a graph (which we will meet in Part VI and Appendix B), and we wish to find the shortest path from one vertex to another in the graph. We shall see how to solve this problem efficiently in Chapter 24.
- We are given two ordered sequences of symbols, $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Y = \langle y_1, y_2, \ldots, y_n \rangle$, and we wish to find a longest common subsequence of X and Y. A subsequence of X is just X with some (or possibly all or none) of its elements removed. For example, one subsequence of $\langle A, B, C, D, E, F, G \rangle$ would be $\langle B, C, E, G \rangle$. The length of a longest common subsequence of X and Y gives one measure of how similar these two sequences are. For example, if the two sequences are base pairs in DNA strands, then we might consider them similar if they have a long common subsequence. If X has m symbols and Y has n symbols, then X and Y have 2^m and 2^n possible subsequences,

respectively. Selecting all possible subsequences of X and Y and matching them up could take a prohibitively long time unless m and n are very small. We shall see in Chapter 15 how to use a general technique known as dynamic programming to solve this problem much more efficiently.

- We are given a mechanical design in terms of a library of parts, where each part may include instances of other parts, and we need to list the parts in order so that each part appears before any part that uses it. If the design comprises n parts, then there are $n!$ possible orders, where $n!$ denotes the factorial function. Because the factorial function grows faster than even an exponential function, we cannot feasibly generate each possible order and then verify that, within that order, each part appears before the parts using it (unless we have only a few parts). This problem is an instance of topological sorting, and we shall see in Chapter 22 how to solve this problem efficiently.
- We are given n points in the plane, and we wish to find the convex hull of these points. The convex hull is the smallest convex polygon containing the points. Intuitively, we can think of each point as being represented by a nail sticking out from a board. The convex hull would be represented by a tight rubber band that surrounds all the nails. Each nail around which the rubber band makes a turn is a vertex of the convex hull. (See Figure 33.6 on page 1029 for an example.) Any of the 2^n subsets of the points might be the vertices of the convex hull. Knowing which points are vertices of the convex hull is not quite enough, either, since we also need to know the order in which they appear. There are many choices, therefore, for the vertices of the convex hull. Chapter 33 gives two good methods for finding the convex hull.

These lists are far from exhaustive (as you again have probably surmised from this book's heft), but exhibit two characteristics that are common to many interesting algorithmic problems:

1. They have many candidate solutions, the overwhelming majority of which do not solve the problem at hand. Finding one that does, or one that is "best," can present quite a challenge.
2. They have practical applications. Of the problems in the above list, finding the shortest path provides the easiest examples. A transportation firm, such as a trucking or railroad company, has a financial interest in finding shortest paths through a road or rail network because taking shorter paths results in lower labor and fuel costs. Or a routing node on the Internet may need to find the shortest path through the network in order to route a message quickly. Or a person wishing to drive from New York to Boston may want to find driving directions from an appropriate Web site, or she may use her GPS while driving.

Not every problem solved by algorithms has an easily identified set of candidate solutions. For example, suppose we are given a set of numerical values representing samples of a signal, and we want to compute the discrete Fourier transform of these samples. The discrete Fourier transform converts the time domain to the frequency domain, producing a set of numerical coefficients, so that we can determine the strength of various frequencies in the sampled signal. In addition to lying at the heart of signal processing, discrete Fourier transforms have applications in data compression and multiplying large polynomials and integers. Chapter 30 gives an efficient algorithm, the fast Fourier transform (commonly called the FFT), for this problem, and the chapter also sketches out the design of a hardware circuit to compute the FFT.

Data structures

This book also contains several data structures. A ***data structure*** is a way to store and organize data in order to facilitate access and modifications. No single data structure works well for all purposes, and so it is important to know the strengths and limitations of several of them.

Technique

Although you can use this book as a "cookbook" for algorithms, you may someday encounter a problem for which you cannot readily find a published algorithm (many of the exercises and problems in this book, for example). This book will teach you techniques of algorithm design and analysis so that you can develop algorithms on your own, show that they give the correct answer, and understand their efficiency. Different chapters address different aspects of algorithmic problem solving. Some chapters address specific problems, such as finding medians and order statistics in Chapter 9, computing minimum spanning trees in Chapter 23, and determining a maximum flow in a network in Chapter 26. Other chapters address techniques, such as divide-and-conquer in Chapter 4, dynamic programming in Chapter 15, and amortized analysis in Chapter 17.

Hard problems

Most of this book is about efficient algorithms. Our usual measure of efficiency is speed, i.e., how long an algorithm takes to produce its result. There are some problems, however, for which no efficient solution is known. Chapter 34 studies an interesting subset of these problems, which are known as NP-complete.

Why are NP-complete problems interesting? First, although no efficient algorithm for an NP-complete problem has ever been found, nobody has ever proven

that an efficient algorithm for one cannot exist. In other words, no one knows whether or not efficient algorithms exist for NP-complete problems. Second, the set of NP-complete problems has the remarkable property that if an efficient algorithm exists for any one of them, then efficient algorithms exist for all of them. This relationship among the NP-complete problems makes the lack of efficient solutions all the more tantalizing. Third, several NP-complete problems are similar, but not identical, to problems for which we do know of efficient algorithms. Computer scientists are intrigued by how a small change to the problem statement can cause a big change to the efficiency of the best known algorithm.

You should know about NP-complete problems because some of them arise surprisingly often in real applications. If you are called upon to produce an efficient algorithm for an NP-complete problem, you are likely to spend a lot of time in a fruitless search. If you can show that the problem is NP-complete, you can instead spend your time developing an efficient algorithm that gives a good, but not the best possible, solution.

As a concrete example, consider a delivery company with a central depot. Each day, it loads up each delivery truck at the depot and sends it around to deliver goods to several addresses. At the end of the day, each truck must end up back at the depot so that it is ready to be loaded for the next day. To reduce costs, the company wants to select an order of delivery stops that yields the lowest overall distance traveled by each truck. This problem is the well-known "traveling-salesman problem," and it is NP-complete. It has no known efficient algorithm. Under certain assumptions, however, we know of efficient algorithms that give an overall distance which is not too far above the smallest possible. Chapter 35 discusses such "approximation algorithms."

Parallelism

For many years, we could count on processor clock speeds increasing at a steady rate. Physical limitations present a fundamental roadblock to ever-increasing clock speeds, however: because power density increases superlinearly with clock speed, chips run the risk of melting once their clock speeds become high enough. In order to perform more computations per second, therefore, chips are being designed to contain not just one but several processing "cores." We can liken these multicore computers to several sequential computers on a single chip; in other words, they are a type of "parallel computer." In order to elicit the best performance from multicore computers, we need to design algorithms with parallelism in mind. Chapter 27 presents a model for "multithreaded" algorithms, which take advantage of multiple cores. This model has advantages from a theoretical standpoint, and it forms the basis of several successful computer programs, including a championship chess program.

Exercises

1.1-1
Give a real-world example that requires sorting or a real-world example that requires computing a convex hull.

1.1-2
Other than speed, what other measures of efficiency might one use in a real-world setting?

1.1-3
Select a data structure that you have seen previously, and discuss its strengths and limitations.

1.1-4
How are the shortest-path and traveling-salesman problems given above similar? How are they different?

1.1-5
Come up with a real-world problem in which only the best solution will do. Then come up with one in which a solution that is "approximately" the best is good enough.

1.2 Algorithms as a technology

Suppose computers were infinitely fast and computer memory was free. Would you have any reason to study algorithms? The answer is yes, if for no other reason than that you would still like to demonstrate that your solution method terminates and does so with the correct answer.

If computers were infinitely fast, any correct method for solving a problem would do. You would probably want your implementation to be within the bounds of good software engineering practice (for example, your implementation should be well designed and documented), but you would most often use whichever method was the easiest to implement.

Of course, computers may be fast, but they are not infinitely fast. And memory may be inexpensive, but it is not free. Computing time is therefore a bounded resource, and so is space in memory. You should use these resources wisely, and algorithms that are efficient in terms of time or space will help you do so.

Efficiency

Different algorithms devised to solve the same problem often differ dramatically in their efficiency. These differences can be much more significant than differences due to hardware and software.

As an example, in Chapter 2, we will see two algorithms for sorting. The first, known as ***insertion sort***, takes time roughly equal to $c_1 n^2$ to sort n items, where c_1 is a constant that does not depend on n. That is, it takes time roughly proportional to n^2. The second, ***merge sort***, takes time roughly equal to $c_2 n \lg n$, where $\lg n$ stands for $\log_2 n$ and c_2 is another constant that also does not depend on n. Insertion sort typically has a smaller constant factor than merge sort, so that $c_1 < c_2$. We shall see that the constant factors can have far less of an impact on the running time than the dependence on the input size n. Let's write insertion sort's running time as $c_1 n \cdot n$ and merge sort's running time as $c_2 n \cdot \lg n$. Then we see that where insertion sort has a factor of n in its running time, merge sort has a factor of $\lg n$, which is much smaller. (For example, when $n = 1000$, $\lg n$ is approximately 10, and when n equals one million, $\lg n$ is approximately only 20.) Although insertion sort usually runs faster than merge sort for small input sizes, once the input size n becomes large enough, merge sort's advantage of $\lg n$ vs. n will more than compensate for the difference in constant factors. No matter how much smaller c_1 is than c_2, there will always be a crossover point beyond which merge sort is faster.

For a concrete example, let us pit a faster computer (computer A) running insertion sort against a slower computer (computer B) running merge sort. They each must sort an array of 10 million numbers. (Although 10 million numbers might seem like a lot, if the numbers are eight-byte integers, then the input occupies about 80 megabytes, which fits in the memory of even an inexpensive laptop computer many times over.) Suppose that computer A executes 10 billion instructions per second (faster than any single sequential computer at the time of this writing) and computer B executes only 10 million instructions per second, so that computer A is 1000 times faster than computer B in raw computing power. To make the difference even more dramatic, suppose that the world's craftiest programmer codes insertion sort in machine language for computer A, and the resulting code requires $2n^2$ instructions to sort n numbers. Suppose further that just an average programmer implements merge sort, using a high-level language with an inefficient compiler, with the resulting code taking $50n \lg n$ instructions. To sort 10 million numbers, computer A takes

$$\frac{2 \cdot (10^7)^2 \text{ instructions}}{10^{10} \text{ instructions/second}} = 20{,}000 \text{ seconds (more than 5.5 hours)} ,$$

while computer B takes

$$\frac{50 \cdot 10^7 \lg 10^7 \text{ instructions}}{10^7 \text{ instructions/second}} \approx 1163 \text{ seconds (less than 20 minutes)} .$$

By using an algorithm whose running time grows more slowly, even with a poor compiler, computer B runs more than 17 times faster than computer A! The advantage of merge sort is even more pronounced when we sort 100 million numbers: where insertion sort takes more than 23 days, merge sort takes under four hours. In general, as the problem size increases, so does the relative advantage of merge sort.

Algorithms and other technologies

The example above shows that we should consider algorithms, like computer hardware, as a ***technology***. Total system performance depends on choosing efficient algorithms as much as on choosing fast hardware. Just as rapid advances are being made in other computer technologies, they are being made in algorithms as well.

You might wonder whether algorithms are truly that important on contemporary computers in light of other advanced technologies, such as

- advanced computer architectures and fabrication technologies,
- easy-to-use, intuitive, graphical user interfaces (GUIs),
- object-oriented systems,
- integrated Web technologies, and
- fast networking, both wired and wireless.

The answer is yes. Although some applications do not explicitly require algorithmic content at the application level (such as some simple, Web-based applications), many do. For example, consider a Web-based service that determines how to travel from one location to another. Its implementation would rely on fast hardware, a graphical user interface, wide-area networking, and also possibly on object orientation. However, it would also require algorithms for certain operations, such as finding routes (probably using a shortest-path algorithm), rendering maps, and interpolating addresses.

Moreover, even an application that does not require algorithmic content at the application level relies heavily upon algorithms. Does the application rely on fast hardware? The hardware design used algorithms. Does the application rely on graphical user interfaces? The design of any GUI relies on algorithms. Does the application rely on networking? Routing in networks relies heavily on algorithms. Was the application written in a language other than machine code? Then it was processed by a compiler, interpreter, or assembler, all of which make extensive use

of algorithms. Algorithms are at the core of most technologies used in contemporary computers.

Furthermore, with the ever-increasing capacities of computers, we use them to solve larger problems than ever before. As we saw in the above comparison between insertion sort and merge sort, it is at larger problem sizes that the differences in efficiency between algorithms become particularly prominent.

Having a solid base of algorithmic knowledge and technique is one characteristic that separates the truly skilled programmers from the novices. With modern computing technology, you can accomplish some tasks without knowing much about algorithms, but with a good background in algorithms, you can do much, much more.

Exercises

1.2-1
Give an example of an application that requires algorithmic content at the application level, and discuss the function of the algorithms involved.

1.2-2
Suppose we are comparing implementations of insertion sort and merge sort on the same machine. For inputs of size n, insertion sort runs in $8n^2$ steps, while merge sort runs in $64n \lg n$ steps. For which values of n does insertion sort beat merge sort?

1.2-3
What is the smallest value of n such that an algorithm whose running time is $100n^2$ runs faster than an algorithm whose running time is 2^n on the same machine?

Problems

1-1 Comparison of running times
For each function $f(n)$ and time t in the following table, determine the largest size n of a problem that can be solved in time t, assuming that the algorithm to solve the problem takes $f(n)$ microseconds.

	1 second	1 minute	1 hour	1 day	1 month	1 year	1 century
$\lg n$							
$\sqrt{n}$							
n							
$n \lg n$							
n^2							
n^3							
2^n							
$n!$							

Chapter notes

There are many excellent texts on the general topic of algorithms, including those by Aho, Hopcroft, and Ullman [5, 6]; Baase and Van Gelder [28]; Brassard and Bratley [54]; Dasgupta, Papadimitriou, and Vazirani [82]; Goodrich and Tamassia [148]; Hofri [175]; Horowitz, Sahni, and Rajasekaran [181]; Johnsonbaugh and Schaefer [193]; Kingston [205]; Kleinberg and Tardos [208]; Knuth [209, 210, 211]; Kozen [220]; Levitin [235]; Manber [242]; Mehlhorn [249, 250, 251]; Purdom and Brown [287]; Reingold, Nievergelt, and Deo [293]; Sedgewick [306]; Sedgewick and Flajolet [307]; Skiena [318]; and Wilf [356]. Some of the more practical aspects of algorithm design are discussed by Bentley [42, 43] and Gonnet [145]. Surveys of the field of algorithms can also be found in the *Handbook of Theoretical Computer Science, Volume A* [342] and the CRC *Algorithms and Theory of Computation Handbook* [25]. Overviews of the algorithms used in computational biology can be found in textbooks by Gusfield [156], Pevzner [275], Setubal and Meidanis [310], and Waterman [350].

2 Getting Started

This chapter will familiarize you with the framework we shall use throughout the book to think about the design and analysis of algorithms. It is self-contained, but it does include several references to material that we introduce in Chapters 3 and 4. (It also contains several summations, which Appendix A shows how to solve.)

We begin by examining the insertion sort algorithm to solve the sorting problem introduced in Chapter 1. We define a "pseudocode" that should be familiar to you if you have done computer programming, and we use it to show how we shall specify our algorithms. Having specified the insertion sort algorithm, we then argue that it correctly sorts, and we analyze its running time. The analysis introduces a notation that focuses on how that time increases with the number of items to be sorted. Following our discussion of insertion sort, we introduce the divide-and-conquer approach to the design of algorithms and use it to develop an algorithm called merge sort. We end with an analysis of merge sort's running time.

2.1 Insertion sort

Our first algorithm, insertion sort, solves the ***sorting problem*** introduced in Chapter 1:

Input: A sequence of n numbers $\langle a_1, a_2, \ldots, a_n \rangle$.

Output: A permutation (reordering) $\langle a'_1, a'_2, \ldots, a'_n \rangle$ of the input sequence such that $a'_1 \leq a'_2 \leq \cdots \leq a'_n$.

The numbers that we wish to sort are also known as the ***keys***. Although conceptually we are sorting a sequence, the input comes to us in the form of an array with n elements.

In this book, we shall typically describe algorithms as programs written in a ***pseudocode*** that is similar in many respects to C, C++, Java, Python, or Pascal. If you have been introduced to any of these languages, you should have little trouble

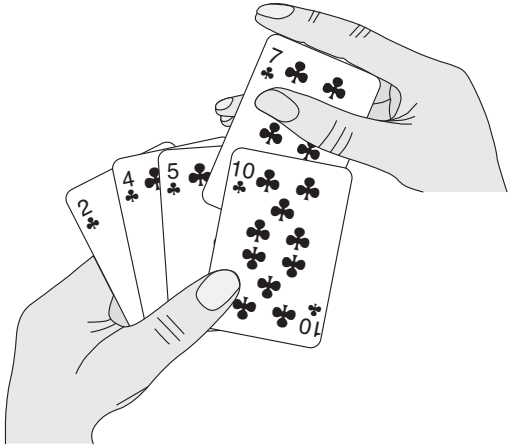


Figure 2.1 Sorting a hand of cards using insertion sort.

reading our algorithms. What separates pseudocode from "real" code is that in pseudocode, we employ whatever expressive method is most clear and concise to specify a given algorithm. Sometimes, the clearest method is English, so do not be surprised if you come across an English phrase or sentence embedded within a section of "real" code. Another difference between pseudocode and real code is that pseudocode is not typically concerned with issues of software engineering. Issues of data abstraction, modularity, and error handling are often ignored in order to convey the essence of the algorithm more concisely.

We start with ***insertion sort***, which is an efficient algorithm for sorting a small number of elements. Insertion sort works the way many people sort a hand of playing cards. We start with an empty left hand and the cards face down on the table. We then remove one card at a time from the table and insert it into the correct position in the left hand. To find the correct position for a card, we compare it with each of the cards already in the hand, from right to left, as illustrated in Figure 2.1. At all times, the cards held in the left hand are sorted, and these cards were originally the top cards of the pile on the table.

We present our pseudocode for insertion sort as a procedure called INSERTION-SORT, which takes as a parameter an array $A[1..n]$ containing a sequence of length n that is to be sorted. (In the code, the number n of elements in A is denoted by $A.length$.) The algorithm sorts the input numbers ***in place***: it rearranges the numbers within the array A, with at most a constant number of them stored outside the array at any time. The input array A contains the sorted output sequence when the INSERTION-SORT procedure is finished.

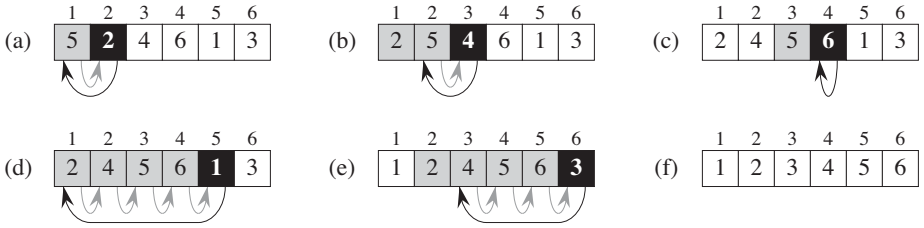


Figure 2.2 The operation of INSERTION-SORT on the array $A = \langle 5, 2, 4, 6, 1, 3 \rangle$. Array indices appear above the rectangles, and values stored in the array positions appear within the rectangles. **(a)–(e)** The iterations of the **for** loop of lines 1–8. In each iteration, the black rectangle holds the key taken from $A[j]$, which is compared with the values in shaded rectangles to its left in the test of line 5. Shaded arrows show array values moved one position to the right in line 6, and black arrows indicate where the key moves to in line 8. **(f)** The final sorted array.

```
INSERTION-SORT(A)
1  for j = 2 to A.length
2      key = A[j]
3      // Insert A[j] into the sorted sequence A[1 .. j − 1].
4      i = j − 1
5      while i > 0 and A[i] > key
6          A[i + 1] = A[i]
7          i = i − 1
8      A[i + 1] = key
```

Loop invariants and the correctness of insertion sort

Figure 2.2 shows how this algorithm works for $A = \langle 5, 2, 4, 6, 1, 3 \rangle$. The index j indicates the "current card" being inserted into the hand. At the beginning of each iteration of the **for** loop, which is indexed by j, the subarray consisting of elements $A[1 \,..\, j-1]$ constitutes the currently sorted hand, and the remaining subarray $A[j+1 \,..\, n]$ corresponds to the pile of cards still on the table. In fact, elements $A[1 \,..\, j-1]$ are the elements *originally* in positions 1 through $j-1$, but now in sorted order. We state these properties of $A[1 \,..\, j-1]$ formally as a ***loop invariant***:

> At the start of each iteration of the **for** loop of lines 1–8, the subarray $A[1 \,..\, j-1]$ consists of the elements originally in $A[1 \,..\, j-1]$, but in sorted order.

We use loop invariants to help us understand why an algorithm is correct. We must show three things about a loop invariant:

Initialization: It is true prior to the first iteration of the loop.

Maintenance: If it is true before an iteration of the loop, it remains true before the next iteration.

Termination: When the loop terminates, the invariant gives us a useful property that helps show that the algorithm is correct.

When the first two properties hold, the loop invariant is true prior to every iteration of the loop. (Of course, we are free to use established facts other than the loop invariant itself to prove that the loop invariant remains true before each iteration.) Note the similarity to mathematical induction, where to prove that a property holds, you prove a base case and an inductive step. Here, showing that the invariant holds before the first iteration corresponds to the base case, and showing that the invariant holds from iteration to iteration corresponds to the inductive step.

The third property is perhaps the most important one, since we are using the loop invariant to show correctness. Typically, we use the loop invariant along with the condition that caused the loop to terminate. The termination property differs from how we usually use mathematical induction, in which we apply the inductive step infinitely; here, we stop the "induction" when the loop terminates.

Let us see how these properties hold for insertion sort.

Initialization: We start by showing that the loop invariant holds before the first loop iteration, when $j = 2$.[1] The subarray $A[1 \,..\, j-1]$, therefore, consists of just the single element $A[1]$, which is in fact the original element in $A[1]$. Moreover, this subarray is sorted (trivially, of course), which shows that the loop invariant holds prior to the first iteration of the loop.

Maintenance: Next, we tackle the second property: showing that each iteration maintains the loop invariant. Informally, the body of the **for** loop works by moving $A[j-1]$, $A[j-2]$, $A[j-3]$, and so on by one position to the right until it finds the proper position for $A[j]$ (lines 4–7), at which point it inserts the value of $A[j]$ (line 8). The subarray $A[1 \,..\, j]$ then consists of the elements originally in $A[1 \,..\, j]$, but in sorted order. Incrementing j for the next iteration of the **for** loop then preserves the loop invariant.

A more formal treatment of the second property would require us to state and show a loop invariant for the **while** loop of lines 5–7. At this point, however,

---

[1] When the loop is a **for** loop, the moment at which we check the loop invariant just prior to the first iteration is immediately after the initial assignment to the loop-counter variable and just before the first test in the loop header. In the case of INSERTION-SORT, this time is after assigning 2 to the variable j but before the first test of whether $j \leq A.length$.

we prefer not to get bogged down in such formalism, and so we rely on our informal analysis to show that the second property holds for the outer loop.

Termination: Finally, we examine what happens when the loop terminates. The condition causing the **for** loop to terminate is that $j > A.length = n$. Because each loop iteration increases j by 1, we must have $j = n + 1$ at that time. Substituting $n + 1$ for j in the wording of loop invariant, we have that the subarray $A[1..n]$ consists of the elements originally in $A[1..n]$, but in sorted order. Observing that the subarray $A[1..n]$ is the entire array, we conclude that the entire array is sorted. Hence, the algorithm is correct.

We shall use this method of loop invariants to show correctness later in this chapter and in other chapters as well.

Pseudocode conventions

We use the following conventions in our pseudocode.

- Indentation indicates block structure. For example, the body of the **for** loop that begins on line 1 consists of lines 2–8, and the body of the **while** loop that begins on line 5 contains lines 6–7 but not line 8. Our indentation style applies to **if-else** statements[2] as well. Using indentation instead of conventional indicators of block structure, such as **begin** and **end** statements, greatly reduces clutter while preserving, or even enhancing, clarity.[3]
- The looping constructs **while**, **for**, and **repeat-until** and the **if-else** conditional construct have interpretations similar to those in C, C++, Java, Python, and Pascal.[4] In this book, the loop counter retains its value after exiting the loop, unlike some situations that arise in C++, Java, and Pascal. Thus, immediately after a **for** loop, the loop counter's value is the value that first exceeded the **for** loop bound. We used this property in our correctness argument for insertion sort. The **for** loop header in line 1 is **for** $j = 2$ **to** $A.length$, and so when this loop terminates, $j = A.length + 1$ (or, equivalently, $j = n + 1$, since $n = A.length$). We use the keyword **to** when a **for** loop increments its loop

---

[2]In an **if-else** statement, we indent **else** at the same level as its matching **if**. Although we omit the keyword **then**, we occasionally refer to the portion executed when the test following **if** is true as a ***then clause***. For multiway tests, we use **elseif** for tests after the first one.

[3]Each pseudocode procedure in this book appears on one page so that you will not have to discern levels of indentation in code that is split across pages.

[4]Most block-structured languages have equivalent constructs, though the exact syntax may differ. Python lacks **repeat-until** loops, and its **for** loops operate a little differently from the **for** loops in this book.

counter in each iteration, and we use the keyword **downto** when a **for** loop decrements its loop counter. When the loop counter changes by an amount greater than 1, the amount of change follows the optional keyword **by**.

- The symbol "**//**" indicates that the remainder of the line is a comment.
- A multiple assignment of the form $i = j = e$ assigns to both variables i and j the value of expression e; it should be treated as equivalent to the assignment $j = e$ followed by the assignment $i = j$.
- Variables (such as i, j, and *key*) are local to the given procedure. We shall not use global variables without explicit indication.
- We access array elements by specifying the array name followed by the index in square brackets. For example, $A[i]$ indicates the ith element of the array A. The notation ". ." is used to indicate a range of values within an array. Thus, $A[1 \,..\, j]$ indicates the subarray of A consisting of the j elements $A[1], A[2], \ldots, A[j]$.
- We typically organize compound data into ***objects***, which are composed of ***attributes***. We access a particular attribute using the syntax found in many object-oriented programming languages: the object name, followed by a dot, followed by the attribute name. For example, we treat an array as an object with the attribute *length* indicating how many elements it contains. To specify the number of elements in an array A, we write $A.length$.

  We treat a variable representing an array or object as a pointer to the data representing the array or object. For all attributes f of an object x, setting $y = x$ causes $y.f$ to equal $x.f$. Moreover, if we now set $x.f = 3$, then afterward not only does $x.f$ equal 3, but $y.f$ equals 3 as well. In other words, x and y point to the same object after the assignment $y = x$.

  Our attribute notation can "cascade." For example, suppose that the attribute f is itself a pointer to some type of object that has an attribute g. Then the notation $x.f.g$ is implicitly parenthesized as $(x.f).g$. In other words, if we had assigned $y = x.f$, then $x.f.g$ is the same as $y.g$.

  Sometimes, a pointer will refer to no object at all. In this case, we give it the special value NIL.
- We pass parameters to a procedure ***by value***: the called procedure receives its own copy of the parameters, and if it assigns a value to a parameter, the change is *not* seen by the calling procedure. When objects are passed, the pointer to the data representing the object is copied, but the object's attributes are not. For example, if x is a parameter of a called procedure, the assignment $x = y$ within the called procedure is not visible to the calling procedure. The assignment $x.f = 3$, however, is visible. Similarly, arrays are passed by pointer, so that

a pointer to the array is passed, rather than the entire array, and changes to individual array elements are visible to the calling procedure.

- A **return** statement immediately transfers control back to the point of call in the calling procedure. Most **return** statements also take a value to pass back to the caller. Our pseudocode differs from many programming languages in that we allow multiple values to be returned in a single **return** statement.
- The boolean operators "and" and "or" are ***short circuiting***. That is, when we evaluate the expression "x and y" we first evaluate x. If x evaluates to FALSE, then the entire expression cannot evaluate to TRUE, and so we do not evaluate y. If, on the other hand, x evaluates to TRUE, we must evaluate y to determine the value of the entire expression. Similarly, in the expression "x or y" we evaluate the expression y only if x evaluates to FALSE. Short-circuiting operators allow us to write boolean expressions such as "$x \neq \text{NIL}$ and $x.f = y$" without worrying about what happens when we try to evaluate $x.f$ when x is NIL.
- The keyword **error** indicates that an error occurred because conditions were wrong for the procedure to have been called. The calling procedure is responsible for handling the error, and so we do not specify what action to take.

Exercises

2.1-1
Using Figure 2.2 as a model, illustrate the operation of INSERTION-SORT on the array $A = \langle 31, 41, 59, 26, 41, 58 \rangle$.

2.1-2
Rewrite the INSERTION-SORT procedure to sort into nonincreasing instead of nondecreasing order.

2.1-3
Consider the ***searching problem***:

Input: A sequence of n numbers $A = \langle a_1, a_2, \ldots, a_n \rangle$ and a value v.

Output: An index i such that $v = A[i]$ or the special value NIL if v does not appear in A.

Write pseudocode for ***linear search***, which scans through the sequence, looking for v. Using a loop invariant, prove that your algorithm is correct. Make sure that your loop invariant fulfills the three necessary properties.

2.1-4
Consider the problem of adding two n-bit binary integers, stored in two n-element arrays A and B. The sum of the two integers should be stored in binary form in

an $(n + 1)$-element array C. State the problem formally and write pseudocode for adding the two integers.

2.2 Analyzing algorithms

Analyzing an algorithm has come to mean predicting the resources that the algorithm requires. Occasionally, resources such as memory, communication bandwidth, or computer hardware are of primary concern, but most often it is computational time that we want to measure. Generally, by analyzing several candidate algorithms for a problem, we can identify a most efficient one. Such analysis may indicate more than one viable candidate, but we can often discard several inferior algorithms in the process.

Before we can analyze an algorithm, we must have a model of the implementation technology that we will use, including a model for the resources of that technology and their costs. For most of this book, we shall assume a generic one-processor, ***random-access machine (RAM)*** model of computation as our implementation technology and understand that our algorithms will be implemented as computer programs. In the RAM model, instructions are executed one after another, with no concurrent operations.

Strictly speaking, we should precisely define the instructions of the RAM model and their costs. To do so, however, would be tedious and would yield little insight into algorithm design and analysis. Yet we must be careful not to abuse the RAM model. For example, what if a RAM had an instruction that sorts? Then we could sort in just one instruction. Such a RAM would be unrealistic, since real computers do not have such instructions. Our guide, therefore, is how real computers are designed. The RAM model contains instructions commonly found in real computers: arithmetic (such as add, subtract, multiply, divide, remainder, floor, ceiling), data movement (load, store, copy), and control (conditional and unconditional branch, subroutine call and return). Each such instruction takes a constant amount of time.

The data types in the RAM model are integer and floating point (for storing real numbers). Although we typically do not concern ourselves with precision in this book, in some applications precision is crucial. We also assume a limit on the size of each word of data. For example, when working with inputs of size n, we typically assume that integers are represented by $c \lg n$ bits for some constant $c \geq 1$. We require $c \geq 1$ so that each word can hold the value of n, enabling us to index the individual input elements, and we restrict c to be a constant so that the word size does not grow arbitrarily. (If the word size could grow arbitrarily, we could store huge amounts of data in one word and operate on it all in constant time—clearly an unrealistic scenario.)

Real computers contain instructions not listed above, and such instructions represent a gray area in the RAM model. For example, is exponentiation a constant-time instruction? In the general case, no; it takes several instructions to compute x^y when x and y are real numbers. In restricted situations, however, exponentiation is a constant-time operation. Many computers have a "shift left" instruction, which in constant time shifts the bits of an integer by k positions to the left. In most computers, shifting the bits of an integer by one position to the left is equivalent to multiplication by 2, so that shifting the bits by k positions to the left is equivalent to multiplication by 2^k. Therefore, such computers can compute 2^k in one constant-time instruction by shifting the integer 1 by k positions to the left, as long as k is no more than the number of bits in a computer word. We will endeavor to avoid such gray areas in the RAM model, but we will treat computation of 2^k as a constant-time operation when k is a small enough positive integer.

In the RAM model, we do not attempt to model the memory hierarchy that is common in contemporary computers. That is, we do not model caches or virtual memory. Several computational models attempt to account for memory-hierarchy effects, which are sometimes significant in real programs on real machines. A handful of problems in this book examine memory-hierarchy effects, but for the most part, the analyses in this book will not consider them. Models that include the memory hierarchy are quite a bit more complex than the RAM model, and so they can be difficult to work with. Moreover, RAM-model analyses are usually excellent predictors of performance on actual machines.

Analyzing even a simple algorithm in the RAM model can be a challenge. The mathematical tools required may include combinatorics, probability theory, algebraic dexterity, and the ability to identify the most significant terms in a formula. Because the behavior of an algorithm may be different for each possible input, we need a means for summarizing that behavior in simple, easily understood formulas.

Even though we typically select only one machine model to analyze a given algorithm, we still face many choices in deciding how to express our analysis. We would like a way that is simple to write and manipulate, shows the important characteristics of an algorithm's resource requirements, and suppresses tedious details.

Analysis of insertion sort

The time taken by the INSERTION-SORT procedure depends on the input: sorting a thousand numbers takes longer than sorting three numbers. Moreover, INSERTION-SORT can take different amounts of time to sort two input sequences of the same size depending on how nearly sorted they already are. In general, the time taken by an algorithm grows with the size of the input, so it is traditional to describe the running time of a program as a function of the size of its input. To do so, we need to define the terms "running time" and "size of input" more carefully.

The best notion for ***input size*** depends on the problem being studied. For many problems, such as sorting or computing discrete Fourier transforms, the most natural measure is the *number of items in the input*—for example, the array size n for sorting. For many other problems, such as multiplying two integers, the best measure of input size is the *total number of bits* needed to represent the input in ordinary binary notation. Sometimes, it is more appropriate to describe the size of the input with two numbers rather than one. For instance, if the input to an algorithm is a graph, the input size can be described by the numbers of vertices and edges in the graph. We shall indicate which input size measure is being used with each problem we study.

The ***running time*** of an algorithm on a particular input is the number of primitive operations or "steps" executed. It is convenient to define the notion of step so that it is as machine-independent as possible. For the moment, let us adopt the following view. A constant amount of time is required to execute each line of our pseudocode. One line may take a different amount of time than another line, but we shall assume that each execution of the ith line takes time c_i, where c_i is a constant. This viewpoint is in keeping with the RAM model, and it also reflects how the pseudocode would be implemented on most actual computers.[5]

In the following discussion, our expression for the running time of INSERTION-SORT will evolve from a messy formula that uses all the statement costs c_i to a much simpler notation that is more concise and more easily manipulated. This simpler notation will also make it easy to determine whether one algorithm is more efficient than another.

We start by presenting the INSERTION-SORT procedure with the time "cost" of each statement and the number of times each statement is executed. For each $j = 2, 3, \ldots, n$, where $n = A.length$, we let t_j denote the number of times the **while** loop test in line 5 is executed for that value of j. When a **for** or **while** loop exits in the usual way (i.e., due to the test in the loop header), the test is executed one time more than the loop body. We assume that comments are not executable statements, and so they take no time.

---

[5]There are some subtleties here. Computational steps that we specify in English are often variants of a procedure that requires more than just a constant amount of time. For example, later in this book we might say "sort the points by x-coordinate," which, as we shall see, takes more than a constant amount of time. Also, note that a statement that calls a subroutine takes constant time, though the subroutine, once invoked, may take more. That is, we separate the process of ***calling*** the subroutine—passing parameters to it, etc.—from the process of ***executing*** the subroutine.

INSERTION-SORT(A)	*cost*	*times*
1 **for** $j = 2$ **to** $A.length$	c_1	n
2 $key = A[j]$	c_2	$n-1$
3 // Insert $A[j]$ into the sorted sequence $A[1..j-1]$.	0	$n-1$
4 $i = j-1$	c_4	$n-1$
5 **while** $i > 0$ and $A[i] > key$	c_5	$\sum_{j=2}^{n} t_j$
6 $A[i+1] = A[i]$	c_6	$\sum_{j=2}^{n}(t_j-1)$
7 $i = i-1$	c_7	$\sum_{j=2}^{n}(t_j-1)$
8 $A[i+1] = key$	c_8	$n-1$

The running time of the algorithm is the sum of running times for each statement executed; a statement that takes c_i steps to execute and executes n times will contribute $c_i n$ to the total running time.[6] To compute $T(n)$, the running time of INSERTION-SORT on an input of n values, we sum the products of the *cost* and *times* columns, obtaining

$$\begin{aligned} T(n) &= c_1 n + c_2(n-1) + c_4(n-1) + c_5 \sum_{j=2}^{n} t_j + c_6 \sum_{j=2}^{n} (t_j - 1) \\ &\quad + c_7 \sum_{j=2}^{n} (t_j - 1) + c_8(n-1) \; . \end{aligned}$$

Even for inputs of a given size, an algorithm's running time may depend on *which* input of that size is given. For example, in INSERTION-SORT, the best case occurs if the array is already sorted. For each $j = 2, 3, \ldots, n$, we then find that $A[i] \le key$ in line 5 when i has its initial value of $j-1$. Thus $t_j = 1$ for $j = 2, 3, \ldots, n$, and the best-case running time is

$$\begin{aligned} T(n) &= c_1 n + c_2(n-1) + c_4(n-1) + c_5(n-1) + c_8(n-1) \\ &= (c_1 + c_2 + c_4 + c_5 + c_8)n - (c_2 + c_4 + c_5 + c_8) \; . \end{aligned}$$

We can express this running time as $an + b$ for *constants* a and b that depend on the statement costs c_i; it is thus a ***linear function*** of n.

If the array is in reverse sorted order—that is, in decreasing order—the worst case results. We must compare each element $A[j]$ with each element in the entire sorted subarray $A[1..j-1]$, and so $t_j = j$ for $j = 2, 3, \ldots, n$. Noting that

[6] This characteristic does not necessarily hold for a resource such as memory. A statement that references m words of memory and is executed n times does not necessarily reference mn distinct words of memory.

$$\sum_{j=2}^{n} j = \frac{n(n+1)}{2} - 1$$

and

$$\sum_{j=2}^{n} (j-1) = \frac{n(n-1)}{2}$$

(see Appendix A for a review of how to solve these summations), we find that in the worst case, the running time of INSERTION-SORT is

$$\begin{aligned} T(n) &= c_1 n + c_2(n-1) + c_4(n-1) + c_5\left(\frac{n(n+1)}{2} - 1\right) \\ &\quad + c_6\left(\frac{n(n-1)}{2}\right) + c_7\left(\frac{n(n-1)}{2}\right) + c_8(n-1) \\ &= \left(\frac{c_5}{2} + \frac{c_6}{2} + \frac{c_7}{2}\right)n^2 + \left(c_1 + c_2 + c_4 + \frac{c_5}{2} - \frac{c_6}{2} - \frac{c_7}{2} + c_8\right)n \\ &\quad - (c_2 + c_4 + c_5 + c_8) \, . \end{aligned}$$

We can express this worst-case running time as $an^2 + bn + c$ for constants a, b, and c that again depend on the statement costs c_i; it is thus a ***quadratic function*** of n.

Typically, as in insertion sort, the running time of an algorithm is fixed for a given input, although in later chapters we shall see some interesting "randomized" algorithms whose behavior can vary even for a fixed input.

Worst-case and average-case analysis

In our analysis of insertion sort, we looked at both the best case, in which the input array was already sorted, and the worst case, in which the input array was reverse sorted. For the remainder of this book, though, we shall usually concentrate on finding only the ***worst-case running time***, that is, the longest running time for *any* input of size n. We give three reasons for this orientation.

- The worst-case running time of an algorithm gives us an upper bound on the running time for any input. Knowing it provides a guarantee that the algorithm will never take any longer. We need not make some educated guess about the running time and hope that it never gets much worse.
- For some algorithms, the worst case occurs fairly often. For example, in searching a database for a particular piece of information, the searching algorithm's worst case will often occur when the information is not present in the database. In some applications, searches for absent information may be frequent.

- The "average case" is often roughly as bad as the worst case. Suppose that we randomly choose n numbers and apply insertion sort. How long does it take to determine where in subarray $A[1 \,..\, j-1]$ to insert element $A[j]$? On average, half the elements in $A[1 \,..\, j-1]$ are less than $A[j]$, and half the elements are greater. On average, therefore, we check half of the subarray $A[1 \,..\, j-1]$, and so t_j is about $j/2$. The resulting average-case running time turns out to be a quadratic function of the input size, just like the worst-case running time.

In some particular cases, we shall be interested in the ***average-case*** running time of an algorithm; we shall see the technique of ***probabilistic analysis*** applied to various algorithms throughout this book. The scope of average-case analysis is limited, because it may not be apparent what constitutes an "average" input for a particular problem. Often, we shall assume that all inputs of a given size are equally likely. In practice, this assumption may be violated, but we can sometimes use a ***randomized algorithm***, which makes random choices, to allow a probabilistic analysis and yield an ***expected*** running time. We explore randomized algorithms more in Chapter 5 and in several other subsequent chapters.

Order of growth

We used some simplifying abstractions to ease our analysis of the INSERTION-SORT procedure. First, we ignored the actual cost of each statement, using the constants c_i to represent these costs. Then, we observed that even these constants give us more detail than we really need: we expressed the worst-case running time as $an^2 + bn + c$ for some constants a, b, and c that depend on the statement costs c_i. We thus ignored not only the actual statement costs, but also the abstract costs c_i.

We shall now make one more simplifying abstraction: it is the ***rate of growth***, or ***order of growth***, of the running time that really interests us. We therefore consider only the leading term of a formula (e.g., an^2), since the lower-order terms are relatively insignificant for large values of n. We also ignore the leading term's constant coefficient, since constant factors are less significant than the rate of growth in determining computational efficiency for large inputs. For insertion sort, when we ignore the lower-order terms and the leading term's constant coefficient, we are left with the factor of n^2 from the leading term. We write that insertion sort has a worst-case running time of $\Theta(n^2)$ (pronounced "theta of n-squared"). We shall use Θ-notation informally in this chapter, and we will define it precisely in Chapter 3.

We usually consider one algorithm to be more efficient than another if its worst-case running time has a lower order of growth. Due to constant factors and lower-order terms, an algorithm whose running time has a higher order of growth might take less time for small inputs than an algorithm whose running time has a lower

order of growth. But for large enough inputs, a $\Theta(n^2)$ algorithm, for example, will run more quickly in the worst case than a $\Theta(n^3)$ algorithm.

Exercises

2.2-1
Express the function $n^3/1000 - 100n^2 - 100n + 3$ in terms of Θ-notation.

2.2-2
Consider sorting n numbers stored in array A by first finding the smallest element of A and exchanging it with the element in $A[1]$. Then find the second smallest element of A, and exchange it with $A[2]$. Continue in this manner for the first $n-1$ elements of A. Write pseudocode for this algorithm, which is known as ***selection sort***. What loop invariant does this algorithm maintain? Why does it need to run for only the first $n-1$ elements, rather than for all n elements? Give the best-case and worst-case running times of selection sort in Θ-notation.

2.2-3
Consider linear search again (see Exercise 2.1-3). How many elements of the input sequence need to be checked on the average, assuming that the element being searched for is equally likely to be any element in the array? How about in the worst case? What are the average-case and worst-case running times of linear search in Θ-notation? Justify your answers.

2.2-4
How can we modify almost any algorithm to have a good best-case running time?

2.3 Designing algorithms

We can choose from a wide range of algorithm design techniques. For insertion sort, we used an ***incremental*** approach: having sorted the subarray $A[1 \mathinner{..} j-1]$, we inserted the single element $A[j]$ into its proper place, yielding the sorted subarray $A[1 \mathinner{..} j]$.

In this section, we examine an alternative design approach, known as "divide-and-conquer," which we shall explore in more detail in Chapter 4. We'll use divide-and-conquer to design a sorting algorithm whose worst-case running time is much less than that of insertion sort. One advantage of divide-and-conquer algorithms is that their running times are often easily determined using techniques that we will see in Chapter 4.

2.3.1 The divide-and-conquer approach

Many useful algorithms are ***recursive*** in structure: to solve a given problem, they call themselves recursively one or more times to deal with closely related subproblems. These algorithms typically follow a ***divide-and-conquer*** approach: they break the problem into several subproblems that are similar to the original problem but smaller in size, solve the subproblems recursively, and then combine these solutions to create a solution to the original problem.

The divide-and-conquer paradigm involves three steps at each level of the recursion:

Divide the problem into a number of subproblems that are smaller instances of the same problem.

Conquer the subproblems by solving them recursively. If the subproblem sizes are small enough, however, just solve the subproblems in a straightforward manner.

Combine the solutions to the subproblems into the solution for the original problem.

The ***merge sort*** algorithm closely follows the divide-and-conquer paradigm. Intuitively, it operates as follows.

Divide: Divide the n-element sequence to be sorted into two subsequences of $n/2$ elements each.

Conquer: Sort the two subsequences recursively using merge sort.

Combine: Merge the two sorted subsequences to produce the sorted answer.

The recursion "bottoms out" when the sequence to be sorted has length 1, in which case there is no work to be done, since every sequence of length 1 is already in sorted order.

The key operation of the merge sort algorithm is the merging of two sorted sequences in the "combine" step. We merge by calling an auxiliary procedure MERGE(A, p, q, r), where A is an array and p, q, and r are indices into the array such that $p \le q < r$. The procedure assumes that the subarrays $A[p\,..\,q]$ and $A[q+1\,..\,r]$ are in sorted order. It ***merges*** them to form a single sorted subarray that replaces the current subarray $A[p\,..\,r]$.

Our MERGE procedure takes time $\Theta(n)$, where $n = r - p + 1$ is the total number of elements being merged, and it works as follows. Returning to our card-playing motif, suppose we have two piles of cards face up on a table. Each pile is sorted, with the smallest cards on top. We wish to merge the two piles into a single sorted output pile, which is to be face down on the table. Our basic step consists of choosing the smaller of the two cards on top of the face-up piles, removing it from its pile (which exposes a new top card), and placing this card face down onto

the output pile. We repeat this step until one input pile is empty, at which time we just take the remaining input pile and place it face down onto the output pile. Computationally, each basic step takes constant time, since we are comparing just the two top cards. Since we perform at most n basic steps, merging takes $\Theta(n)$ time.

The following pseudocode implements the above idea, but with an additional twist that avoids having to check whether either pile is empty in each basic step. We place on the bottom of each pile a ***sentinel*** card, which contains a special value that we use to simplify our code. Here, we use ∞ as the sentinel value, so that whenever a card with ∞ is exposed, it cannot be the smaller card unless both piles have their sentinel cards exposed. But once that happens, all the nonsentinel cards have already been placed onto the output pile. Since we know in advance that exactly $r - p + 1$ cards will be placed onto the output pile, we can stop once we have performed that many basic steps.

```
MERGE(A, p, q, r)
 1  n_1 = q − p + 1
 2  n_2 = r − q
 3  let L[1 .. n_1 + 1] and R[1 .. n_2 + 1] be new arrays
 4  for i = 1 to n_1
 5      L[i] = A[p + i − 1]
 6  for j = 1 to n_2
 7      R[j] = A[q + j]
 8  L[n_1 + 1] = ∞
 9  R[n_2 + 1] = ∞
10  i = 1
11  j = 1
12  for k = p to r
13      if L[i] ≤ R[j]
14          A[k] = L[i]
15          i = i + 1
16      else A[k] = R[j]
17          j = j + 1
```

In detail, the MERGE procedure works as follows. Line 1 computes the length n_1 of the subarray $A[p \,..\, q]$, and line 2 computes the length n_2 of the subarray $A[q + 1 \,..\, r]$. We create arrays L and R ("left" and "right"), of lengths $n_1 + 1$ and $n_2 + 1$, respectively, in line 3; the extra position in each array will hold the sentinel. The **for** loop of lines 4–5 copies the subarray $A[p \,..\, q]$ into $L[1 \,..\, n_1]$, and the **for** loop of lines 6–7 copies the subarray $A[q + 1 \,..\, r]$ into $R[1 \,..\, n_2]$. Lines 8–9 put the sentinels at the ends of the arrays L and R. Lines 10–17, illus-

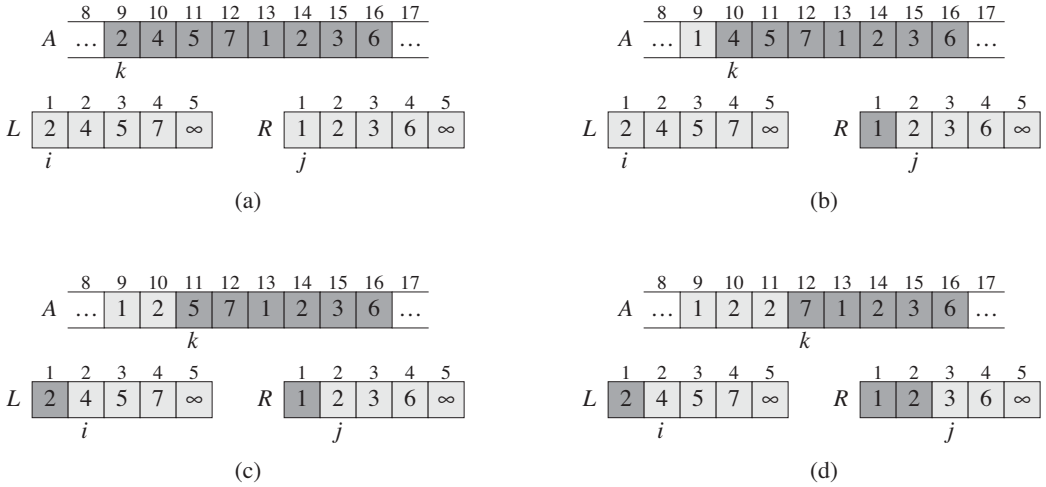


Figure 2.3 The operation of lines 10–17 in the call MERGE$(A, 9, 12, 16)$, when the subarray $A[9\,..\,16]$ contains the sequence $\langle 2, 4, 5, 7, 1, 2, 3, 6\rangle$. After copying and inserting sentinels, the array L contains $\langle 2, 4, 5, 7, \infty\rangle$, and the array R contains $\langle 1, 2, 3, 6, \infty\rangle$. Lightly shaded positions in A contain their final values, and lightly shaded positions in L and R contain values that have yet to be copied back into A. Taken together, the lightly shaded positions always comprise the values originally in $A[9\,..\,16]$, along with the two sentinels. Heavily shaded positions in A contain values that will be copied over, and heavily shaded positions in L and R contain values that have already been copied back into A. **(a)–(h)** The arrays A, L, and R, and their respective indices k, i, and j prior to each iteration of the loop of lines 12–17.

trated in Figure 2.3, perform the $r - p + 1$ basic steps by maintaining the following loop invariant:

> At the start of each iteration of the **for** loop of lines 12–17, the subarray $A[p\,..\,k-1]$ contains the $k - p$ smallest elements of $L[1\,..\,n_1 + 1]$ and $R[1\,..\,n_2 + 1]$, in sorted order. Moreover, $L[i]$ and $R[j]$ are the smallest elements of their arrays that have not been copied back into A.

We must show that this loop invariant holds prior to the first iteration of the **for** loop of lines 12–17, that each iteration of the loop maintains the invariant, and that the invariant provides a useful property to show correctness when the loop terminates.

Initialization: Prior to the first iteration of the loop, we have $k = p$, so that the subarray $A[p\,..\,k-1]$ is empty. This empty subarray contains the $k - p = 0$ smallest elements of L and R, and since $i = j = 1$, both $L[i]$ and $R[j]$ are the smallest elements of their arrays that have not been copied back into A.

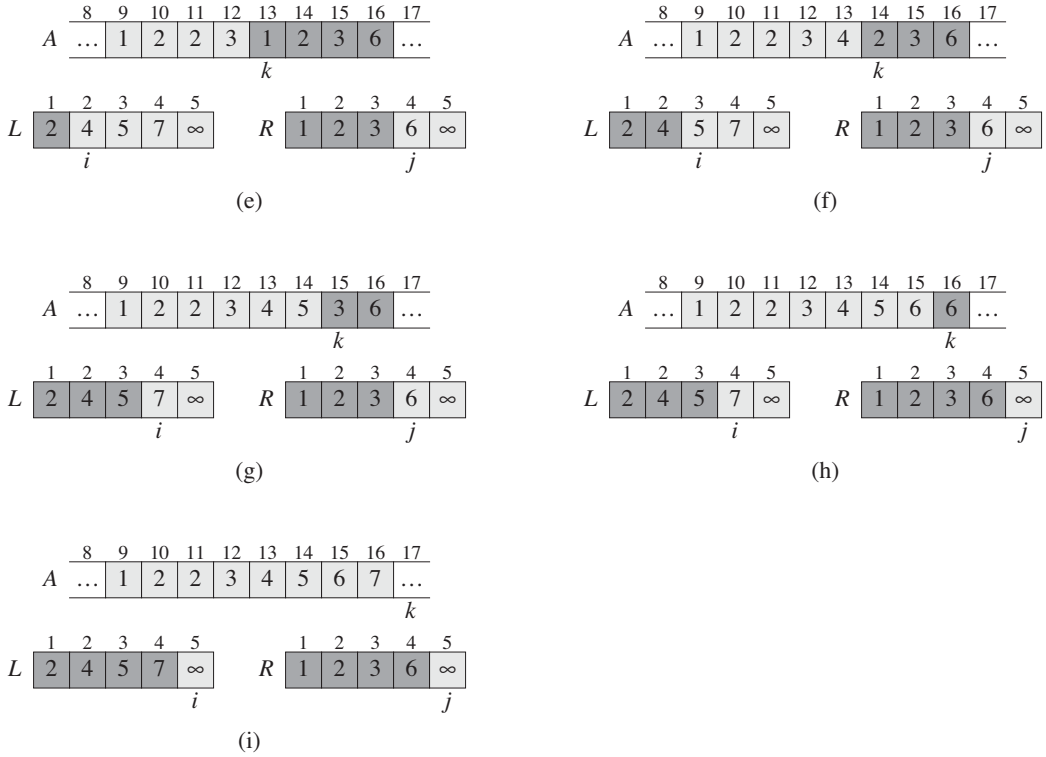


Figure 2.3, continued **(i)** The arrays and indices at termination. At this point, the subarray in $A[9\,..\,16]$ is sorted, and the two sentinels in L and R are the only two elements in these arrays that have not been copied into A.

Maintenance: To see that each iteration maintains the loop invariant, let us first suppose that $L[i] \le R[j]$. Then $L[i]$ is the smallest element not yet copied back into A. Because $A[p\,..\,k-1]$ contains the $k-p$ smallest elements, after line 14 copies $L[i]$ into $A[k]$, the subarray $A[p\,..\,k]$ will contain the $k-p+1$ smallest elements. Incrementing k (in the **for** loop update) and i (in line 15) reestablishes the loop invariant for the next iteration. If instead $L[i] > R[j]$, then lines 16–17 perform the appropriate action to maintain the loop invariant.

Termination: At termination, $k = r+1$. By the loop invariant, the subarray $A[p\,..\,k-1]$, which is $A[p\,..\,r]$, contains the $k-p = r-p+1$ smallest elements of $L[1\,..\,n_1+1]$ and $R[1\,..\,n_2+1]$, in sorted order. The arrays L and R together contain $n_1+n_2+2 = r-p+3$ elements. All but the two largest have been copied back into A, and these two largest elements are the sentinels.

To see that the MERGE procedure runs in $\Theta(n)$ time, where $n = r - p + 1$, observe that each of lines 1–3 and 8–11 takes constant time, the **for** loops of lines 4–7 take $\Theta(n_1 + n_2) = \Theta(n)$ time,[7] and there are n iterations of the **for** loop of lines 12–17, each of which takes constant time.

We can now use the MERGE procedure as a subroutine in the merge sort algorithm. The procedure MERGE-SORT(A, p, r) sorts the elements in the subarray $A[p..r]$. If $p \geq r$, the subarray has at most one element and is therefore already sorted. Otherwise, the divide step simply computes an index q that partitions $A[p..r]$ into two subarrays: $A[p..q]$, containing $\lceil n/2 \rceil$ elements, and $A[q+1..r]$, containing $\lfloor n/2 \rfloor$ elements.[8]

```
MERGE-SORT(A, p, r)
1  if p < r
2      q = ⌊(p + r)/2⌋
3      MERGE-SORT(A, p, q)
4      MERGE-SORT(A, q + 1, r)
5      MERGE(A, p, q, r)
```

To sort the entire sequence $A = \langle A[1], A[2], \ldots, A[n] \rangle$, we make the initial call MERGE-SORT$(A, 1, A.length)$, where once again $A.length = n$. Figure 2.4 illustrates the operation of the procedure bottom-up when n is a power of 2. The algorithm consists of merging pairs of 1-item sequences to form sorted sequences of length 2, merging pairs of sequences of length 2 to form sorted sequences of length 4, and so on, until two sequences of length $n/2$ are merged to form the final sorted sequence of length n.

2.3.2 Analyzing divide-and-conquer algorithms

When an algorithm contains a recursive call to itself, we can often describe its running time by a ***recurrence equation*** or ***recurrence***, which describes the overall running time on a problem of size n in terms of the running time on smaller inputs. We can then use mathematical tools to solve the recurrence and provide bounds on the performance of the algorithm.

---

[7] We shall see in Chapter 3 how to formally interpret equations containing Θ-notation.

[8] The expression $\lceil x \rceil$ denotes the least integer greater than or equal to x, and $\lfloor x \rfloor$ denotes the greatest integer less than or equal to x. These notations are defined in Chapter 3. The easiest way to verify that setting q to $\lfloor (p + r)/2 \rfloor$ yields subarrays $A[p..q]$ and $A[q+1..r]$ of sizes $\lceil n/2 \rceil$ and $\lfloor n/2 \rfloor$, respectively, is to examine the four cases that arise depending on whether each of p and r is odd or even.

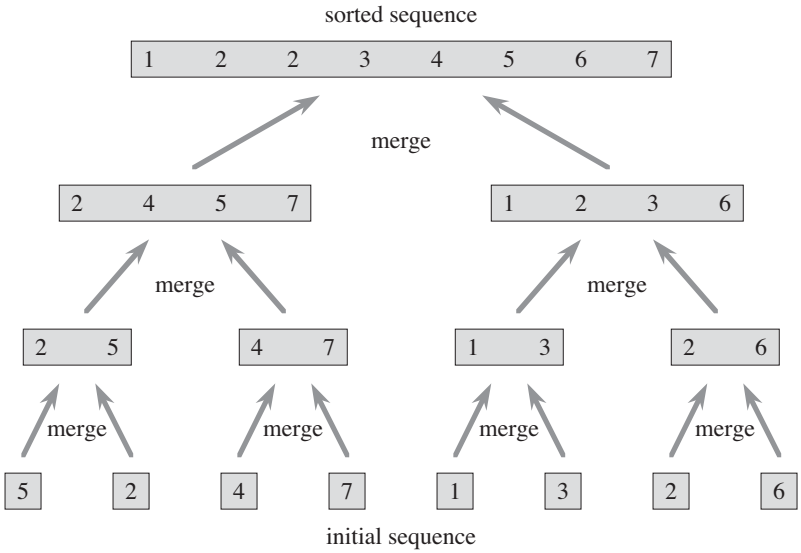


Figure 2.4 The operation of merge sort on the array $A = \langle 5, 2, 4, 7, 1, 3, 2, 6 \rangle$. The lengths of the sorted sequences being merged increase as the algorithm progresses from bottom to top.

A recurrence for the running time of a divide-and-conquer algorithm falls out from the three steps of the basic paradigm. As before, we let $T(n)$ be the running time on a problem of size n. If the problem size is small enough, say $n \leq c$ for some constant c, the straightforward solution takes constant time, which we write as $\Theta(1)$. Suppose that our division of the problem yields a subproblems, each of which is $1/b$ the size of the original. (For merge sort, both a and b are 2, but we shall see many divide-and-conquer algorithms in which $a \neq b$.) It takes time $T(n/b)$ to solve one subproblem of size n/b, and so it takes time $aT(n/b)$ to solve a of them. If we take $D(n)$ time to divide the problem into subproblems and $C(n)$ time to combine the solutions to the subproblems into the solution to the original problem, we get the recurrence

$$T(n) = \begin{cases} \Theta(1) & \text{if } n \leq c \ , \\ aT(n/b) + D(n) + C(n) & \text{otherwise} \ . \end{cases}$$

In Chapter 4, we shall see how to solve common recurrences of this form.

Analysis of merge sort

Although the pseudocode for MERGE-SORT works correctly when the number of elements is not even, our recurrence-based analysis is simplified if we assume that

the original problem size is a power of 2. Each divide step then yields two subsequences of size exactly $n/2$. In Chapter 4, we shall see that this assumption does not affect the order of growth of the solution to the recurrence.

We reason as follows to set up the recurrence for $T(n)$, the worst-case running time of merge sort on n numbers. Merge sort on just one element takes constant time. When we have $n > 1$ elements, we break down the running time as follows.

Divide: The divide step just computes the middle of the subarray, which takes constant time. Thus, $D(n) = \Theta(1)$.

Conquer: We recursively solve two subproblems, each of size $n/2$, which contributes $2T(n/2)$ to the running time.

Combine: We have already noted that the MERGE procedure on an n-element subarray takes time $\Theta(n)$, and so $C(n) = \Theta(n)$.

When we add the functions $D(n)$ and $C(n)$ for the merge sort analysis, we are adding a function that is $\Theta(n)$ and a function that is $\Theta(1)$. This sum is a linear function of n, that is, $\Theta(n)$. Adding it to the $2T(n/2)$ term from the "conquer" step gives the recurrence for the worst-case running time $T(n)$ of merge sort:

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 , \\ 2T(n/2) + \Theta(n) & \text{if } n > 1 . \end{cases} \tag{2.1}$$

In Chapter 4, we shall see the "master theorem," which we can use to show that $T(n)$ is $\Theta(n \lg n)$, where $\lg n$ stands for $\log_2 n$. Because the logarithm function grows more slowly than any linear function, for large enough inputs, merge sort, with its $\Theta(n \lg n)$ running time, outperforms insertion sort, whose running time is $\Theta(n^2)$, in the worst case.

We do not need the master theorem to intuitively understand why the solution to the recurrence (2.1) is $T(n) = \Theta(n \lg n)$. Let us rewrite recurrence (2.1) as

$$T(n) = \begin{cases} c & \text{if } n = 1 , \\ 2T(n/2) + cn & \text{if } n > 1 , \end{cases} \tag{2.2}$$

where the constant c represents the time required to solve problems of size 1 as well as the time per array element of the divide and combine steps.[9]

[9] It is unlikely that the same constant exactly represents both the time to solve problems of size 1 and the time per array element of the divide and combine steps. We can get around this problem by letting c be the larger of these times and understanding that our recurrence gives an upper bound on the running time, or by letting c be the lesser of these times and understanding that our recurrence gives a lower bound on the running time. Both bounds are on the order of $n \lg n$ and, taken together, give a $\Theta(n \lg n)$ running time.

Figure 2.5 shows how we can solve recurrence (2.2). For convenience, we assume that n is an exact power of 2. Part (a) of the figure shows $T(n)$, which we expand in part (b) into an equivalent tree representing the recurrence. The cn term is the root (the cost incurred at the top level of recursion), and the two subtrees of the root are the two smaller recurrences $T(n/2)$. Part (c) shows this process carried one step further by expanding $T(n/2)$. The cost incurred at each of the two subnodes at the second level of recursion is $cn/2$. We continue expanding each node in the tree by breaking it into its constituent parts as determined by the recurrence, until the problem sizes get down to 1, each with a cost of c. Part (d) shows the resulting ***recursion tree***.

Next, we add the costs across each level of the tree. The top level has total cost cn, the next level down has total cost $c(n/2) + c(n/2) = cn$, the level after that has total cost $c(n/4)+c(n/4)+c(n/4)+c(n/4) = cn$, and so on. In general, the level i below the top has 2^i nodes, each contributing a cost of $c(n/2^i)$, so that the ith level below the top has total cost $2^i\, c(n/2^i) = cn$. The bottom level has n nodes, each contributing a cost of c, for a total cost of cn.

The total number of levels of the recursion tree in Figure 2.5 is $\lg n + 1$, where n is the number of leaves, corresponding to the input size. An informal inductive argument justifies this claim. The base case occurs when $n = 1$, in which case the tree has only one level. Since $\lg 1 = 0$, we have that $\lg n + 1$ gives the correct number of levels. Now assume as an inductive hypothesis that the number of levels of a recursion tree with 2^i leaves is $\lg 2^i + 1 = i + 1$ (since for any value of i, we have that $\lg 2^i = i$). Because we are assuming that the input size is a power of 2, the next input size to consider is 2^{i+1}. A tree with $n = 2^{i+1}$ leaves has one more level than a tree with 2^i leaves, and so the total number of levels is $(i + 1) + 1 = \lg 2^{i+1} + 1$.

To compute the total cost represented by the recurrence (2.2), we simply add up the costs of all the levels. The recursion tree has $\lg n + 1$ levels, each costing cn, for a total cost of $cn(\lg n + 1) = cn \lg n + cn$. Ignoring the low-order term and the constant c gives the desired result of $\Theta(n \lg n)$.

Exercises

2.3-1

Using Figure 2.4 as a model, illustrate the operation of merge sort on the array $A = \langle 3, 41, 52, 26, 38, 57, 9, 49\rangle$.

2.3-2

Rewrite the MERGE procedure so that it does not use sentinels, instead stopping once either array L or R has had all its elements copied back to A and then copying the remainder of the other array back into A.

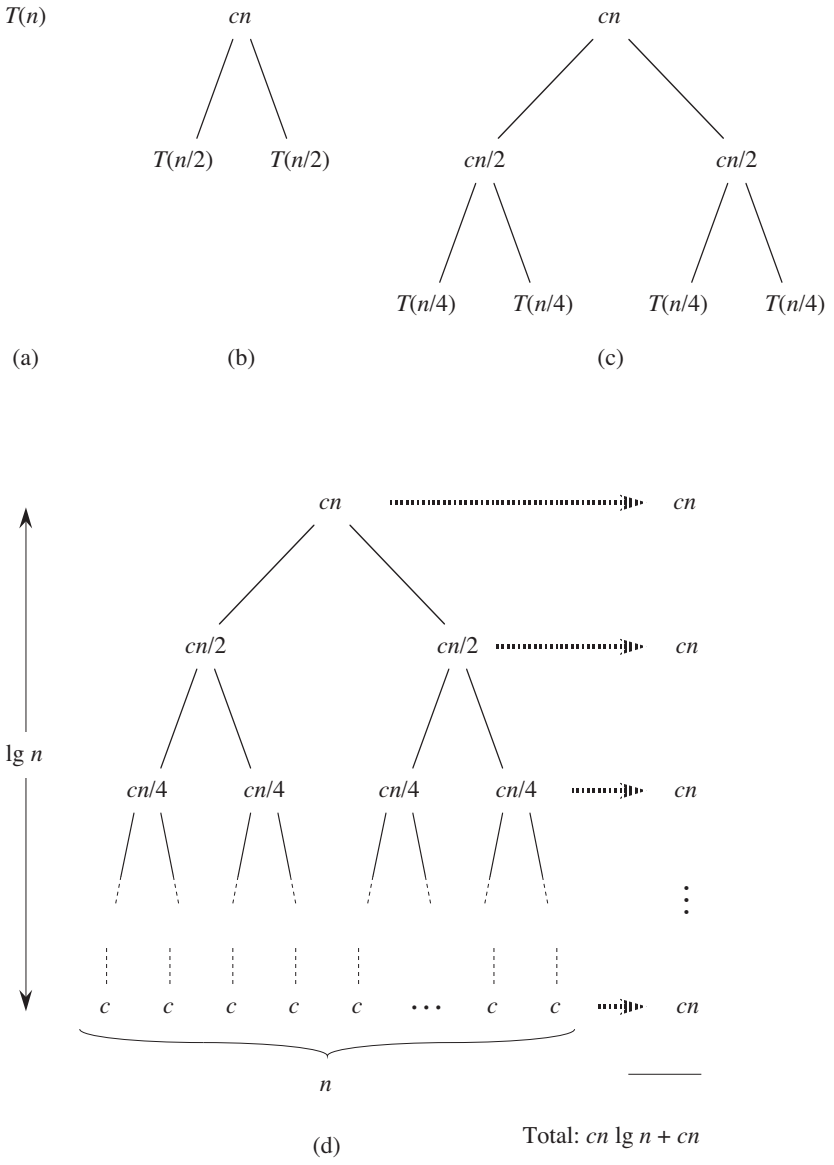


Figure 2.5 How to construct a recursion tree for the recurrence $T(n) = 2T(n/2) + cn$. Part **(a)** shows $T(n)$, which progressively expands in **(b)–(d)** to form the recursion tree. The fully expanded tree in part (d) has $\lg n + 1$ levels (i.e., it has height $\lg n$, as indicated), and each level contributes a total cost of cn. The total cost, therefore, is $cn \lg n + cn$, which is $\Theta(n \lg n)$.

2.3-3
Use mathematical induction to show that when n is an exact power of 2, the solution of the recurrence

$$T(n) = \begin{cases} 2 & \text{if } n = 2\,, \\ 2T(n/2) + n & \text{if } n = 2^k, \text{ for } k > 1 \end{cases}$$

is $T(n) = n \lg n$.

2.3-4
We can express insertion sort as a recursive procedure as follows. In order to sort $A[1\,..\,n]$, we recursively sort $A[1\,..\,n-1]$ and then insert $A[n]$ into the sorted array $A[1\,..\,n-1]$. Write a recurrence for the running time of this recursive version of insertion sort.

2.3-5
Referring back to the searching problem (see Exercise 2.1-3), observe that if the sequence A is sorted, we can check the midpoint of the sequence against v and eliminate half of the sequence from further consideration. The ***binary search*** algorithm repeats this procedure, halving the size of the remaining portion of the sequence each time. Write pseudocode, either iterative or recursive, for binary search. Argue that the worst-case running time of binary search is $\Theta(\lg n)$.

2.3-6
Observe that the **while** loop of lines 5–7 of the INSERTION-SORT procedure in Section 2.1 uses a linear search to scan (backward) through the sorted subarray $A[1\,..\,j-1]$. Can we use a binary search (see Exercise 2.3-5) instead to improve the overall worst-case running time of insertion sort to $\Theta(n \lg n)$?

2.3-7 ⋆
Describe a $\Theta(n \lg n)$-time algorithm that, given a set S of n integers and another integer x, determines whether or not there exist two elements in S whose sum is exactly x.

Problems

2-1 Insertion sort on small arrays in merge sort
Although merge sort runs in $\Theta(n \lg n)$ worst-case time and insertion sort runs in $\Theta(n^2)$ worst-case time, the constant factors in insertion sort can make it faster in practice for small problem sizes on many machines. Thus, it makes sense to ***coarsen*** the leaves of the recursion by using insertion sort within merge sort when

subproblems become sufficiently small. Consider a modification to merge sort in which n/k sublists of length k are sorted using insertion sort and then merged using the standard merging mechanism, where k is a value to be determined.

a. Show that insertion sort can sort the n/k sublists, each of length k, in $\Theta(nk)$ worst-case time.

b. Show how to merge the sublists in $\Theta(n \lg(n/k))$ worst-case time.

c. Given that the modified algorithm runs in $\Theta(nk + n \lg(n/k))$ worst-case time, what is the largest value of k as a function of n for which the modified algorithm has the same running time as standard merge sort, in terms of Θ-notation?

d. How should we choose k in practice?

2-2 Correctness of bubblesort

Bubblesort is a popular, but inefficient, sorting algorithm. It works by repeatedly swapping adjacent elements that are out of order.

```
BUBBLESORT(A)
1  for i = 1 to A.length − 1
2      for j = A.length downto i + 1
3          if A[j] < A[j − 1]
4              exchange A[j] with A[j − 1]
```

a. Let A' denote the output of BUBBLESORT(A). To prove that BUBBLESORT is correct, we need to prove that it terminates and that

$$A'[1] \le A'[2] \le \cdots \le A'[n] \,, \tag{2.3}$$

where $n = A.length$. In order to show that BUBBLESORT actually sorts, what else do we need to prove?

The next two parts will prove inequality (2.3).

b. State precisely a loop invariant for the **for** loop in lines 2–4, and prove that this loop invariant holds. Your proof should use the structure of the loop invariant proof presented in this chapter.

c. Using the termination condition of the loop invariant proved in part (b), state a loop invariant for the **for** loop in lines 1–4 that will allow you to prove inequality (2.3). Your proof should use the structure of the loop invariant proof presented in this chapter.

d. What is the worst-case running time of bubblesort? How does it compare to the running time of insertion sort?

2-3 Correctness of Horner's rule

The following code fragment implements Horner's rule for evaluating a polynomial

$$\begin{aligned} P(x) &= \sum_{k=0}^{n} a_k x^k \\ &= a_0 + x(a_1 + x(a_2 + \cdots + x(a_{n-1} + x a_n)\cdots)) \,, \end{aligned}$$

given the coefficients $a_0, a_1, \ldots, a_n$ and a value for x:

```
1  y = 0
2  for i = n downto 0
3      y = a_i + x · y
```

a. In terms of Θ-notation, what is the running time of this code fragment for Horner's rule?

b. Write pseudocode to implement the naive polynomial-evaluation algorithm that computes each term of the polynomial from scratch. What is the running time of this algorithm? How does it compare to Horner's rule?

c. Consider the following loop invariant:

> At the start of each iteration of the **for** loop of lines 2–3,
>
> $$y = \sum_{k=0}^{n-(i+1)} a_{k+i+1} x^k \,.$$
>
> Interpret a summation with no terms as equaling 0. Following the structure of the loop invariant proof presented in this chapter, use this loop invariant to show that, at termination, $y = \sum_{k=0}^{n} a_k x^k$.

d. Conclude by arguing that the given code fragment correctly evaluates a polynomial characterized by the coefficients $a_0, a_1, \ldots, a_n$.

2-4 Inversions

Let $A[1..n]$ be an array of n distinct numbers. If $i < j$ and $A[i] > A[j]$, then the pair (i, j) is called an ***inversion*** of A.

a. List the five inversions of the array $\langle 2, 3, 8, 6, 1 \rangle$.

b. What array with elements from the set $\{1, 2, \ldots, n\}$ has the most inversions? How many does it have?

c. What is the relationship between the running time of insertion sort and the number of inversions in the input array? Justify your answer.

d. Give an algorithm that determines the number of inversions in any permutation on n elements in $\Theta(n \lg n)$ worst-case time. (*Hint:* Modify merge sort.)

Chapter notes

In 1968, Knuth published the first of three volumes with the general title *The Art of Computer Programming* [209, 210, 211]. The first volume ushered in the modern study of computer algorithms with a focus on the analysis of running time, and the full series remains an engaging and worthwhile reference for many of the topics presented here. According to Knuth, the word "algorithm" is derived from the name "al-Khowârizmî," a ninth-century Persian mathematician.

Aho, Hopcroft, and Ullman [5] advocated the asymptotic analysis of algorithms—using notations that Chapter 3 introduces, including Θ-notation—as a means of comparing relative performance. They also popularized the use of recurrence relations to describe the running times of recursive algorithms.

Knuth [211] provides an encyclopedic treatment of many sorting algorithms. His comparison of sorting algorithms (page 381) includes exact step-counting analyses, like the one we performed here for insertion sort. Knuth's discussion of insertion sort encompasses several variations of the algorithm. The most important of these is Shell's sort, introduced by D. L. Shell, which uses insertion sort on periodic subsequences of the input to produce a faster sorting algorithm.

Merge sort is also described by Knuth. He mentions that a mechanical collator capable of merging two decks of punched cards in a single pass was invented in 1938. J. von Neumann, one of the pioneers of computer science, apparently wrote a program for merge sort on the EDVAC computer in 1945.

The early history of proving programs correct is described by Gries [153], who credits P. Naur with the first article in this field. Gries attributes loop invariants to R. W. Floyd. The textbook by Mitchell [256] describes more recent progress in proving programs correct.

3 Growth of Functions

The order of growth of the running time of an algorithm, defined in Chapter 2, gives a simple characterization of the algorithm's efficiency and also allows us to compare the relative performance of alternative algorithms. Once the input size n becomes large enough, merge sort, with its $\Theta(n \lg n)$ worst-case running time, beats insertion sort, whose worst-case running time is $\Theta(n^2)$. Although we can sometimes determine the exact running time of an algorithm, as we did for insertion sort in Chapter 2, the extra precision is not usually worth the effort of computing it. For large enough inputs, the multiplicative constants and lower-order terms of an exact running time are dominated by the effects of the input size itself.

When we look at input sizes large enough to make only the order of growth of the running time relevant, we are studying the ***asymptotic*** efficiency of algorithms. That is, we are concerned with how the running time of an algorithm increases with the size of the input *in the limit*, as the size of the input increases without bound. Usually, an algorithm that is asymptotically more efficient will be the best choice for all but very small inputs.

This chapter gives several standard methods for simplifying the asymptotic analysis of algorithms. The next section begins by defining several types of "asymptotic notation," of which we have already seen an example in Θ-notation. We then present several notational conventions used throughout this book, and finally we review the behavior of functions that commonly arise in the analysis of algorithms.

3.1 Asymptotic notation

The notations we use to describe the asymptotic running time of an algorithm are defined in terms of functions whose domains are the set of natural numbers $\mathbb{N} = \{0, 1, 2, \ldots\}$. Such notations are convenient for describing the worst-case running-time function $T(n)$, which usually is defined only on integer input sizes. We sometimes find it convenient, however, to *abuse* asymptotic notation in a va-

riety of ways. For example, we might extend the notation to the domain of real numbers or, alternatively, restrict it to a subset of the natural numbers. We should make sure, however, to understand the precise meaning of the notation so that when we abuse, we do not *misuse* it. This section defines the basic asymptotic notations and also introduces some common abuses.

Asymptotic notation, functions, and running times

We will use asymptotic notation primarily to describe the running times of algorithms, as when we wrote that insertion sort's worst-case running time is $\Theta(n^2)$. Asymptotic notation actually applies to functions, however. Recall that we characterized insertion sort's worst-case running time as an^2+bn+c, for some constants a, b, and c. By writing that insertion sort's running time is $\Theta(n^2)$, we abstracted away some details of this function. Because asymptotic notation applies to functions, what we were writing as $\Theta(n^2)$ was the function $an^2 + bn + c$, which in that case happened to characterize the worst-case running time of insertion sort.

In this book, the functions to which we apply asymptotic notation will usually characterize the running times of algorithms. But asymptotic notation can apply to functions that characterize some other aspect of algorithms (the amount of space they use, for example), or even to functions that have nothing whatsoever to do with algorithms.

Even when we use asymptotic notation to apply to the running time of an algorithm, we need to understand *which* running time we mean. Sometimes we are interested in the worst-case running time. Often, however, we wish to characterize the running time no matter what the input. In other words, we often wish to make a blanket statement that covers all inputs, not just the worst case. We shall see asymptotic notations that are well suited to characterizing running times no matter what the input.

Θ-notation

In Chapter 2, we found that the worst-case running time of insertion sort is $T(n) = \Theta(n^2)$. Let us define what this notation means. For a given function $g(n)$, we denote by $\Theta(g(n))$ the *set of functions*

$$\Theta(g(n)) = \{f(n) : \text{ there exist positive constants } c_1, c_2, \text{ and } n_0 \text{ such that } 0 \le c_1 g(n) \le f(n) \le c_2 g(n) \text{ for all } n \ge n_0\}.$$[1]

[1] Within set notation, a colon means "such that."

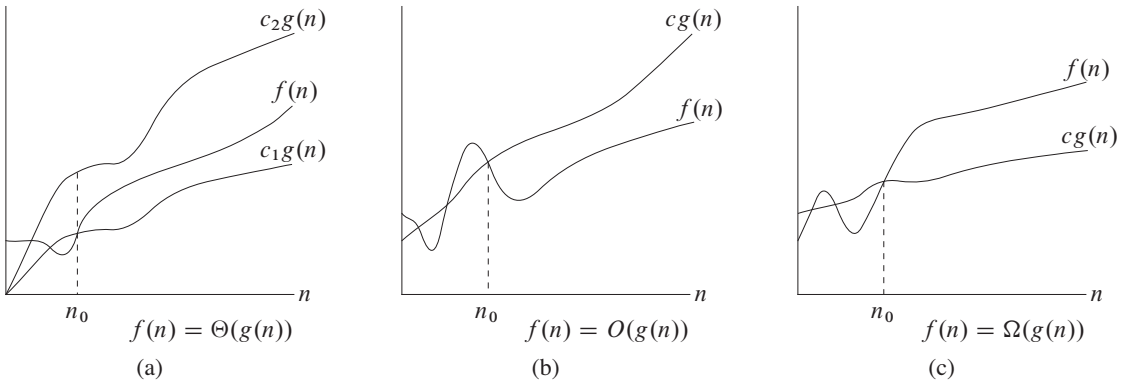


Figure 3.1 Graphic examples of the Θ, O, and Ω notations. In each part, the value of n_0 shown is the minimum possible value; any greater value would also work. **(a)** Θ-notation bounds a function to within constant factors. We write $f(n) = \Theta(g(n))$ if there exist positive constants n_0, c_1, and c_2 such that at and to the right of n_0, the value of $f(n)$ always lies between $c_1 g(n)$ and $c_2 g(n)$ inclusive. **(b)** O-notation gives an upper bound for a function to within a constant factor. We write $f(n) = O(g(n))$ if there are positive constants n_0 and c such that at and to the right of n_0, the value of $f(n)$ always lies on or below $cg(n)$. **(c)** Ω-notation gives a lower bound for a function to within a constant factor. We write $f(n) = \Omega(g(n))$ if there are positive constants n_0 and c such that at and to the right of n_0, the value of $f(n)$ always lies on or above $cg(n)$.

A function $f(n)$ belongs to the set $\Theta(g(n))$ if there exist positive constants c_1 and c_2 such that it can be "sandwiched" between $c_1 g(n)$ and $c_2 g(n)$, for sufficiently large n. Because $\Theta(g(n))$ is a set, we could write "$f(n) \in \Theta(g(n))$" to indicate that $f(n)$ is a member of $\Theta(g(n))$. Instead, we will usually write "$f(n) = \Theta(g(n))$" to express the same notion. You might be confused because we abuse equality in this way, but we shall see later in this section that doing so has its advantages.

Figure 3.1(a) gives an intuitive picture of functions $f(n)$ and $g(n)$, where $f(n) = \Theta(g(n))$. For all values of n at and to the right of n_0, the value of $f(n)$ lies at or above $c_1 g(n)$ and at or below $c_2 g(n)$. In other words, for all $n \geq n_0$, the function $f(n)$ is equal to $g(n)$ to within a constant factor. We say that $g(n)$ is an ***asymptotically tight bound*** for $f(n)$.

The definition of $\Theta(g(n))$ requires that every member $f(n) \in \Theta(g(n))$ be ***asymptotically nonnegative***, that is, that $f(n)$ be nonnegative whenever n is sufficiently large. (An ***asymptotically positive*** function is one that is positive for all sufficiently large n.) Consequently, the function $g(n)$ itself must be asymptotically nonnegative, or else the set $\Theta(g(n))$ is empty. We shall therefore assume that every function used within Θ-notation is asymptotically nonnegative. This assumption holds for the other asymptotic notations defined in this chapter as well.

In Chapter 2, we introduced an informal notion of Θ-notation that amounted to throwing away lower-order terms and ignoring the leading coefficient of the highest-order term. Let us briefly justify this intuition by using the formal definition to show that $\frac{1}{2}n^2 - 3n = \Theta(n^2)$. To do so, we must determine positive constants c_1, c_2, and n_0 such that

$$c_1 n^2 \leq \frac{1}{2}n^2 - 3n \leq c_2 n^2$$

for all $n \geq n_0$. Dividing by n^2 yields

$$c_1 \leq \frac{1}{2} - \frac{3}{n} \leq c_2 .$$

We can make the right-hand inequality hold for any value of $n \geq 1$ by choosing any constant $c_2 \geq 1/2$. Likewise, we can make the left-hand inequality hold for any value of $n \geq 7$ by choosing any constant $c_1 \leq 1/14$. Thus, by choosing $c_1 = 1/14$, $c_2 = 1/2$, and $n_0 = 7$, we can verify that $\frac{1}{2}n^2 - 3n = \Theta(n^2)$. Certainly, other choices for the constants exist, but the important thing is that *some* choice exists. Note that these constants depend on the function $\frac{1}{2}n^2 - 3n$; a different function belonging to $\Theta(n^2)$ would usually require different constants.

We can also use the formal definition to verify that $6n^3 \neq \Theta(n^2)$. Suppose for the purpose of contradiction that c_2 and n_0 exist such that $6n^3 \leq c_2 n^2$ for all $n \geq n_0$. But then dividing by n^2 yields $n \leq c_2/6$, which cannot possibly hold for arbitrarily large n, since c_2 is constant.

Intuitively, the lower-order terms of an asymptotically positive function can be ignored in determining asymptotically tight bounds because they are insignificant for large n. When n is large, even a tiny fraction of the highest-order term suffices to dominate the lower-order terms. Thus, setting c_1 to a value that is slightly smaller than the coefficient of the highest-order term and setting c_2 to a value that is slightly larger permits the inequalities in the definition of Θ-notation to be satisfied. The coefficient of the highest-order term can likewise be ignored, since it only changes c_1 and c_2 by a constant factor equal to the coefficient.

As an example, consider any quadratic function $f(n) = an^2 + bn + c$, where a, b, and c are constants and $a > 0$. Throwing away the lower-order terms and ignoring the constant yields $f(n) = \Theta(n^2)$. Formally, to show the same thing, we take the constants $c_1 = a/4$, $c_2 = 7a/4$, and $n_0 = 2 \cdot \max(|b|/a, \sqrt{|c|/a})$. You may verify that $0 \leq c_1 n^2 \leq an^2 + bn + c \leq c_2 n^2$ for all $n \geq n_0$. In general, for any polynomial $p(n) = \sum_{i=0}^{d} a_i n^i$, where the a_i are constants and $a_d > 0$, we have $p(n) = \Theta(n^d)$ (see Problem 3-1).

Since any constant is a degree-0 polynomial, we can express any constant function as $\Theta(n^0)$, or $\Theta(1)$. This latter notation is a minor abuse, however, because the

expression does not indicate what variable is tending to infinity.[2] We shall often use the notation $\Theta(1)$ to mean either a constant or a constant function with respect to some variable.

O-notation

The Θ-notation asymptotically bounds a function from above and below. When we have only an ***asymptotic upper bound***, we use O-notation. For a given function $g(n)$, we denote by $O(g(n))$ (pronounced "big-oh of g of n" or sometimes just "oh of g of n") the set of functions

$$O(g(n)) = \{f(n) : \text{ there exist positive constants } c \text{ and } n_0 \text{ such that } 0 \le f(n) \le cg(n) \text{ for all } n \ge n_0\} .$$

We use O-notation to give an upper bound on a function, to within a constant factor. Figure 3.1(b) shows the intuition behind O-notation. For all values n at and to the right of n_0, the value of the function $f(n)$ is on or below $cg(n)$.

We write $f(n) = O(g(n))$ to indicate that a function $f(n)$ is a member of the set $O(g(n))$. Note that $f(n) = \Theta(g(n))$ implies $f(n) = O(g(n))$, since Θ-notation is a stronger notion than O-notation. Written set-theoretically, we have $\Theta(g(n)) \subseteq O(g(n))$. Thus, our proof that any quadratic function $an^2 + bn + c$, where $a > 0$, is in $\Theta(n^2)$ also shows that any such quadratic function is in $O(n^2)$. What may be more surprising is that when $a > 0$, any *linear* function $an + b$ is in $O(n^2)$, which is easily verified by taking $c = a + |b|$ and $n_0 = \max(1, -b/a)$.

If you have seen O-notation before, you might find it strange that we should write, for example, $n = O(n^2)$. In the literature, we sometimes find O-notation informally describing asymptotically tight bounds, that is, what we have defined using Θ-notation. In this book, however, when we write $f(n) = O(g(n))$, we are merely claiming that some constant multiple of $g(n)$ is an asymptotic upper bound on $f(n)$, with no claim about how tight an upper bound it is. Distinguishing asymptotic upper bounds from asymptotically tight bounds is standard in the algorithms literature.

Using O-notation, we can often describe the running time of an algorithm merely by inspecting the algorithm's overall structure. For example, the doubly nested loop structure of the insertion sort algorithm from Chapter 2 immediately yields an $O(n^2)$ upper bound on the worst-case running time: the cost of each iteration of the inner loop is bounded from above by $O(1)$ (constant), the indices i

---

[2] The real problem is that our ordinary notation for functions does not distinguish functions from values. In λ-calculus, the parameters to a function are clearly specified: the function n^2 could be written as $\lambda n.n^2$, or even $\lambda r.r^2$. Adopting a more rigorous notation, however, would complicate algebraic manipulations, and so we choose to tolerate the abuse.

and j are both at most n, and the inner loop is executed at most once for each of the n^2 pairs of values for i and j.

Since O-notation describes an upper bound, when we use it to bound the worst-case running time of an algorithm, we have a bound on the running time of the algorithm on every input—the blanket statement we discussed earlier. Thus, the $O(n^2)$ bound on worst-case running time of insertion sort also applies to its running time on every input. The $\Theta(n^2)$ bound on the worst-case running time of insertion sort, however, does not imply a $\Theta(n^2)$ bound on the running time of insertion sort on *every* input. For example, we saw in Chapter 2 that when the input is already sorted, insertion sort runs in $\Theta(n)$ time.

Technically, it is an abuse to say that the running time of insertion sort is $O(n^2)$, since for a given n, the actual running time varies, depending on the particular input of size n. When we say "the running time is $O(n^2)$," we mean that there is a function $f(n)$ that is $O(n^2)$ such that for any value of n, no matter what particular input of size n is chosen, the running time on that input is bounded from above by the value $f(n)$. Equivalently, we mean that the worst-case running time is $O(n^2)$.

Ω-notation

Just as O-notation provides an asymptotic *upper* bound on a function, Ω-notation provides an ***asymptotic lower bound***. For a given function $g(n)$, we denote by $\Omega(g(n))$ (pronounced "big-omega of g of n" or sometimes just "omega of g of n") the set of functions

$$\Omega(g(n)) = \{f(n) : \text{ there exist positive constants } c \text{ and } n_0 \text{ such that } 0 \le cg(n) \le f(n) \text{ for all } n \ge n_0\} .$$

Figure 3.1(c) shows the intuition behind Ω-notation. For all values n at or to the right of n_0, the value of $f(n)$ is on or above $cg(n)$.

From the definitions of the asymptotic notations we have seen thus far, it is easy to prove the following important theorem (see Exercise 3.1-5).

Theorem 3.1

For any two functions $f(n)$ and $g(n)$, we have $f(n) = \Theta(g(n))$ if and only if $f(n) = O(g(n))$ and $f(n) = \Omega(g(n))$. ■

As an example of the application of this theorem, our proof that $an^2 + bn + c = \Theta(n^2)$ for any constants a, b, and c, where $a > 0$, immediately implies that $an^2 + bn + c = \Omega(n^2)$ and $an^2 + bn + c = O(n^2)$. In practice, rather than using Theorem 3.1 to obtain asymptotic upper and lower bounds from asymptotically tight bounds, as we did for this example, we usually use it to prove asymptotically tight bounds from asymptotic upper and lower bounds.

When we say that the *running time* (no modifier) of an algorithm is $\Omega(g(n))$, we mean that *no matter what particular input of size n is chosen for each value of n*, the running time on that input is at least a constant times $g(n)$, for sufficiently large n. Equivalently, we are giving a lower bound on the best-case running time of an algorithm. For example, the best-case running time of insertion sort is $\Omega(n)$, which implies that the running time of insertion sort is $\Omega(n)$.

The running time of insertion sort therefore belongs to both $\Omega(n)$ and $O(n^2)$, since it falls anywhere between a linear function of n and a quadratic function of n. Moreover, these bounds are asymptotically as tight as possible: for instance, the running time of insertion sort is not $\Omega(n^2)$, since there exists an input for which insertion sort runs in $\Theta(n)$ time (e.g., when the input is already sorted). It is not contradictory, however, to say that the *worst-case* running time of insertion sort is $\Omega(n^2)$, since there exists an input that causes the algorithm to take $\Omega(n^2)$ time.

Asymptotic notation in equations and inequalities

We have already seen how asymptotic notation can be used within mathematical formulas. For example, in introducing O-notation, we wrote "$n = O(n^2)$." We might also write $2n^2 + 3n + 1 = 2n^2 + \Theta(n)$. How do we interpret such formulas?

When the asymptotic notation stands alone (that is, not within a larger formula) on the right-hand side of an equation (or inequality), as in $n = O(n^2)$, we have already defined the equal sign to mean set membership: $n \in O(n^2)$. In general, however, when asymptotic notation appears in a formula, we interpret it as standing for some anonymous function that we do not care to name. For example, the formula $2n^2 + 3n + 1 = 2n^2 + \Theta(n)$ means that $2n^2 + 3n + 1 = 2n^2 + f(n)$, where $f(n)$ is some function in the set $\Theta(n)$. In this case, we let $f(n) = 3n + 1$, which indeed is in $\Theta(n)$.

Using asymptotic notation in this manner can help eliminate inessential detail and clutter in an equation. For example, in Chapter 2 we expressed the worst-case running time of merge sort as the recurrence

$$T(n) = 2T(n/2) + \Theta(n) .$$

If we are interested only in the asymptotic behavior of $T(n)$, there is no point in specifying all the lower-order terms exactly; they are all understood to be included in the anonymous function denoted by the term $\Theta(n)$.

The number of anonymous functions in an expression is understood to be equal to the number of times the asymptotic notation appears. For example, in the expression

$$\sum_{i=1}^{n} O(i) ,$$

there is only a single anonymous function (a function of i). This expression is thus *not* the same as $O(1) + O(2) + \cdots + O(n)$, which doesn't really have a clean interpretation.

In some cases, asymptotic notation appears on the left-hand side of an equation, as in

$$2n^2 + \Theta(n) = \Theta(n^2) .$$

We interpret such equations using the following rule: *No matter how the anonymous functions are chosen on the left of the equal sign, there is a way to choose the anonymous functions on the right of the equal sign to make the equation valid.* Thus, our example means that for *any* function $f(n) \in \Theta(n)$, there is *some* function $g(n) \in \Theta(n^2)$ such that $2n^2 + f(n) = g(n)$ for all n. In other words, the right-hand side of an equation provides a coarser level of detail than the left-hand side.

We can chain together a number of such relationships, as in

$$\begin{aligned} 2n^2 + 3n + 1 &= 2n^2 + \Theta(n) \\ &= \Theta(n^2) . \end{aligned}$$

We can interpret each equation separately by the rules above. The first equation says that there is *some* function $f(n) \in \Theta(n)$ such that $2n^2 + 3n + 1 = 2n^2 + f(n)$ for all n. The second equation says that for *any* function $g(n) \in \Theta(n)$ (such as the $f(n)$ just mentioned), there is *some* function $h(n) \in \Theta(n^2)$ such that $2n^2 + g(n) = h(n)$ for all n. Note that this interpretation implies that $2n^2 + 3n + 1 = \Theta(n^2)$, which is what the chaining of equations intuitively gives us.

o-notation

The asymptotic upper bound provided by O-notation may or may not be asymptotically tight. The bound $2n^2 = O(n^2)$ is asymptotically tight, but the bound $2n = O(n^2)$ is not. We use o-notation to denote an upper bound that is not asymptotically tight. We formally define $o(g(n))$ ("little-oh of g of n") as the set

$$\begin{aligned} o(g(n)) = \{ f(n) : &\text{ for any positive constant } c > 0, \text{ there exists a constant} \\ &n_0 > 0 \text{ such that } 0 \le f(n) < cg(n) \text{ for all } n \ge n_0 \} . \end{aligned}$$

For example, $2n = o(n^2)$, but $2n^2 \neq o(n^2)$.

The definitions of O-notation and o-notation are similar. The main difference is that in $f(n) = O(g(n))$, the bound $0 \le f(n) \le cg(n)$ holds for *some* constant $c > 0$, but in $f(n) = o(g(n))$, the bound $0 \le f(n) < cg(n)$ holds for *all* constants $c > 0$. Intuitively, in o-notation, the function $f(n)$ becomes insignificant relative to $g(n)$ as n approaches infinity; that is,

$$\lim_{n\to\infty} \frac{f(n)}{g(n)} = 0 \,. \tag{3.1}$$

Some authors use this limit as a definition of the o-notation; the definition in this book also restricts the anonymous functions to be asymptotically nonnegative.

ω-notation

By analogy, ω-notation is to Ω-notation as o-notation is to O-notation. We use ω-notation to denote a lower bound that is not asymptotically tight. One way to define it is by

$f(n) \in \omega(g(n))$ if and only if $g(n) \in o(f(n))$.

Formally, however, we define $\omega(g(n))$ ("little-omega of g of n") as the set

$$\omega(g(n)) = \{f(n) : \text{for any positive constant } c > 0, \text{ there exists a constant } n_0 > 0 \text{ such that } 0 \le cg(n) < f(n) \text{ for all } n \ge n_0\} \,.$$

For example, $n^2/2 = \omega(n)$, but $n^2/2 \neq \omega(n^2)$. The relation $f(n) = \omega(g(n))$ implies that

$$\lim_{n\to\infty} \frac{f(n)}{g(n)} = \infty \,,$$

if the limit exists. That is, $f(n)$ becomes arbitrarily large relative to $g(n)$ as n approaches infinity.

Comparing functions

Many of the relational properties of real numbers apply to asymptotic comparisons as well. For the following, assume that $f(n)$ and $g(n)$ are asymptotically positive.

Transitivity:

$$\begin{aligned}
&f(n) = \Theta(g(n)) \text{ and } g(n) = \Theta(h(n)) \quad \text{imply} \quad f(n) = \Theta(h(n)) \,,\\
&f(n) = O(g(n)) \text{ and } g(n) = O(h(n)) \quad \text{imply} \quad f(n) = O(h(n)) \,,\\
&f(n) = \Omega(g(n)) \text{ and } g(n) = \Omega(h(n)) \quad \text{imply} \quad f(n) = \Omega(h(n)) \,,\\
&f(n) = o(g(n)) \text{ and } g(n) = o(h(n)) \quad \text{imply} \quad f(n) = o(h(n)) \,,\\
&f(n) = \omega(g(n)) \text{ and } g(n) = \omega(h(n)) \quad \text{imply} \quad f(n) = \omega(h(n)) \,.
\end{aligned}$$

Reflexivity:

$$\begin{aligned}
f(n) &= \Theta(f(n)) \,,\\
f(n) &= O(f(n)) \,,\\
f(n) &= \Omega(f(n)) \,.
\end{aligned}$$

Symmetry:

$$f(n) = \Theta(g(n)) \text{ if and only if } g(n) = \Theta(f(n)) .$$

Transpose symmetry:

$$f(n) = O(g(n)) \text{ if and only if } g(n) = \Omega(f(n)) ,$$
$$f(n) = o(g(n)) \text{ if and only if } g(n) = \omega(f(n)) .$$

Because these properties hold for asymptotic notations, we can draw an analogy between the asymptotic comparison of two functions f and g and the comparison of two real numbers a and b:

$$f(n) = O(g(n)) \quad \text{is like} \quad a \leq b ,$$
$$f(n) = \Omega(g(n)) \quad \text{is like} \quad a \geq b ,$$
$$f(n) = \Theta(g(n)) \quad \text{is like} \quad a = b ,$$
$$f(n) = o(g(n)) \quad \text{is like} \quad a < b ,$$
$$f(n) = \omega(g(n)) \quad \text{is like} \quad a > b .$$

We say that $f(n)$ is ***asymptotically smaller*** than $g(n)$ if $f(n) = o(g(n))$, and $f(n)$ is ***asymptotically larger*** than $g(n)$ if $f(n) = \omega(g(n))$.

One property of real numbers, however, does not carry over to asymptotic notation:

Trichotomy: For any two real numbers a and b, exactly one of the following must hold: $a < b$, $a = b$, or $a > b$.

Although any two real numbers can be compared, not all functions are asymptotically comparable. That is, for two functions $f(n)$ and $g(n)$, it may be the case that neither $f(n) = O(g(n))$ nor $f(n) = \Omega(g(n))$ holds. For example, we cannot compare the functions n and $n^{1+\sin n}$ using asymptotic notation, since the value of the exponent in $n^{1+\sin n}$ oscillates between 0 and 2, taking on all values in between.

Exercises

3.1-1

Let $f(n)$ and $g(n)$ be asymptotically nonnegative functions. Using the basic definition of Θ-notation, prove that $\max(f(n), g(n)) = \Theta(f(n) + g(n))$.

3.1-2

Show that for any real constants a and b, where $b > 0$,

$$(n + a)^b = \Theta(n^b) . \tag{3.2}$$

3.1-3
Explain why the statement, "The running time of algorithm A is at least $O(n^2)$," is meaningless.

3.1-4
Is $2^{n+1} = O(2^n)$? Is $2^{2n} = O(2^n)$?

3.1-5
Prove Theorem 3.1.

3.1-6
Prove that the running time of an algorithm is $\Theta(g(n))$ if and only if its worst-case running time is $O(g(n))$ and its best-case running time is $\Omega(g(n))$.

3.1-7
Prove that $o(g(n)) \cap \omega(g(n))$ is the empty set.

3.1-8
We can extend our notation to the case of two parameters n and m that can go to infinity independently at different rates. For a given function $g(n,m)$, we denote by $O(g(n,m))$ the set of functions

$$O(g(n,m)) = \{f(n,m) : \text{there exist positive constants } c, n_0, \text{ and } m_0 \text{ such that } 0 \le f(n,m) \le cg(n,m) \text{ for all } n \ge n_0 \text{ or } m \ge m_0\}.$$

Give corresponding definitions for $\Omega(g(n,m))$ and $\Theta(g(n,m))$.

3.2 Standard notations and common functions

This section reviews some standard mathematical functions and notations and explores the relationships among them. It also illustrates the use of the asymptotic notations.

Monotonicity

A function $f(n)$ is ***monotonically increasing*** if $m \le n$ implies $f(m) \le f(n)$. Similarly, it is ***monotonically decreasing*** if $m \le n$ implies $f(m) \ge f(n)$. A function $f(n)$ is ***strictly increasing*** if $m < n$ implies $f(m) < f(n)$ and ***strictly decreasing*** if $m < n$ implies $f(m) > f(n)$.

Floors and ceilings

For any real number x, we denote the greatest integer less than or equal to x by $\lfloor x \rfloor$ (read "the floor of x") and the least integer greater than or equal to x by $\lceil x \rceil$ (read "the ceiling of x"). For all real x,

$$x - 1 \ < \ \lfloor x \rfloor \ \leq \ x \ \leq \ \lceil x \rceil \ < \ x + 1 \ . \tag{3.3}$$

For any integer n,

$$\lceil n/2 \rceil + \lfloor n/2 \rfloor = n \ ,$$

and for any real number $x \geq 0$ and integers $a, b > 0$,

$$\left\lceil \frac{\lceil x/a \rceil}{b} \right\rceil \ = \ \left\lceil \frac{x}{ab} \right\rceil \ , \tag{3.4}$$

$$\left\lfloor \frac{\lfloor x/a \rfloor}{b} \right\rfloor \ = \ \left\lfloor \frac{x}{ab} \right\rfloor \ , \tag{3.5}$$

$$\left\lceil \frac{a}{b} \right\rceil \ \leq \ \frac{a + (b-1)}{b} \ , \tag{3.6}$$

$$\left\lfloor \frac{a}{b} \right\rfloor \ \geq \ \frac{a - (b-1)}{b} \ . \tag{3.7}$$

The floor function $f(x) = \lfloor x \rfloor$ is monotonically increasing, as is the ceiling function $f(x) = \lceil x \rceil$.

Modular arithmetic

For any integer a and any positive integer n, the value $a \bmod n$ is the ***remainder*** (or ***residue***) of the quotient a/n:

$$a \bmod n = a - n \lfloor a/n \rfloor \ . \tag{3.8}$$

It follows that

$$0 \leq a \bmod n < n \ . \tag{3.9}$$

Given a well-defined notion of the remainder of one integer when divided by another, it is convenient to provide special notation to indicate equality of remainders. If $(a \bmod n) = (b \bmod n)$, we write $a \equiv b \pmod{n}$ and say that a is ***equivalent*** to b, modulo n. In other words, $a \equiv b \pmod{n}$ if a and b have the same remainder when divided by n. Equivalently, $a \equiv b \pmod{n}$ if and only if n is a divisor of $b - a$. We write $a \not\equiv b \pmod{n}$ if a is not equivalent to b, modulo n.

Polynomials

Given a nonnegative integer d, a ***polynomial in n of degree d*** is a function $p(n)$ of the form

$$p(n) = \sum_{i=0}^{d} a_i n^i ,$$

where the constants $a_0, a_1, \ldots, a_d$ are the ***coefficients*** of the polynomial and $a_d \neq 0$. A polynomial is asymptotically positive if and only if $a_d > 0$. For an asymptotically positive polynomial $p(n)$ of degree d, we have $p(n) = \Theta(n^d)$. For any real constant $a \geq 0$, the function n^a is monotonically increasing, and for any real constant $a \leq 0$, the function n^a is monotonically decreasing. We say that a function $f(n)$ is ***polynomially bounded*** if $f(n) = O(n^k)$ for some constant k.

Exponentials

For all real $a > 0$, m, and n, we have the following identities:

$$\begin{aligned} a^0 &= 1 , \\ a^1 &= a , \\ a^{-1} &= 1/a , \\ (a^m)^n &= a^{mn} , \\ (a^m)^n &= (a^n)^m , \\ a^m a^n &= a^{m+n} . \end{aligned}$$

For all n and $a \geq 1$, the function a^n is monotonically increasing in n. When convenient, we shall assume $0^0 = 1$.

We can relate the rates of growth of polynomials and exponentials by the following fact. For all real constants a and b such that $a > 1$,

$$\lim_{n \to \infty} \frac{n^b}{a^n} = 0 , \tag{3.10}$$

from which we can conclude that

$$n^b = o(a^n) .$$

Thus, any exponential function with a base strictly greater than 1 grows faster than any polynomial function.

Using e to denote 2.71828..., the base of the natural logarithm function, we have for all real x,

$$e^x = 1 + x + \frac{x^2}{2!} + \frac{x^3}{3!} + \cdots = \sum_{i=0}^{\infty} \frac{x^i}{i!} , \tag{3.11}$$

where "!" denotes the factorial function defined later in this section. For all real x, we have the inequality

$$e^x \geq 1 + x \,, \tag{3.12}$$

where equality holds only when $x = 0$. When $|x| \leq 1$, we have the approximation

$$1 + x \leq e^x \leq 1 + x + x^2 \,. \tag{3.13}$$

When $x \to 0$, the approximation of e^x by $1 + x$ is quite good:

$$e^x = 1 + x + \Theta(x^2) \,.$$

(In this equation, the asymptotic notation is used to describe the limiting behavior as $x \to 0$ rather than as $x \to \infty$.) We have for all x,

$$\lim_{n \to \infty} \left(1 + \frac{x}{n}\right)^n = e^x \,. \tag{3.14}$$

Logarithms

We shall use the following notations:

$$\begin{aligned}
\lg n &= \log_2 n && \text{(binary logarithm)} \,, \\
\ln n &= \log_e n && \text{(natural logarithm)} \,, \\
\lg^k n &= (\lg n)^k && \text{(exponentiation)} \,, \\
\lg \lg n &= \lg(\lg n) && \text{(composition)} \,.
\end{aligned}$$

An important notational convention we shall adopt is that *logarithm functions will apply only to the next term in the formula*, so that $\lg n + k$ will mean $(\lg n) + k$ and not $\lg(n + k)$. If we hold $b > 1$ constant, then for $n > 0$, the function $\log_b n$ is strictly increasing.

For all real $a > 0$, $b > 0$, $c > 0$, and n,

$$\begin{aligned}
a &= b^{\log_b a} \,, \\
\log_c(ab) &= \log_c a + \log_c b \,, \\
\log_b a^n &= n \log_b a \,, \\
\log_b a &= \frac{\log_c a}{\log_c b} \,, && (3.15) \\
\log_b(1/a) &= -\log_b a \,, \\
\log_b a &= \frac{1}{\log_a b} \,, \\
a^{\log_b c} &= c^{\log_b a} \,, && (3.16)
\end{aligned}$$

where, in each equation above, logarithm bases are not 1.

By equation (3.15), changing the base of a logarithm from one constant to another changes the value of the logarithm by only a constant factor, and so we shall often use the notation "$\lg n$" when we don't care about constant factors, such as in O-notation. Computer scientists find 2 to be the most natural base for logarithms because so many algorithms and data structures involve splitting a problem into two parts.

There is a simple series expansion for $\ln(1+x)$ when $|x| < 1$:

$$\ln(1+x) = x - \frac{x^2}{2} + \frac{x^3}{3} - \frac{x^4}{4} + \frac{x^5}{5} - \cdots .$$

We also have the following inequalities for $x > -1$:

$$\frac{x}{1+x} \le \ln(1+x) \le x , \tag{3.17}$$

where equality holds only for $x = 0$.

We say that a function $f(n)$ is ***polylogarithmically bounded*** if $f(n) = O(\lg^k n)$ for some constant k. We can relate the growth of polynomials and polylogarithms by substituting $\lg n$ for n and 2^a for a in equation (3.10), yielding

$$\lim_{n\to\infty} \frac{\lg^b n}{(2^a)^{\lg n}} = \lim_{n\to\infty} \frac{\lg^b n}{n^a} = 0 .$$

From this limit, we can conclude that

$$\lg^b n = o(n^a)$$

for any constant $a > 0$. Thus, any positive polynomial function grows faster than any polylogarithmic function.

Factorials

The notation $n!$ (read "n factorial") is defined for integers $n \ge 0$ as

$$n! = \begin{cases} 1 & \text{if } n = 0 , \\ n \cdot (n-1)! & \text{if } n > 0 . \end{cases}$$

Thus, $n! = 1 \cdot 2 \cdot 3 \cdots n$.

A weak upper bound on the factorial function is $n! \le n^n$, since each of the n terms in the factorial product is at most n. ***Stirling's approximation***,

$$n! = \sqrt{2\pi n}\left(\frac{n}{e}\right)^n \left(1 + \Theta\left(\frac{1}{n}\right)\right) , \tag{3.18}$$

where e is the base of the natural logarithm, gives us a tighter upper bound, and a lower bound as well. As Exercise 3.2-3 asks you to prove,

$$\begin{aligned} n! &= o(n^n) , \\ n! &= \omega(2^n) , \\ \lg(n!) &= \Theta(n \lg n) , \end{aligned} \tag{3.19}$$

where Stirling's approximation is helpful in proving equation (3.19). The following equation also holds for all $n \geq 1$:

$$n! = \sqrt{2\pi n} \left(\frac{n}{e}\right)^n e^{\alpha_n} \tag{3.20}$$

where

$$\frac{1}{12n+1} < \alpha_n < \frac{1}{12n} . \tag{3.21}$$

Functional iteration

We use the notation $f^{(i)}(n)$ to denote the function $f(n)$ iteratively applied i times to an initial value of n. Formally, let $f(n)$ be a function over the reals. For nonnegative integers i, we recursively define

$$f^{(i)}(n) = \begin{cases} n & \text{if } i = 0 , \\ f(f^{(i-1)}(n)) & \text{if } i > 0 . \end{cases}$$

For example, if $f(n) = 2n$, then $f^{(i)}(n) = 2^i n$.

The iterated logarithm function

We use the notation $\lg^* n$ (read "log star of n") to denote the iterated logarithm, defined as follows. Let $\lg^{(i)} n$ be as defined above, with $f(n) = \lg n$. Because the logarithm of a nonpositive number is undefined, $\lg^{(i)} n$ is defined only if $\lg^{(i-1)} n > 0$. Be sure to distinguish $\lg^{(i)} n$ (the logarithm function applied i times in succession, starting with argument n) from $\lg^i n$ (the logarithm of n raised to the ith power). Then we define the iterated logarithm function as

$$\lg^* n = \min \left\{ i \geq 0 : \lg^{(i)} n \leq 1 \right\} .$$

The iterated logarithm is a *very* slowly growing function:

$$\begin{aligned} \lg^* 2 &= 1 , \\ \lg^* 4 &= 2 , \\ \lg^* 16 &= 3 , \\ \lg^* 65536 &= 4 , \\ \lg^*(2^{65536}) &= 5 . \end{aligned}$$

Since the number of atoms in the observable universe is estimated to be about 10^{80}, which is much less than 2^{65536}, we rarely encounter an input size n such that $\lg^* n > 5$.

Fibonacci numbers

We define the ***Fibonacci numbers*** by the following recurrence:

$$\begin{aligned} F_0 &= 0 , \\ F_1 &= 1 , \\ F_i &= F_{i-1} + F_{i-2} \qquad \text{for } i \geq 2 . \end{aligned} \tag{3.22}$$

Thus, each Fibonacci number is the sum of the two previous ones, yielding the sequence

$$0,\ 1,\ 1,\ 2,\ 3,\ 5,\ 8,\ 13,\ 21,\ 34,\ 55,\ \ldots\ .$$

Fibonacci numbers are related to the ***golden ratio*** ϕ and to its conjugate $\widehat{\phi}$, which are the two roots of the equation

$$x^2 = x + 1 \tag{3.23}$$

and are given by the following formulas (see Exercise 3.2-6):

$$\begin{aligned} \phi &= \frac{1+\sqrt{5}}{2} \\ &= 1.61803\ldots , \\ \widehat{\phi} &= \frac{1-\sqrt{5}}{2} \\ &= -.61803\ldots . \end{aligned} \tag{3.24}$$

Specifically, we have

$$F_i = \frac{\phi^i - \widehat{\phi}^i}{\sqrt{5}} ,$$

which we can prove by induction (Exercise 3.2-7). Since $|\widehat{\phi}| < 1$, we have

$$\begin{aligned} \frac{|\widehat{\phi}^i|}{\sqrt{5}} &< \frac{1}{\sqrt{5}} \\ &< \frac{1}{2} , \end{aligned}$$

which implies that

$$F_i = \left\lfloor \frac{\phi^i}{\sqrt{5}} + \frac{1}{2} \right\rfloor , \tag{3.25}$$

which is to say that the ith Fibonacci number F_i is equal to $\phi^i / \sqrt{5}$ rounded to the nearest integer. Thus, Fibonacci numbers grow exponentially.

Exercises

3.2-1
Show that if $f(n)$ and $g(n)$ are monotonically increasing functions, then so are the functions $f(n) + g(n)$ and $f(g(n))$, and if $f(n)$ and $g(n)$ are in addition nonnegative, then $f(n) \cdot g(n)$ is monotonically increasing.

3.2-2
Prove equation (3.16).

3.2-3
Prove equation (3.19). Also prove that $n! = \omega(2^n)$ and $n! = o(n^n)$.

3.2-4 ⋆
Is the function $\lceil \lg n \rceil !$ polynomially bounded? Is the function $\lceil \lg \lg n \rceil !$ polynomially bounded?

3.2-5 ⋆
Which is asymptotically larger: $\lg(\lg^* n)$ or $\lg^*(\lg n)$?

3.2-6
Show that the golden ratio ϕ and its conjugate $\widehat{\phi}$ both satisfy the equation $x^2 = x + 1$.

3.2-7
Prove by induction that the ith Fibonacci number satisfies the equality

$$F_i = \frac{\phi^i - \widehat{\phi}^i}{\sqrt{5}} ,$$

where ϕ is the golden ratio and $\widehat{\phi}$ is its conjugate.

3.2-8
Show that $k \ln k = \Theta(n)$ implies $k = \Theta(n / \ln n)$.

Problems

3-1 Asymptotic behavior of polynomials

Let

$$p(n) = \sum_{i=0}^{d} a_i n^i \ ,$$

where $a_d > 0$, be a degree-d polynomial in n, and let k be a constant. Use the definitions of the asymptotic notations to prove the following properties.

a. If $k \geq d$, then $p(n) = O(n^k)$.

b. If $k \leq d$, then $p(n) = \Omega(n^k)$.

c. If $k = d$, then $p(n) = \Theta(n^k)$.

d. If $k > d$, then $p(n) = o(n^k)$.

e. If $k < d$, then $p(n) = \omega(n^k)$.

3-2 Relative asymptotic growths

Indicate, for each pair of expressions (A, B) in the table below, whether A is O, o, Ω, ω, or Θ of B. Assume that $k \geq 1$, $\epsilon > 0$, and $c > 1$ are constants. Your answer should be in the form of the table with "yes" or "no" written in each box.

	A	B	O	o	Ω	ω	Θ
a.	$\lg^k n$	n^ϵ					
b.	n^k	c^n					
c.	$\sqrt{n}$	$n^{\sin n}$					
d.	2^n	$2^{n/2}$					
e.	$n^{\lg c}$	$c^{\lg n}$					
f.	$\lg(n!)$	$\lg(n^n)$					

3-3 Ordering by asymptotic growth rates

a. Rank the following functions by order of growth; that is, find an arrangement $g_1, g_2, \ldots, g_{30}$ of the functions satisfying $g_1 = \Omega(g_2)$, $g_2 = \Omega(g_3)$, $\ldots$, $g_{29} = \Omega(g_{30})$. Partition your list into equivalence classes such that functions $f(n)$ and $g(n)$ are in the same class if and only if $f(n) = \Theta(g(n))$.

$\lg(\lg^* n)$	$2^{\lg^* n}$	$(\sqrt{2})^{\lg n}$	n^2	$n!$	$(\lg n)!$
$(\frac{3}{2})^n$	n^3	$\lg^2 n$	$\lg(n!)$	2^{2^n}	$n^{1/\lg n}$
$\ln\ln n$	$\lg^* n$	$n \cdot 2^n$	$n^{\lg\lg n}$	$\ln n$	1
$2^{\lg n}$	$(\lg n)^{\lg n}$	e^n	$4^{\lg n}$	$(n+1)!$	$\sqrt{\lg n}$
$\lg^*(\lg n)$	$2^{\sqrt{2\lg n}}$	n	2^n	$n \lg n$	$2^{2^{n+1}}$

b. Give an example of a single nonnegative function $f(n)$ such that for all functions $g_i(n)$ in part (a), $f(n)$ is neither $O(g_i(n))$ nor $\Omega(g_i(n))$.

3-4 Asymptotic notation properties

Let $f(n)$ and $g(n)$ be asymptotically positive functions. Prove or disprove each of the following conjectures.

a. $f(n) = O(g(n))$ implies $g(n) = O(f(n))$.

b. $f(n) + g(n) = \Theta(\min(f(n), g(n)))$.

c. $f(n) = O(g(n))$ implies $\lg(f(n)) = O(\lg(g(n)))$, where $\lg(g(n)) \geq 1$ and $f(n) \geq 1$ for all sufficiently large n.

d. $f(n) = O(g(n))$ implies $2^{f(n)} = O\left(2^{g(n)}\right)$.

e. $f(n) = O\left((f(n))^2\right)$.

f. $f(n) = O(g(n))$ implies $g(n) = \Omega(f(n))$.

g. $f(n) = \Theta(f(n/2))$.

h. $f(n) + o(f(n)) = \Theta(f(n))$.

3-5 Variations on O and Ω

Some authors define Ω in a slightly different way than we do; let's use $\overset{\infty}{\Omega}$ (read "omega infinity") for this alternative definition. We say that $f(n) = \overset{\infty}{\Omega}(g(n))$ if there exists a positive constant c such that $f(n) \geq cg(n) \geq 0$ for infinitely many integers n.

a. Show that for any two functions $f(n)$ and $g(n)$ that are asymptotically nonnegative, either $f(n) = O(g(n))$ or $f(n) = \overset{\infty}{\Omega}(g(n))$ or both, whereas this is not true if we use Ω in place of $\overset{\infty}{\Omega}$.

b. Describe the potential advantages and disadvantages of using $\overset{\infty}{\Omega}$ instead of Ω to characterize the running times of programs.

Some authors also define O in a slightly different manner; let's use O' for the alternative definition. We say that $f(n) = O'(g(n))$ if and only if $|f(n)| = O(g(n))$.

c. What happens to each direction of the "if and only if" in Theorem 3.1 if we substitute O' for O but still use Ω?

Some authors define $\widetilde{O}$ (read "soft-oh") to mean O with logarithmic factors ignored:

$$\widetilde{O}(g(n)) = \{f(n) : \text{ there exist positive constants } c, k, \text{ and } n_0 \text{ such that } 0 \le f(n) \le cg(n)\lg^k(n) \text{ for all } n \ge n_0\} .$$

d. Define $\widetilde{\Omega}$ and $\widetilde{\Theta}$ in a similar manner. Prove the corresponding analog to Theorem 3.1.

3-6 Iterated functions

We can apply the iteration operator * used in the $\lg^*$ function to any monotonically increasing function $f(n)$ over the reals. For a given constant $c \in \mathbb{R}$, we define the iterated function f_c^* by

$$f_c^*(n) = \min\left\{i \ge 0 : f^{(i)}(n) \le c\right\} ,$$

which need not be well defined in all cases. In other words, the quantity $f_c^*(n)$ is the number of iterated applications of the function f required to reduce its argument down to c or less.

For each of the following functions $f(n)$ and constants c, give as tight a bound as possible on $f_c^*(n)$.

	$f(n)$	c	$f_c^*(n)$
a.	$n-1$	0	
b.	$\lg n$	1	
c.	$n/2$	1	
d.	$n/2$	2	
e.	$\sqrt{n}$	2	
f.	$\sqrt{n}$	1	
g.	$n^{1/3}$	2	
h.	$n/\lg n$	2	

Chapter notes

Knuth [209] traces the origin of the O-notation to a number-theory text by P. Bachmann in 1892. The o-notation was invented by E. Landau in 1909 for his discussion of the distribution of prime numbers. The Ω and Θ notations were advocated by Knuth [213] to correct the popular, but technically sloppy, practice in the literature of using O-notation for both upper and lower bounds. Many people continue to use the O-notation where the Θ-notation is more technically precise. Further discussion of the history and development of asymptotic notations appears in works by Knuth [209, 213] and Brassard and Bratley [54].

Not all authors define the asymptotic notations in the same way, although the various definitions agree in most common situations. Some of the alternative definitions encompass functions that are not asymptotically nonnegative, as long as their absolute values are appropriately bounded.

Equation (3.20) is due to Robbins [297]. Other properties of elementary mathematical functions can be found in any good mathematical reference, such as Abramowitz and Stegun [1] or Zwillinger [362], or in a calculus book, such as Apostol [18] or Thomas et al. [334]. Knuth [209] and Graham, Knuth, and Patashnik [152] contain a wealth of material on discrete mathematics as used in computer science.

4 Divide-and-Conquer

In Section 2.3.1, we saw how merge sort serves as an example of the divide-and-conquer paradigm. Recall that in divide-and-conquer, we solve a problem recursively, applying three steps at each level of the recursion:

Divide the problem into a number of subproblems that are smaller instances of the same problem.

Conquer the subproblems by solving them recursively. If the subproblem sizes are small enough, however, just solve the subproblems in a straightforward manner.

Combine the solutions to the subproblems into the solution for the original problem.

When the subproblems are large enough to solve recursively, we call that the ***recursive case***. Once the subproblems become small enough that we no longer recurse, we say that the recursion "bottoms out" and that we have gotten down to the ***base case***. Sometimes, in addition to subproblems that are smaller instances of the same problem, we have to solve subproblems that are not quite the same as the original problem. We consider solving such subproblems as part of the combine step.

In this chapter, we shall see more algorithms based on divide-and-conquer. The first one solves the maximum-subarray problem: it takes as input an array of numbers, and it determines the contiguous subarray whose values have the greatest sum. Then we shall see two divide-and-conquer algorithms for multiplying $n \times n$ matrices. One runs in $\Theta(n^3)$ time, which is no better than the straightforward method of multiplying square matrices. But the other, Strassen's algorithm, runs in $O(n^{2.81})$ time, which beats the straightforward method asymptotically.

Recurrences

Recurrences go hand in hand with the divide-and-conquer paradigm, because they give us a natural way to characterize the running times of divide-and-conquer algorithms. A ***recurrence*** is an equation or inequality that describes a function in terms

of its value on smaller inputs. For example, in Section 2.3.2 we described the worst-case running time $T(n)$ of the MERGE-SORT procedure by the recurrence

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 , \\ 2T(n/2) + \Theta(n) & \text{if } n > 1 , \end{cases} \tag{4.1}$$

whose solution we claimed to be $T(n) = \Theta(n \lg n)$.

Recurrences can take many forms. For example, a recursive algorithm might divide subproblems into unequal sizes, such as a $2/3$-to-$1/3$ split. If the divide and combine steps take linear time, such an algorithm would give rise to the recurrence $T(n) = T(2n/3) + T(n/3) + \Theta(n)$.

Subproblems are not necessarily constrained to being a constant fraction of the original problem size. For example, a recursive version of linear search (see Exercise 2.1-3) would create just one subproblem containing only one element fewer than the original problem. Each recursive call would take constant time plus the time for the recursive calls it makes, yielding the recurrence $T(n) = T(n-1) + \Theta(1)$.

This chapter offers three methods for solving recurrences—that is, for obtaining asymptotic "Θ" or "O" bounds on the solution:

- In the ***substitution method***, we guess a bound and then use mathematical induction to prove our guess correct.
- The ***recursion-tree method*** converts the recurrence into a tree whose nodes represent the costs incurred at various levels of the recursion. We use techniques for bounding summations to solve the recurrence.
- The ***master method*** provides bounds for recurrences of the form

  $$T(n) = aT(n/b) + f(n) , \tag{4.2}$$

  where $a \geq 1$, $b > 1$, and $f(n)$ is a given function. Such recurrences arise frequently. A recurrence of the form in equation (4.2) characterizes a divide-and-conquer algorithm that creates a subproblems, each of which is $1/b$ the size of the original problem, and in which the divide and combine steps together take $f(n)$ time.

  To use the master method, you will need to memorize three cases, but once you do that, you will easily be able to determine asymptotic bounds for many simple recurrences. We will use the master method to determine the running times of the divide-and-conquer algorithms for the maximum-subarray problem and for matrix multiplication, as well as for other algorithms based on divide-and-conquer elsewhere in this book.

Occasionally, we shall see recurrences that are not equalities but rather inequalities, such as $T(n) \le 2T(n/2) + \Theta(n)$. Because such a recurrence states only an upper bound on $T(n)$, we will couch its solution using O-notation rather than Θ-notation. Similarly, if the inequality were reversed to $T(n) \ge 2T(n/2) + \Theta(n)$, then because the recurrence gives only a lower bound on $T(n)$, we would use Ω-notation in its solution.

Technicalities in recurrences

In practice, we neglect certain technical details when we state and solve recurrences. For example, if we call MERGE-SORT on n elements when n is odd, we end up with subproblems of size $\lfloor n/2 \rfloor$ and $\lceil n/2 \rceil$. Neither size is actually $n/2$, because $n/2$ is not an integer when n is odd. Technically, the recurrence describing the worst-case running time of MERGE-SORT is really

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 , \\ T(\lceil n/2 \rceil) + T(\lfloor n/2 \rfloor) + \Theta(n) & \text{if } n > 1 . \end{cases} \tag{4.3}$$

Boundary conditions represent another class of details that we typically ignore. Since the running time of an algorithm on a constant-sized input is a constant, the recurrences that arise from the running times of algorithms generally have $T(n) = \Theta(1)$ for sufficiently small n. Consequently, for convenience, we shall generally omit statements of the boundary conditions of recurrences and assume that $T(n)$ is constant for small n. For example, we normally state recurrence (4.1) as

$$T(n) = 2T(n/2) + \Theta(n) , \tag{4.4}$$

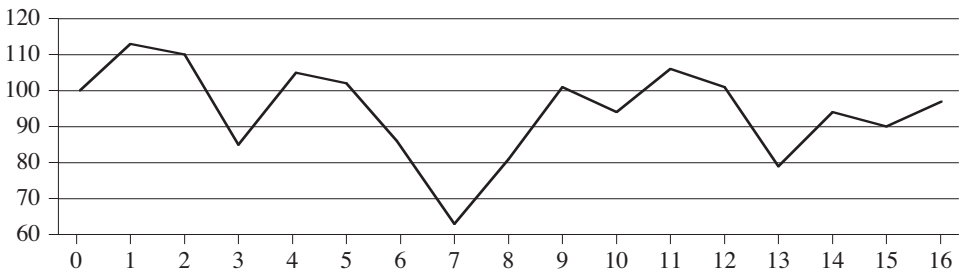
without explicitly giving values for small n. The reason is that although changing the value of $T(1)$ changes the exact solution to the recurrence, the solution typically doesn't change by more than a constant factor, and so the order of growth is unchanged.

When we state and solve recurrences, we often omit floors, ceilings, and boundary conditions. We forge ahead without these details and later determine whether or not they matter. They usually do not, but you should know when they do. Experience helps, and so do some theorems stating that these details do not affect the asymptotic bounds of many recurrences characterizing divide-and-conquer algorithms (see Theorem 4.1). In this chapter, however, we shall address some of these details and illustrate the fine points of recurrence solution methods.

4.1 The maximum-subarray problem

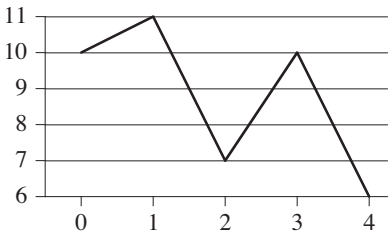
Suppose that you been offered the opportunity to invest in the Volatile Chemical Corporation. Like the chemicals the company produces, the stock price of the Volatile Chemical Corporation is rather volatile. You are allowed to buy one unit of stock only one time and then sell it at a later date, buying and selling after the close of trading for the day. To compensate for this restriction, you are allowed to learn what the price of the stock will be in the future. Your goal is to maximize your profit. Figure 4.1 shows the price of the stock over a 17-day period. You may buy the stock at any one time, starting after day 0, when the price is \$100 per share. Of course, you would want to "buy low, sell high"—buy at the lowest possible price and later on sell at the highest possible price—to maximize your profit. Unfortunately, you might not be able to buy at the lowest price and then sell at the highest price within a given period. In Figure 4.1, the lowest price occurs after day 7, which occurs after the highest price, after day 1.

You might think that you can always maximize profit by either buying at the lowest price or selling at the highest price. For example, in Figure 4.1, we would maximize profit by buying at the lowest price, after day 7. If this strategy always worked, then it would be easy to determine how to maximize profit: find the highest and lowest prices, and then work left from the highest price to find the lowest prior price, work right from the lowest price to find the highest later price, and take the pair with the greater difference. Figure 4.2 shows a simple counterexample,



Day	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Price	100	113	110	85	105	102	86	63	81	101	94	106	101	79	94	90	97
Change		13	−3	−25	20	−3	−16	−23	18	20	−7	12	−5	−22	15	−4	7

Figure 4.1 Information about the price of stock in the Volatile Chemical Corporation after the close of trading over a period of 17 days. The horizontal axis of the chart indicates the day, and the vertical axis shows the price. The bottom row of the table gives the change in price from the previous day.



Day	0	1	2	3	4
Price	10	11	7	10	6
Change		1	−4	3	−4

Figure 4.2 An example showing that the maximum profit does not always start at the lowest price or end at the highest price. Again, the horizontal axis indicates the day, and the vertical axis shows the price. Here, the maximum profit of \$3 per share would be earned by buying after day 2 and selling after day 3. The price of \$7 after day 2 is not the lowest price overall, and the price of \$10 after day 3 is not the highest price overall.

demonstrating that the maximum profit sometimes comes neither by buying at the lowest price nor by selling at the highest price.

A brute-force solution

We can easily devise a brute-force solution to this problem: just try every possible pair of buy and sell dates in which the buy date precedes the sell date. A period of n days has $\binom{n}{2}$ such pairs of dates. Since $\binom{n}{2}$ is $\Theta(n^2)$, and the best we can hope for is to evaluate each pair of dates in constant time, this approach would take $\Omega(n^2)$ time. Can we do better?

A transformation

In order to design an algorithm with an $o(n^2)$ running time, we will look at the input in a slightly different way. We want to find a sequence of days over which the net change from the first day to the last is maximum. Instead of looking at the daily prices, let us instead consider the daily change in price, where the change on day i is the difference between the prices after day $i-1$ and after day i. The table in Figure 4.1 shows these daily changes in the bottom row. If we treat this row as an array A, shown in Figure 4.3, we now want to find the nonempty, contiguous subarray of A whose values have the largest sum. We call this contiguous subarray the ***maximum subarray***. For example, in the array of Figure 4.3, the maximum subarray of $A[1\,..\,16]$ is $A[8\,..\,11]$, with the sum 43. Thus, you would want to buy the stock just before day 8 (that is, after day 7) and sell it after day 11, earning a profit of \$43 per share.

At first glance, this transformation does not help. We still need to check $\binom{n-1}{2} = \Theta(n^2)$ subarrays for a period of n days. Exercise 4.1-2 asks you to show

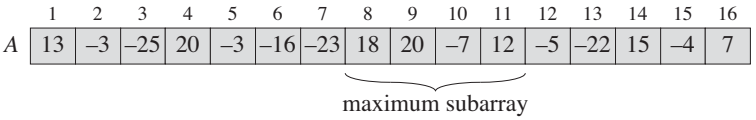


Figure 4.3 The change in stock prices as a maximum-subarray problem. Here, the subarray $A[8\,..\,11]$, with sum 43, has the greatest sum of any contiguous subarray of array A.

that although computing the cost of one subarray might take time proportional to the length of the subarray, when computing all $\Theta(n^2)$ subarray sums, we can organize the computation so that each subarray sum takes $O(1)$ time, given the values of previously computed subarray sums, so that the brute-force solution takes $\Theta(n^2)$ time.

So let us seek a more efficient solution to the maximum-subarray problem. When doing so, we will usually speak of "a" maximum subarray rather than "the" maximum subarray, since there could be more than one subarray that achieves the maximum sum.

The maximum-subarray problem is interesting only when the array contains some negative numbers. If all the array entries were nonnegative, then the maximum-subarray problem would present no challenge, since the entire array would give the greatest sum.

A solution using divide-and-conquer

Let's think about how we might solve the maximum-subarray problem using the divide-and-conquer technique. Suppose we want to find a maximum subarray of the subarray $A[low\,..\,high]$. Divide-and-conquer suggests that we divide the subarray into two subarrays of as equal size as possible. That is, we find the midpoint, say mid, of the subarray, and consider the subarrays $A[low\,..\,mid]$ and $A[mid + 1\,..\,high]$. As Figure 4.4(a) shows, any contiguous subarray $A[i\,..\,j]$ of $A[low\,..\,high]$ must lie in exactly one of the following places:

- entirely in the subarray $A[low\,..\,mid]$, so that $low \le i \le j \le mid$,
- entirely in the subarray $A[mid + 1\,..\,high]$, so that $mid < i \le j \le high$, or
- crossing the midpoint, so that $low \le i \le mid < j \le high$.

Therefore, a maximum subarray of $A[low\,..\,high]$ must lie in exactly one of these places. In fact, a maximum subarray of $A[low\,..\,high]$ must have the greatest sum over all subarrays entirely in $A[low\,..\,mid]$, entirely in $A[mid + 1\,..\,high]$, or crossing the midpoint. We can find maximum subarrays of $A[low\,..\,mid]$ and $A[mid+1\,..\,high]$ recursively, because these two subproblems are smaller instances of the problem of finding a maximum subarray. Thus, all that is left to do is find a

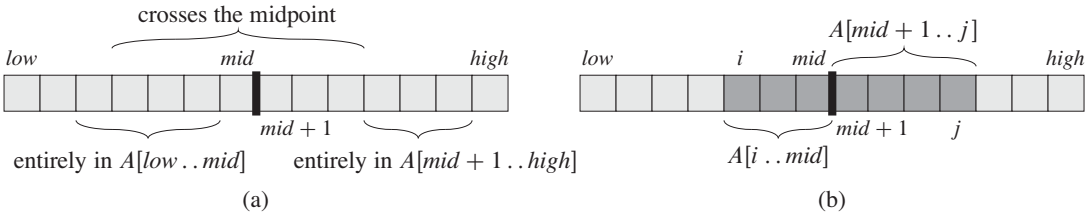


Figure 4.4 **(a)** Possible locations of subarrays of $A[low\,..\,high]$: entirely in $A[low\,..\,mid]$, entirely in $A[mid+1\,..\,high]$, or crossing the midpoint mid. **(b)** Any subarray of $A[low\,..\,high]$ crossing the midpoint comprises two subarrays $A[i\,..\,mid]$ and $A[mid+1\,..\,j]$, where $low \le i \le mid$ and $mid < j \le high$.

maximum subarray that crosses the midpoint, and take a subarray with the largest sum of the three.

We can easily find a maximum subarray crossing the midpoint in time linear in the size of the subarray $A[low\,..\,high]$. This problem is *not* a smaller instance of our original problem, because it has the added restriction that the subarray it chooses must cross the midpoint. As Figure 4.4(b) shows, any subarray crossing the midpoint is itself made of two subarrays $A[i\,..\,mid]$ and $A[mid+1\,..\,j]$, where $low \le i \le mid$ and $mid < j \le high$. Therefore, we just need to find maximum subarrays of the form $A[i\,..\,mid]$ and $A[mid+1\,..\,j]$ and then combine them. The procedure FIND-MAX-CROSSING-SUBARRAY takes as input the array A and the indices low, mid, and $high$, and it returns a tuple containing the indices demarcating a maximum subarray that crosses the midpoint, along with the sum of the values in a maximum subarray.

```
FIND-MAX-CROSSING-SUBARRAY(A, low, mid, high)
 1  left-sum = −∞
 2  sum = 0
 3  for i = mid downto low
 4       sum = sum + A[i]
 5       if sum > left-sum
 6            left-sum = sum
 7            max-left = i
 8  right-sum = −∞
 9  sum = 0
10  for j = mid + 1 to high
11       sum = sum + A[j]
12       if sum > right-sum
13            right-sum = sum
14            max-right = j
15  return (max-left, max-right, left-sum + right-sum)
```

This procedure works as follows. Lines 1–7 find a maximum subarray of the left half, $A[low\,..\,mid]$. Since this subarray must contain $A[mid]$, the **for** loop of lines 3–7 starts the index i at mid and works down to low, so that every subarray it considers is of the form $A[i\,..\,mid]$. Lines 1–2 initialize the variables *left-sum*, which holds the greatest sum found so far, and *sum*, holding the sum of the entries in $A[i\,..\,mid]$. Whenever we find, in line 5, a subarray $A[i\,..\,mid]$ with a sum of values greater than *left-sum*, we update *left-sum* to this subarray's sum in line 6, and in line 7 we update the variable *max-left* to record this index i. Lines 8–14 work analogously for the right half, $A[mid+1\,..\,high]$. Here, the **for** loop of lines 10–14 starts the index j at $mid+1$ and works up to $high$, so that every subarray it considers is of the form $A[mid+1\,..\,j]$. Finally, line 15 returns the indices *max-left* and *max-right* that demarcate a maximum subarray crossing the midpoint, along with the sum *left-sum* + *right-sum* of the values in the subarray $A[max\text{-}left\,..\,max\text{-}right]$.

If the subarray $A[low\,..\,high]$ contains n entries (so that $n = high - low + 1$), we claim that the call FIND-MAX-CROSSING-SUBARRAY$(A, low, mid, high)$ takes $\Theta(n)$ time. Since each iteration of each of the two **for** loops takes $\Theta(1)$ time, we just need to count up how many iterations there are altogether. The **for** loop of lines 3–7 makes $mid - low + 1$ iterations, and the **for** loop of lines 10–14 makes $high - mid$ iterations, and so the total number of iterations is

$$\begin{aligned}(mid - low + 1) + (high - mid) &= high - low + 1 \\ &= n\,.\end{aligned}$$

With a linear-time FIND-MAX-CROSSING-SUBARRAY procedure in hand, we can write pseudocode for a divide-and-conquer algorithm to solve the maximum-subarray problem:

```
FIND-MAXIMUM-SUBARRAY(A, low, high)
 1  if high == low
 2      return (low, high, A[low])          // base case: only one element
 3  else mid = ⌊(low + high)/2⌋
 4      (left-low, left-high, left-sum) =
            FIND-MAXIMUM-SUBARRAY(A, low, mid)
 5      (right-low, right-high, right-sum) =
            FIND-MAXIMUM-SUBARRAY(A, mid + 1, high)
 6      (cross-low, cross-high, cross-sum) =
            FIND-MAX-CROSSING-SUBARRAY(A, low, mid, high)
 7      if left-sum ≥ right-sum and left-sum ≥ cross-sum
 8          return (left-low, left-high, left-sum)
 9      elseif right-sum ≥ left-sum and right-sum ≥ cross-sum
10          return (right-low, right-high, right-sum)
11      else return (cross-low, cross-high, cross-sum)
```

The initial call FIND-MAXIMUM-SUBARRAY$(A, 1, A.length)$ will find a maximum subarray of $A[1..n]$.

Similar to FIND-MAX-CROSSING-SUBARRAY, the recursive procedure FIND-MAXIMUM-SUBARRAY returns a tuple containing the indices that demarcate a maximum subarray, along with the sum of the values in a maximum subarray. Line 1 tests for the base case, where the subarray has just one element. A subarray with just one element has only one subarray—itself—and so line 2 returns a tuple with the starting and ending indices of just the one element, along with its value. Lines 3–11 handle the recursive case. Line 3 does the divide part, computing the index *mid* of the midpoint. Let's refer to the subarray $A[low..mid]$ as the ***left subarray*** and to $A[mid + 1..high]$ as the ***right subarray***. Because we know that the subarray $A[low..high]$ contains at least two elements, each of the left and right subarrays must have at least one element. Lines 4 and 5 conquer by recursively finding maximum subarrays within the left and right subarrays, respectively. Lines 6–11 form the combine part. Line 6 finds a maximum subarray that crosses the midpoint. (Recall that because line 6 solves a subproblem that is not a smaller instance of the original problem, we consider it to be in the combine part.) Line 7 tests whether the left subarray contains a subarray with the maximum sum, and line 8 returns that maximum subarray. Otherwise, line 9 tests whether the right subarray contains a subarray with the maximum sum, and line 10 returns that maximum subarray. If neither the left nor right subarrays contain a subarray achieving the maximum sum, then a maximum subarray must cross the midpoint, and line 11 returns it.

Analyzing the divide-and-conquer algorithm

Next we set up a recurrence that describes the running time of the recursive FIND-MAXIMUM-SUBARRAY procedure. As we did when we analyzed merge sort in Section 2.3.2, we make the simplifying assumption that the original problem size is a power of 2, so that all subproblem sizes are integers. We denote by $T(n)$ the running time of FIND-MAXIMUM-SUBARRAY on a subarray of n elements. For starters, line 1 takes constant time. The base case, when $n = 1$, is easy: line 2 takes constant time, and so

$$T(1) = \Theta(1) . \tag{4.5}$$

The recursive case occurs when $n > 1$. Lines 1 and 3 take constant time. Each of the subproblems solved in lines 4 and 5 is on a subarray of $n/2$ elements (our assumption that the original problem size is a power of 2 ensures that $n/2$ is an integer), and so we spend $T(n/2)$ time solving each of them. Because we have to solve two subproblems—for the left subarray and for the right subarray—the contribution to the running time from lines 4 and 5 comes to $2T(n/2)$. As we have

already seen, the call to FIND-MAX-CROSSING-SUBARRAY in line 6 takes $\Theta(n)$ time. Lines 7–11 take only $\Theta(1)$ time. For the recursive case, therefore, we have

$$\begin{aligned} T(n) &= \Theta(1) + 2T(n/2) + \Theta(n) + \Theta(1) \\ &= 2T(n/2) + \Theta(n) \,. \end{aligned} \tag{4.6}$$

Combining equations (4.5) and (4.6) gives us a recurrence for the running time $T(n)$ of FIND-MAXIMUM-SUBARRAY:

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 \,, \\ 2T(n/2) + \Theta(n) & \text{if } n > 1 \,. \end{cases} \tag{4.7}$$

This recurrence is the same as recurrence (4.1) for merge sort. As we shall see from the master method in Section 4.5, this recurrence has the solution $T(n) = \Theta(n \lg n)$. You might also revisit the recursion tree in Figure 2.5 to understand why the solution should be $T(n) = \Theta(n \lg n)$.

Thus, we see that the divide-and-conquer method yields an algorithm that is asymptotically faster than the brute-force method. With merge sort and now the maximum-subarray problem, we begin to get an idea of how powerful the divide-and-conquer method can be. Sometimes it will yield the asymptotically fastest algorithm for a problem, and other times we can do even better. As Exercise 4.1-5 shows, there is in fact a linear-time algorithm for the maximum-subarray problem, and it does not use divide-and-conquer.

Exercises

4.1-1

What does FIND-MAXIMUM-SUBARRAY return when all elements of A are negative?

4.1-2

Write pseudocode for the brute-force method of solving the maximum-subarray problem. Your procedure should run in $\Theta(n^2)$ time.

4.1-3

Implement both the brute-force and recursive algorithms for the maximum-subarray problem on your own computer. What problem size n_0 gives the crossover point at which the recursive algorithm beats the brute-force algorithm? Then, change the base case of the recursive algorithm to use the brute-force algorithm whenever the problem size is less than n_0. Does that change the crossover point?

4.1-4

Suppose we change the definition of the maximum-subarray problem to allow the result to be an empty subarray, where the sum of the values of an empty subar-

ray is 0. How would you change any of the algorithms that do not allow empty subarrays to permit an empty subarray to be the result?

4.1-5
Use the following ideas to develop a nonrecursive, linear-time algorithm for the maximum-subarray problem. Start at the left end of the array, and progress toward the right, keeping track of the maximum subarray seen so far. Knowing a maximum subarray of $A[1\,..\,j]$, extend the answer to find a maximum subarray ending at index $j+1$ by using the following observation: a maximum subarray of $A[1\,..\,j+1]$ is either a maximum subarray of $A[1\,..\,j]$ or a subarray $A[i\,..\,j+1]$, for some $1 \le i \le j+1$. Determine a maximum subarray of the form $A[i\,..\,j+1]$ in constant time based on knowing a maximum subarray ending at index j.

4.2 Strassen's algorithm for matrix multiplication

If you have seen matrices before, then you probably know how to multiply them. (Otherwise, you should read Section D.1 in Appendix D.) If $A = (a_{ij})$ and $B = (b_{ij})$ are square $n \times n$ matrices, then in the product $C = A \cdot B$, we define the entry c_{ij}, for $i, j = 1, 2, \ldots, n$, by

$$c_{ij} = \sum_{k=1}^{n} a_{ik} \cdot b_{kj} \; . \tag{4.8}$$

We must compute n^2 matrix entries, and each is the sum of n values. The following procedure takes $n \times n$ matrices A and B and multiplies them, returning their $n \times n$ product C. We assume that each matrix has an attribute *rows*, giving the number of rows in the matrix.

```
SQUARE-MATRIX-MULTIPLY(A, B)
1  n = A.rows
2  let C be a new n × n matrix
3  for i = 1 to n
4      for j = 1 to n
5          c_ij = 0
6          for k = 1 to n
7              c_ij = c_ij + a_ik · b_kj
8  return C
```

The SQUARE-MATRIX-MULTIPLY procedure works as follows. The **for** loop of lines 3–7 computes the entries of each row i, and within a given row i, the

for loop of lines 4–7 computes each of the entries c_{ij}, for each column j. Line 5 initializes c_{ij} to 0 as we start computing the sum given in equation (4.8), and each iteration of the **for** loop of lines 6–7 adds in one more term of equation (4.8).

Because each of the triply-nested **for** loops runs exactly n iterations, and each execution of line 7 takes constant time, the SQUARE-MATRIX-MULTIPLY procedure takes $\Theta(n^3)$ time.

You might at first think that any matrix multiplication algorithm must take $\Omega(n^3)$ time, since the natural definition of matrix multiplication requires that many multiplications. You would be incorrect, however: we have a way to multiply matrices in $o(n^3)$ time. In this section, we shall see Strassen's remarkable recursive algorithm for multiplying $n \times n$ matrices. It runs in $\Theta(n^{\lg 7})$ time, which we shall show in Section 4.5. Since $\lg 7$ lies between 2.80 and 2.81, Strassen's algorithm runs in $O(n^{2.81})$ time, which is asymptotically better than the simple SQUARE-MATRIX-MULTIPLY procedure.

A simple divide-and-conquer algorithm

To keep things simple, when we use a divide-and-conquer algorithm to compute the matrix product $C = A \cdot B$, we assume that n is an exact power of 2 in each of the $n \times n$ matrices. We make this assumption because in each divide step, we will divide $n \times n$ matrices into four $n/2 \times n/2$ matrices, and by assuming that n is an exact power of 2, we are guaranteed that as long as $n \geq 2$, the dimension $n/2$ is an integer.

Suppose that we partition each of A, B, and C into four $n/2 \times n/2$ matrices

$$A = \begin{pmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{pmatrix}, \quad B = \begin{pmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{pmatrix}, \quad C = \begin{pmatrix} C_{11} & C_{12} \\ C_{21} & C_{22} \end{pmatrix}, \tag{4.9}$$

so that we rewrite the equation $C = A \cdot B$ as

$$\begin{pmatrix} C_{11} & C_{12} \\ C_{21} & C_{22} \end{pmatrix} = \begin{pmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{pmatrix} \cdot \begin{pmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{pmatrix}. \tag{4.10}$$

Equation (4.10) corresponds to the four equations

$$C_{11} = A_{11} \cdot B_{11} + A_{12} \cdot B_{21}\,, \tag{4.11}$$
$$C_{12} = A_{11} \cdot B_{12} + A_{12} \cdot B_{22}\,, \tag{4.12}$$
$$C_{21} = A_{21} \cdot B_{11} + A_{22} \cdot B_{21}\,, \tag{4.13}$$
$$C_{22} = A_{21} \cdot B_{12} + A_{22} \cdot B_{22}\,. \tag{4.14}$$

Each of these four equations specifies two multiplications of $n/2 \times n/2$ matrices and the addition of their $n/2 \times n/2$ products. We can use these equations to create a straightforward, recursive, divide-and-conquer algorithm:

```
SQUARE-MATRIX-MULTIPLY-RECURSIVE(A, B)
 1  n = A.rows
 2  let C be a new n × n matrix
 3  if n == 1
 4      c_11 = a_11 · b_11
 5  else partition A, B, and C as in equations (4.9)
 6      C_11 = SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_11, B_11)
              + SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_12, B_21)
 7      C_12 = SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_11, B_12)
              + SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_12, B_22)
 8      C_21 = SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_21, B_11)
              + SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_22, B_21)
 9      C_22 = SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_21, B_12)
              + SQUARE-MATRIX-MULTIPLY-RECURSIVE(A_22, B_22)
10  return C
```

This pseudocode glosses over one subtle but important implementation detail. How do we partition the matrices in line 5? If we were to create 12 new $n/2 \times n/2$ matrices, we would spend $\Theta(n^2)$ time copying entries. In fact, we can partition the matrices without copying entries. The trick is to use index calculations. We identify a submatrix by a range of row indices and a range of column indices of the original matrix. We end up representing a submatrix a little differently from how we represent the original matrix, which is the subtlety we are glossing over. The advantage is that, since we can specify submatrices by index calculations, executing line 5 takes only $\Theta(1)$ time (although we shall see that it makes no difference asymptotically to the overall running time whether we copy or partition in place).

Now, we derive a recurrence to characterize the running time of SQUARE-MATRIX-MULTIPLY-RECURSIVE. Let $T(n)$ be the time to multiply two $n \times n$ matrices using this procedure. In the base case, when $n = 1$, we perform just the one scalar multiplication in line 4, and so

$$T(1) = \Theta(1) . \tag{4.15}$$

The recursive case occurs when $n > 1$. As discussed, partitioning the matrices in line 5 takes $\Theta(1)$ time, using index calculations. In lines 6–9, we recursively call SQUARE-MATRIX-MULTIPLY-RECURSIVE a total of eight times. Because each recursive call multiplies two $n/2 \times n/2$ matrices, thereby contributing $T(n/2)$ to the overall running time, the time taken by all eight recursive calls is $8T(n/2)$. We also must account for the four matrix additions in lines 6–9. Each of these matrices contains $n^2/4$ entries, and so each of the four matrix additions takes $\Theta(n^2)$ time. Since the number of matrix additions is a constant, the total time spent adding ma-

trices in lines 6–9 is $\Theta(n^2)$. (Again, we use index calculations to place the results of the matrix additions into the correct positions of matrix C, with an overhead of $\Theta(1)$ time per entry.) The total time for the recursive case, therefore, is the sum of the partitioning time, the time for all the recursive calls, and the time to add the matrices resulting from the recursive calls:

$$\begin{aligned} T(n) &= \Theta(1) + 8T(n/2) + \Theta(n^2) \\ &= 8T(n/2) + \Theta(n^2) \ . \end{aligned} \tag{4.16}$$

Notice that if we implemented partitioning by copying matrices, which would cost $\Theta(n^2)$ time, the recurrence would not change, and hence the overall running time would increase by only a constant factor.

Combining equations (4.15) and (4.16) gives us the recurrence for the running time of SQUARE-MATRIX-MULTIPLY-RECURSIVE:

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 \ , \\ 8T(n/2) + \Theta(n^2) & \text{if } n > 1 \ . \end{cases} \tag{4.17}$$

As we shall see from the master method in Section 4.5, recurrence (4.17) has the solution $T(n) = \Theta(n^3)$. Thus, this simple divide-and-conquer approach is no faster than the straightforward SQUARE-MATRIX-MULTIPLY procedure.

Before we continue on to examining Strassen's algorithm, let us review where the components of equation (4.16) came from. Partitioning each $n \times n$ matrix by index calculation takes $\Theta(1)$ time, but we have two matrices to partition. Although you could say that partitioning the two matrices takes $\Theta(2)$ time, the constant of 2 is subsumed by the Θ-notation. Adding two matrices, each with, say, k entries, takes $\Theta(k)$ time. Since the matrices we add each have $n^2/4$ entries, you could say that adding each pair takes $\Theta(n^2/4)$ time. Again, however, the Θ-notation subsumes the constant factor of $1/4$, and we say that adding two $n^2/4 \times n^2/4$ matrices takes $\Theta(n^2)$ time. We have four such matrix additions, and once again, instead of saying that they take $\Theta(4n^2)$ time, we say that they take $\Theta(n^2)$ time. (Of course, you might observe that we could say that the four matrix additions take $\Theta(4n^2/4)$ time, and that $4n^2/4 = n^2$, but the point here is that Θ-notation subsumes constant factors, whatever they are.) Thus, we end up with two terms of $\Theta(n^2)$, which we can combine into one.

When we account for the eight recursive calls, however, we cannot just subsume the constant factor of 8. In other words, we must say that together they take $8T(n/2)$ time, rather than just $T(n/2)$ time. You can get a feel for why by looking back at the recursion tree in Figure 2.5, for recurrence (2.1) (which is identical to recurrence (4.7)), with the recursive case $T(n) = 2T(n/2) + \Theta(n)$. The factor of 2 determined how many children each tree node had, which in turn determined how many terms contributed to the sum at each level of the tree. If we were to ignore

the factor of 8 in equation (4.16) or the factor of 2 in recurrence (4.1), the recursion tree would just be linear, rather than "bushy," and each level would contribute only one term to the sum.

Bear in mind, therefore, that although asymptotic notation subsumes constant multiplicative factors, recursive notation such as $T(n/2)$ does not.

Strassen's method

The key to Strassen's method is to make the recursion tree slightly less bushy. That is, instead of performing eight recursive multiplications of $n/2 \times n/2$ matrices, it performs only seven. The cost of eliminating one matrix multiplication will be several new additions of $n/2 \times n/2$ matrices, but still only a constant number of additions. As before, the constant number of matrix additions will be subsumed by Θ-notation when we set up the recurrence equation to characterize the running time.

Strassen's method is not at all obvious. (This might be the biggest understatement in this book.) It has four steps:

1. Divide the input matrices A and B and output matrix C into $n/2 \times n/2$ submatrices, as in equation (4.9). This step takes $\Theta(1)$ time by index calculation, just as in SQUARE-MATRIX-MULTIPLY-RECURSIVE.
2. Create 10 matrices $S_1, S_2, \ldots, S_{10}$, each of which is $n/2 \times n/2$ and is the sum or difference of two matrices created in step 1. We can create all 10 matrices in $\Theta(n^2)$ time.
3. Using the submatrices created in step 1 and the 10 matrices created in step 2, recursively compute seven matrix products $P_1, P_2, \ldots, P_7$. Each matrix P_i is $n/2 \times n/2$.
4. Compute the desired submatrices $C_{11}, C_{12}, C_{21}, C_{22}$ of the result matrix C by adding and subtracting various combinations of the P_i matrices. We can compute all four submatrices in $\Theta(n^2)$ time.

We shall see the details of steps 2–4 in a moment, but we already have enough information to set up a recurrence for the running time of Strassen's method. Let us assume that once the matrix size n gets down to 1, we perform a simple scalar multiplication, just as in line 4 of SQUARE-MATRIX-MULTIPLY-RECURSIVE. When $n > 1$, steps 1, 2, and 4 take a total of $\Theta(n^2)$ time, and step 3 requires us to perform seven multiplications of $n/2 \times n/2$ matrices. Hence, we obtain the following recurrence for the running time $T(n)$ of Strassen's algorithm:

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 \,, \\ 7T(n/2) + \Theta(n^2) & \text{if } n > 1 \,. \end{cases} \tag{4.18}$$

We have traded off one matrix multiplication for a constant number of matrix additions. Once we understand recurrences and their solutions, we shall see that this tradeoff actually leads to a lower asymptotic running time. By the master method in Section 4.5, recurrence (4.18) has the solution $T(n) = \Theta(n^{\lg 7})$.

We now proceed to describe the details. In step 2, we create the following 10 matrices:

$$\begin{aligned}
S_1 &= B_{12} - B_{22} , \\
S_2 &= A_{11} + A_{12} , \\
S_3 &= A_{21} + A_{22} , \\
S_4 &= B_{21} - B_{11} , \\
S_5 &= A_{11} + A_{22} , \\
S_6 &= B_{11} + B_{22} , \\
S_7 &= A_{12} - A_{22} , \\
S_8 &= B_{21} + B_{22} , \\
S_9 &= A_{11} - A_{21} , \\
S_{10} &= B_{11} + B_{12} .
\end{aligned}$$

Since we must add or subtract $n/2 \times n/2$ matrices 10 times, this step does indeed take $\Theta(n^2)$ time.

In step 3, we recursively multiply $n/2 \times n/2$ matrices seven times to compute the following $n/2 \times n/2$ matrices, each of which is the sum or difference of products of A and B submatrices:

$$\begin{aligned}
P_1 &= A_{11} \cdot S_1 &&= A_{11} \cdot B_{12} - A_{11} \cdot B_{22} , \\
P_2 &= S_2 \cdot B_{22} &&= A_{11} \cdot B_{22} + A_{12} \cdot B_{22} , \\
P_3 &= S_3 \cdot B_{11} &&= A_{21} \cdot B_{11} + A_{22} \cdot B_{11} , \\
P_4 &= A_{22} \cdot S_4 &&= A_{22} \cdot B_{21} - A_{22} \cdot B_{11} , \\
P_5 &= S_5 \cdot S_6 &&= A_{11} \cdot B_{11} + A_{11} \cdot B_{22} + A_{22} \cdot B_{11} + A_{22} \cdot B_{22} , \\
P_6 &= S_7 \cdot S_8 &&= A_{12} \cdot B_{21} + A_{12} \cdot B_{22} - A_{22} \cdot B_{21} - A_{22} \cdot B_{22} , \\
P_7 &= S_9 \cdot S_{10} &&= A_{11} \cdot B_{11} + A_{11} \cdot B_{12} - A_{21} \cdot B_{11} - A_{21} \cdot B_{12} .
\end{aligned}$$

Note that the only multiplications we need to perform are those in the middle column of the above equations. The right-hand column just shows what these products equal in terms of the original submatrices created in step 1.

Step 4 adds and subtracts the P_i matrices created in step 3 to construct the four $n/2 \times n/2$ submatrices of the product C. We start with

$$C_{11} = P_5 + P_4 - P_2 + P_6 .$$

Expanding out the right-hand side, with the expansion of each P_i on its own line and vertically aligning terms that cancel out, we see that C_{11} equals

$$\begin{array}{rrrr}
A_{11}\cdot B_{11} + A_{11}\cdot B_{22} + A_{22}\cdot B_{11} + A_{22}\cdot B_{22} & & & \\
- A_{22}\cdot B_{11} & & + A_{22}\cdot B_{21} & \\
- A_{11}\cdot B_{22} & & & - A_{12}\cdot B_{22} \\
- A_{22}\cdot B_{22} & - A_{22}\cdot B_{21} & + A_{12}\cdot B_{22} & + A_{12}\cdot B_{21} \\
\hline
A_{11}\cdot B_{11} & & & + A_{12}\cdot B_{21}\ ,
\end{array}$$

which corresponds to equation (4.11).

Similarly, we set

$$C_{12} = P_1 + P_2\ ,$$

and so C_{12} equals

$$\begin{array}{rrrr}
A_{11}\cdot B_{12} - A_{11}\cdot B_{22} & & & \\
+ A_{11}\cdot B_{22} & & + A_{12}\cdot B_{22} & \\
\hline
A_{11}\cdot B_{12} & & & + A_{12}\cdot B_{22}\ ,
\end{array}$$

corresponding to equation (4.12).

Setting

$$C_{21} = P_3 + P_4$$

makes C_{21} equal

$$\begin{array}{rrrr}
A_{21}\cdot B_{11} + A_{22}\cdot B_{11} & & & \\
- A_{22}\cdot B_{11} & & + A_{22}\cdot B_{21} & \\
\hline
A_{21}\cdot B_{11} & & & + A_{22}\cdot B_{21}\ ,
\end{array}$$

corresponding to equation (4.13).

Finally, we set

$$C_{22} = P_5 + P_1 - P_3 - P_7\ ,$$

so that C_{22} equals

$$\begin{array}{rrrr}
A_{11}\cdot B_{11} + A_{11}\cdot B_{22} + A_{22}\cdot B_{11} + A_{22}\cdot B_{22} & & & \\
- A_{11}\cdot B_{22} & & + A_{11}\cdot B_{12} & \\
- A_{22}\cdot B_{11} & & & - A_{21}\cdot B_{11} \\
- A_{11}\cdot B_{11} & & - A_{11}\cdot B_{12} + A_{21}\cdot B_{11} & + A_{21}\cdot B_{12} \\
\hline
A_{22}\cdot B_{22} & & & + A_{21}\cdot B_{12}\ ,
\end{array}$$

which corresponds to equation (4.14). Altogether, we add or subtract $n/2 \times n/2$ matrices eight times in step 4, and so this step indeed takes $\Theta(n^2)$ time.

Thus, we see that Strassen's algorithm, comprising steps 1–4, produces the correct matrix product and that recurrence (4.18) characterizes its running time. Since we shall see in Section 4.5 that this recurrence has the solution $T(n) = \Theta(n^{\lg 7})$, Strassen's method is asymptotically faster than the straightforward SQUARE-MATRIX-MULTIPLY procedure. The notes at the end of this chapter discuss some of the practical aspects of Strassen's algorithm.

Exercises

Note: Although Exercises 4.2-3, 4.2-4, and 4.2-5 are about variants on Strassen's algorithm, you should read Section 4.5 before trying to solve them.

4.2-1
Use Strassen's algorithm to compute the matrix product

$$\begin{pmatrix} 1 & 3 \\ 7 & 5 \end{pmatrix} \begin{pmatrix} 6 & 8 \\ 4 & 2 \end{pmatrix}.$$

Show your work.

4.2-2
Write pseudocode for Strassen's algorithm.

4.2-3
How would you modify Strassen's algorithm to multiply $n \times n$ matrices in which n is not an exact power of 2? Show that the resulting algorithm runs in time $\Theta(n^{\lg 7})$.

4.2-4
What is the largest k such that if you can multiply 3×3 matrices using k multiplications (not assuming commutativity of multiplication), then you can multiply $n \times n$ matrices in time $o(n^{\lg 7})$? What would the running time of this algorithm be?

4.2-5
V. Pan has discovered a way of multiplying 68×68 matrices using 132,464 multiplications, a way of multiplying 70×70 matrices using 143,640 multiplications, and a way of multiplying 72×72 matrices using 155,424 multiplications. Which method yields the best asymptotic running time when used in a divide-and-conquer matrix-multiplication algorithm? How does it compare to Strassen's algorithm?

4.2-6

How quickly can you multiply a $kn \times n$ matrix by an $n \times kn$ matrix, using Strassen's algorithm as a subroutine? Answer the same question with the order of the input matrices reversed.

4.2-7

Show how to multiply the complex numbers $a + bi$ and $c + di$ using only three multiplications of real numbers. The algorithm should take a, b, c, and d as input and produce the real component $ac - bd$ and the imaginary component $ad + bc$ separately.

4.3 The substitution method for solving recurrences

Now that we have seen how recurrences characterize the running times of divide-and-conquer algorithms, we will learn how to solve recurrences. We start in this section with the "substitution" method.

The ***substitution method*** for solving recurrences comprises two steps:

1. Guess the form of the solution.
2. Use mathematical induction to find the constants and show that the solution works.

We substitute the guessed solution for the function when applying the inductive hypothesis to smaller values; hence the name "substitution method." This method is powerful, but we must be able to guess the form of the answer in order to apply it.

We can use the substitution method to establish either upper or lower bounds on a recurrence. As an example, let us determine an upper bound on the recurrence

$$T(n) = 2T(\lfloor n/2 \rfloor) + n \,, \tag{4.19}$$

which is similar to recurrences (4.3) and (4.4). We guess that the solution is $T(n) = O(n \lg n)$. The substitution method requires us to prove that $T(n) \leq cn \lg n$ for an appropriate choice of the constant $c > 0$. We start by assuming that this bound holds for all positive $m < n$, in particular for $m = \lfloor n/2 \rfloor$, yielding $T(\lfloor n/2 \rfloor) \leq c \lfloor n/2 \rfloor \lg(\lfloor n/2 \rfloor)$. Substituting into the recurrence yields

$$\begin{aligned} T(n) &\leq 2(c \lfloor n/2 \rfloor \lg(\lfloor n/2 \rfloor)) + n \\ &\leq cn \lg(n/2) + n \\ &= cn \lg n - cn \lg 2 + n \\ &= cn \lg n - cn + n \\ &\leq cn \lg n \,, \end{aligned}$$

where the last step holds as long as $c \geq 1$.

Mathematical induction now requires us to show that our solution holds for the boundary conditions. Typically, we do so by showing that the boundary conditions are suitable as base cases for the inductive proof. For the recurrence (4.19), we must show that we can choose the constant c large enough so that the bound $T(n) \leq cn \lg n$ works for the boundary conditions as well. This requirement can sometimes lead to problems. Let us assume, for the sake of argument, that $T(1) = 1$ is the sole boundary condition of the recurrence. Then for $n = 1$, the bound $T(n) \leq cn \lg n$ yields $T(1) \leq c1 \lg 1 = 0$, which is at odds with $T(1) = 1$. Consequently, the base case of our inductive proof fails to hold.

We can overcome this obstacle in proving an inductive hypothesis for a specific boundary condition with only a little more effort. In the recurrence (4.19), for example, we take advantage of asymptotic notation requiring us only to prove $T(n) \leq cn \lg n$ for $n \geq n_0$, where n_0 is a constant *that we get to choose*. We keep the troublesome boundary condition $T(1) = 1$, but remove it from consideration in the inductive proof. We do so by first observing that for $n > 3$, the recurrence does not depend directly on $T(1)$. Thus, we can replace $T(1)$ by $T(2)$ and $T(3)$ as the base cases in the inductive proof, letting $n_0 = 2$. Note that we make a distinction between the base case of the recurrence ($n = 1$) and the base cases of the inductive proof ($n = 2$ and $n = 3$). With $T(1) = 1$, we derive from the recurrence that $T(2) = 4$ and $T(3) = 5$. Now we can complete the inductive proof that $T(n) \leq cn \lg n$ for some constant $c \geq 1$ by choosing c large enough so that $T(2) \leq c2 \lg 2$ and $T(3) \leq c3 \lg 3$. As it turns out, any choice of $c \geq 2$ suffices for the base cases of $n = 2$ and $n = 3$ to hold. For most of the recurrences we shall examine, it is straightforward to extend boundary conditions to make the inductive assumption work for small n, and we shall not always explicitly work out the details.

Making a good guess

Unfortunately, there is no general way to guess the correct solutions to recurrences. Guessing a solution takes experience and, occasionally, creativity. Fortunately, though, you can use some heuristics to help you become a good guesser. You can also use recursion trees, which we shall see in Section 4.4, to generate good guesses.

If a recurrence is similar to one you have seen before, then guessing a similar solution is reasonable. As an example, consider the recurrence

$$T(n) = 2T(\lfloor n/2 \rfloor + 17) + n \ ,$$

which looks difficult because of the added "17" in the argument to T on the right-hand side. Intuitively, however, this additional term cannot substantially affect the

solution to the recurrence. When n is large, the difference between $\lfloor n/2 \rfloor$ and $\lfloor n/2 \rfloor + 17$ is not that large: both cut n nearly evenly in half. Consequently, we make the guess that $T(n) = O(n \lg n)$, which you can verify as correct by using the substitution method (see Exercise 4.3-6).

Another way to make a good guess is to prove loose upper and lower bounds on the recurrence and then reduce the range of uncertainty. For example, we might start with a lower bound of $T(n) = \Omega(n)$ for the recurrence (4.19), since we have the term n in the recurrence, and we can prove an initial upper bound of $T(n) = O(n^2)$. Then, we can gradually lower the upper bound and raise the lower bound until we converge on the correct, asymptotically tight solution of $T(n) = \Theta(n \lg n)$.

Subtleties

Sometimes you might correctly guess an asymptotic bound on the solution of a recurrence, but somehow the math fails to work out in the induction. The problem frequently turns out to be that the inductive assumption is not strong enough to prove the detailed bound. If you revise the guess by subtracting a lower-order term when you hit such a snag, the math often goes through.

Consider the recurrence

$$T(n) = T(\lfloor n/2 \rfloor) + T(\lceil n/2 \rceil) + 1 \; .$$

We guess that the solution is $T(n) = O(n)$, and we try to show that $T(n) \le cn$ for an appropriate choice of the constant c. Substituting our guess in the recurrence, we obtain

$$\begin{aligned} T(n) &\le c \lfloor n/2 \rfloor + c \lceil n/2 \rceil + 1 \\ &= cn + 1 \; , \end{aligned}$$

which does not imply $T(n) \le cn$ for any choice of c. We might be tempted to try a larger guess, say $T(n) = O(n^2)$. Although we can make this larger guess work, our original guess of $T(n) = O(n)$ is correct. In order to show that it is correct, however, we must make a stronger inductive hypothesis.

Intuitively, our guess is nearly right: we are off only by the constant 1, a lower-order term. Nevertheless, mathematical induction does not work unless we prove the exact form of the inductive hypothesis. We overcome our difficulty by *subtracting* a lower-order term from our previous guess. Our new guess is $T(n) \le cn - d$, where $d \ge 0$ is a constant. We now have

$$\begin{aligned} T(n) &\le (c \lfloor n/2 \rfloor - d) + (c \lceil n/2 \rceil - d) + 1 \\ &= cn - 2d + 1 \\ &\le cn - d \; , \end{aligned}$$

as long as $d \geq 1$. As before, we must choose the constant c large enough to handle the boundary conditions.

You might find the idea of subtracting a lower-order term counterintuitive. After all, if the math does not work out, we should increase our guess, right? Not necessarily! When proving an upper bound by induction, it may actually be more difficult to prove that a weaker upper bound holds, because in order to prove the weaker bound, we must use the same weaker bound inductively in the proof. In our current example, when the recurrence has more than one recursive term, we get to subtract out the lower-order term of the proposed bound once per recursive term. In the above example, we subtracted out the constant d twice, once for the $T(\lfloor n/2 \rfloor)$ term and once for the $T(\lceil n/2 \rceil)$ term. We ended up with the inequality $T(n) \leq cn - 2d + 1$, and it was easy to find values of d to make $cn - 2d + 1$ be less than or equal to $cn - d$.

Avoiding pitfalls

It is easy to err in the use of asymptotic notation. For example, in the recurrence (4.19) we can falsely "prove" $T(n) = O(n)$ by guessing $T(n) \leq cn$ and then arguing

$$\begin{aligned} T(n) &\leq 2(c\lfloor n/2 \rfloor) + n \\ &\leq cn + n \\ &= O(n) , \qquad \Longleftarrow \textit{wrong!!} \end{aligned}$$

since c is a constant. The error is that we have not proved the *exact form* of the inductive hypothesis, that is, that $T(n) \leq cn$. We therefore will explicitly prove that $T(n) \leq cn$ when we want to show that $T(n) = O(n)$.

Changing variables

Sometimes, a little algebraic manipulation can make an unknown recurrence similar to one you have seen before. As an example, consider the recurrence

$$T(n) = 2T\left(\lfloor \sqrt{n} \rfloor\right) + \lg n ,$$

which looks difficult. We can simplify this recurrence, though, with a change of variables. For convenience, we shall not worry about rounding off values, such as $\sqrt{n}$, to be integers. Renaming $m = \lg n$ yields

$$T(2^m) = 2T(2^{m/2}) + m .$$

We can now rename $S(m) = T(2^m)$ to produce the new recurrence

$$S(m) = 2S(m/2) + m ,$$

which is very much like recurrence (4.19). Indeed, this new recurrence has the same solution: $S(m) = O(m \lg m)$. Changing back from $S(m)$ to $T(n)$, we obtain

$$T(n) = T(2^m) = S(m) = O(m \lg m) = O(\lg n \lg \lg n) .$$

Exercises

4.3-1
Show that the solution of $T(n) = T(n-1) + n$ is $O(n^2)$.

4.3-2
Show that the solution of $T(n) = T(\lceil n/2 \rceil) + 1$ is $O(\lg n)$.

4.3-3
We saw that the solution of $T(n) = 2T(\lfloor n/2 \rfloor) + n$ is $O(n \lg n)$. Show that the solution of this recurrence is also $\Omega(n \lg n)$. Conclude that the solution is $\Theta(n \lg n)$.

4.3-4
Show that by making a different inductive hypothesis, we can overcome the difficulty with the boundary condition $T(1) = 1$ for recurrence (4.19) without adjusting the boundary conditions for the inductive proof.

4.3-5
Show that $\Theta(n \lg n)$ is the solution to the "exact" recurrence (4.3) for merge sort.

4.3-6
Show that the solution to $T(n) = 2T(\lfloor n/2 \rfloor + 17) + n$ is $O(n \lg n)$.

4.3-7
Using the master method in Section 4.5, you can show that the solution to the recurrence $T(n) = 4T(n/3) + n$ is $T(n) = \Theta(n^{\log_3 4})$. Show that a substitution proof with the assumption $T(n) \leq cn^{\log_3 4}$ fails. Then show how to subtract off a lower-order term to make a substitution proof work.

4.3-8
Using the master method in Section 4.5, you can show that the solution to the recurrence $T(n) = 4T(n/2) + n^2$ is $T(n) = \Theta(n^2)$. Show that a substitution proof with the assumption $T(n) \leq cn^2$ fails. Then show how to subtract off a lower-order term to make a substitution proof work.

4.3-9

Solve the recurrence $T(n) = 3T(\sqrt{n}) + \log n$ by making a change of variables. Your solution should be asymptotically tight. Do not worry about whether values are integral.

4.4 The recursion-tree method for solving recurrences

Although you can use the substitution method to provide a succinct proof that a solution to a recurrence is correct, you might have trouble coming up with a good guess. Drawing out a recursion tree, as we did in our analysis of the merge sort recurrence in Section 2.3.2, serves as a straightforward way to devise a good guess. In a ***recursion tree***, each node represents the cost of a single subproblem somewhere in the set of recursive function invocations. We sum the costs within each level of the tree to obtain a set of per-level costs, and then we sum all the per-level costs to determine the total cost of all levels of the recursion.

A recursion tree is best used to generate a good guess, which you can then verify by the substitution method. When using a recursion tree to generate a good guess, you can often tolerate a small amount of "sloppiness," since you will be verifying your guess later on. If you are very careful when drawing out a recursion tree and summing the costs, however, you can use a recursion tree as a direct proof of a solution to a recurrence. In this section, we will use recursion trees to generate good guesses, and in Section 4.6, we will use recursion trees directly to prove the theorem that forms the basis of the master method.

For example, let us see how a recursion tree would provide a good guess for the recurrence $T(n) = 3T(\lfloor n/4 \rfloor) + \Theta(n^2)$. We start by focusing on finding an upper bound for the solution. Because we know that floors and ceilings usually do not matter when solving recurrences (here's an example of sloppiness that we can tolerate), we create a recursion tree for the recurrence $T(n) = 3T(n/4) + cn^2$, having written out the implied constant coefficient $c > 0$.

Figure 4.5 shows how we derive the recursion tree for $T(n) = 3T(n/4) + cn^2$. For convenience, we assume that n is an exact power of 4 (another example of tolerable sloppiness) so that all subproblem sizes are integers. Part (a) of the figure shows $T(n)$, which we expand in part (b) into an equivalent tree representing the recurrence. The cn^2 term at the root represents the cost at the top level of recursion, and the three subtrees of the root represent the costs incurred by the subproblems of size $n/4$. Part (c) shows this process carried one step further by expanding each node with cost $T(n/4)$ from part (b). The cost for each of the three children of the root is $c(n/4)^2$. We continue expanding each node in the tree by breaking it into its constituent parts as determined by the recurrence.

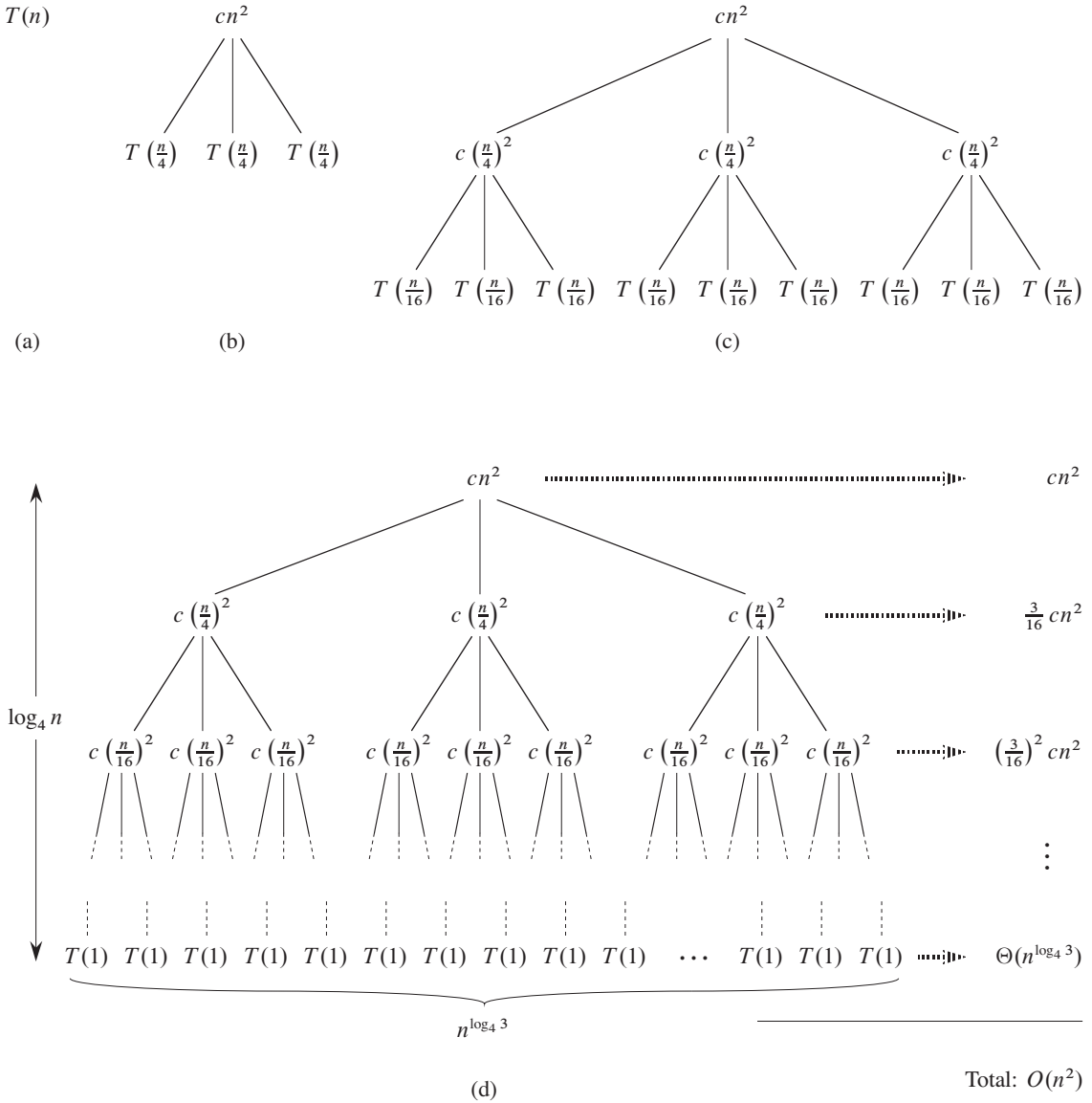


Figure 4.5 Constructing a recursion tree for the recurrence $T(n) = 3T(n/4) + cn^2$. Part **(a)** shows $T(n)$, which progressively expands in **(b)–(d)** to form the recursion tree. The fully expanded tree in part (d) has height $\log_4 n$ (it has $\log_4 n + 1$ levels).

Because subproblem sizes decrease by a factor of 4 each time we go down one level, we eventually must reach a boundary condition. How far from the root do we reach one? The subproblem size for a node at depth i is $n/4^i$. Thus, the subproblem size hits $n = 1$ when $n/4^i = 1$ or, equivalently, when $i = \log_4 n$. Thus, the tree has $\log_4 n + 1$ levels (at depths $0, 1, 2, \ldots, \log_4 n$).

Next we determine the cost at each level of the tree. Each level has three times more nodes than the level above, and so the number of nodes at depth i is 3^i. Because subproblem sizes reduce by a factor of 4 for each level we go down from the root, each node at depth i, for $i = 0, 1, 2, \ldots, \log_4 n - 1$, has a cost of $c(n/4^i)^2$. Multiplying, we see that the total cost over all nodes at depth i, for $i = 0, 1, 2, \ldots, \log_4 n - 1$, is $3^i c(n/4^i)^2 = (3/16)^i cn^2$. The bottom level, at depth $\log_4 n$, has $3^{\log_4 n} = n^{\log_4 3}$ nodes, each contributing cost $T(1)$, for a total cost of $n^{\log_4 3} T(1)$, which is $\Theta(n^{\log_4 3})$, since we assume that $T(1)$ is a constant.

Now we add up the costs over all levels to determine the cost for the entire tree:

$$\begin{aligned}
T(n) &= cn^2 + \frac{3}{16}cn^2 + \left(\frac{3}{16}\right)^2 cn^2 + \cdots + \left(\frac{3}{16}\right)^{\log_4 n - 1} cn^2 + \Theta(n^{\log_4 3}) \\
&= \sum_{i=0}^{\log_4 n - 1} \left(\frac{3}{16}\right)^i cn^2 + \Theta(n^{\log_4 3}) \\
&= \frac{(3/16)^{\log_4 n} - 1}{(3/16) - 1} cn^2 + \Theta(n^{\log_4 3}) \qquad \text{(by equation (A.5))} .
\end{aligned}$$

This last formula looks somewhat messy until we realize that we can again take advantage of small amounts of sloppiness and use an infinite decreasing geometric series as an upper bound. Backing up one step and applying equation (A.6), we have

$$\begin{aligned}
T(n) &= \sum_{i=0}^{\log_4 n - 1} \left(\frac{3}{16}\right)^i cn^2 + \Theta(n^{\log_4 3}) \\
&< \sum_{i=0}^{\infty} \left(\frac{3}{16}\right)^i cn^2 + \Theta(n^{\log_4 3}) \\
&= \frac{1}{1 - (3/16)} cn^2 + \Theta(n^{\log_4 3}) \\
&= \frac{16}{13} cn^2 + \Theta(n^{\log_4 3}) \\
&= O(n^2) .
\end{aligned}$$

Thus, we have derived a guess of $T(n) = O(n^2)$ for our original recurrence $T(n) = 3T(\lfloor n/4 \rfloor) + \Theta(n^2)$. In this example, the coefficients of cn^2 form a decreasing geometric series and, by equation (A.6), the sum of these coefficients

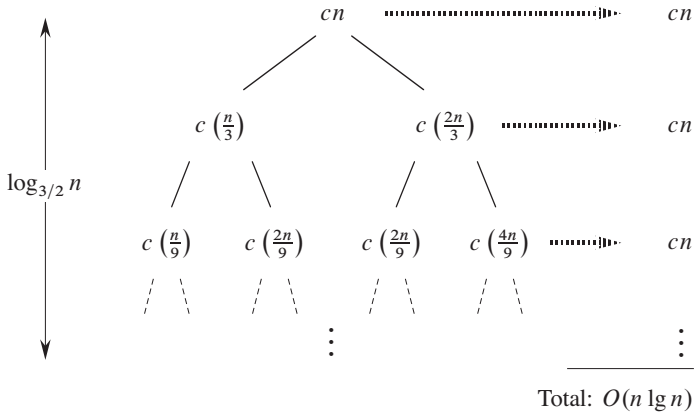


Figure 4.6 A recursion tree for the recurrence $T(n) = T(n/3) + T(2n/3) + cn$.

is bounded from above by the constant 16/13. Since the root's contribution to the total cost is cn^2, the root contributes a constant fraction of the total cost. In other words, the cost of the root dominates the total cost of the tree.

In fact, if $O(n^2)$ is indeed an upper bound for the recurrence (as we shall verify in a moment), then it must be a tight bound. Why? The first recursive call contributes a cost of $\Theta(n^2)$, and so $\Omega(n^2)$ must be a lower bound for the recurrence.

Now we can use the substitution method to verify that our guess was correct, that is, $T(n) = O(n^2)$ is an upper bound for the recurrence $T(n) = 3T(\lfloor n/4 \rfloor) + \Theta(n^2)$. We want to show that $T(n) \le dn^2$ for some constant $d > 0$. Using the same constant $c > 0$ as before, we have

$$\begin{aligned} T(n) &\le 3T(\lfloor n/4 \rfloor) + cn^2 \\ &\le 3d \lfloor n/4 \rfloor^2 + cn^2 \\ &\le 3d(n/4)^2 + cn^2 \\ &= \frac{3}{16} dn^2 + cn^2 \\ &\le dn^2 , \end{aligned}$$

where the last step holds as long as $d \ge (16/13)c$.

In another, more intricate, example, Figure 4.6 shows the recursion tree for

$$T(n) = T(n/3) + T(2n/3) + O(n) .$$

(Again, we omit floor and ceiling functions for simplicity.) As before, we let c represent the constant factor in the $O(n)$ term. When we add the values across the levels of the recursion tree shown in the figure, we get a value of cn for every level.

The longest simple path from the root to a leaf is $n \to (2/3)n \to (2/3)^2 n \to \cdots \to 1$. Since $(2/3)^k n = 1$ when $k = \log_{3/2} n$, the height of the tree is $\log_{3/2} n$.

Intuitively, we expect the solution to the recurrence to be at most the number of levels times the cost of each level, or $O(cn \log_{3/2} n) = O(n \lg n)$. Figure 4.6 shows only the top levels of the recursion tree, however, and not every level in the tree contributes a cost of cn. Consider the cost of the leaves. If this recursion tree were a complete binary tree of height $\log_{3/2} n$, there would be $2^{\log_{3/2} n} = n^{\log_{3/2} 2}$ leaves. Since the cost of each leaf is a constant, the total cost of all leaves would then be $\Theta(n^{\log_{3/2} 2})$ which, since $\log_{3/2} 2$ is a constant strictly greater than 1, is $\omega(n \lg n)$. This recursion tree is not a complete binary tree, however, and so it has fewer than $n^{\log_{3/2} 2}$ leaves. Moreover, as we go down from the root, more and more internal nodes are absent. Consequently, levels toward the bottom of the recursion tree contribute less than cn to the total cost. We could work out an accurate accounting of all costs, but remember that we are just trying to come up with a guess to use in the substitution method. Let us tolerate the sloppiness and attempt to show that a guess of $O(n \lg n)$ for the upper bound is correct.

Indeed, we can use the substitution method to verify that $O(n \lg n)$ is an upper bound for the solution to the recurrence. We show that $T(n) \le dn \lg n$, where d is a suitable positive constant. We have

$$\begin{aligned}
T(n) &\le T(n/3) + T(2n/3) + cn \\
&\le d(n/3)\lg(n/3) + d(2n/3)\lg(2n/3) + cn \\
&= (d(n/3)\lg n - d(n/3)\lg 3) \\
&\qquad + (d(2n/3)\lg n - d(2n/3)\lg(3/2)) + cn \\
&= dn\lg n - d((n/3)\lg 3 + (2n/3)\lg(3/2)) + cn \\
&= dn\lg n - d((n/3)\lg 3 + (2n/3)\lg 3 - (2n/3)\lg 2) + cn \\
&= dn\lg n - dn(\lg 3 - 2/3) + cn \\
&\le dn\lg n\ ,
\end{aligned}$$

as long as $d \ge c/(\lg 3 - (2/3))$. Thus, we did not need to perform a more accurate accounting of costs in the recursion tree.

Exercises

4.4-1

Use a recursion tree to determine a good asymptotic upper bound on the recurrence $T(n) = 3T(\lfloor n/2 \rfloor) + n$. Use the substitution method to verify your answer.

4.4-2

Use a recursion tree to determine a good asymptotic upper bound on the recurrence $T(n) = T(n/2) + n^2$. Use the substitution method to verify your answer.

4.4-3
Use a recursion tree to determine a good asymptotic upper bound on the recurrence $T(n) = 4T(n/2 + 2) + n$. Use the substitution method to verify your answer.

4.4-4
Use a recursion tree to determine a good asymptotic upper bound on the recurrence $T(n) = 2T(n - 1) + 1$. Use the substitution method to verify your answer.

4.4-5
Use a recursion tree to determine a good asymptotic upper bound on the recurrence $T(n) = T(n-1) + T(n/2) + n$. Use the substitution method to verify your answer.

4.4-6
Argue that the solution to the recurrence $T(n) = T(n/3) + T(2n/3) + cn$, where c is a constant, is $\Omega(n \lg n)$ by appealing to a recursion tree.

4.4-7
Draw the recursion tree for $T(n) = 4T(\lfloor n/2 \rfloor) + cn$, where c is a constant, and provide a tight asymptotic bound on its solution. Verify your bound by the substitution method.

4.4-8
Use a recursion tree to give an asymptotically tight solution to the recurrence $T(n) = T(n - a) + T(a) + cn$, where $a \geq 1$ and $c > 0$ are constants.

4.4-9
Use a recursion tree to give an asymptotically tight solution to the recurrence $T(n) = T(\alpha n) + T((1 - \alpha)n) + cn$, where α is a constant in the range $0 < \alpha < 1$ and $c > 0$ is also a constant.

4.5 The master method for solving recurrences

The master method provides a "cookbook" method for solving recurrences of the form

$$T(n) = aT(n/b) + f(n)\,, \tag{4.20}$$

where $a \geq 1$ and $b > 1$ are constants and $f(n)$ is an asymptotically positive function. To use the master method, you will need to memorize three cases, but then you will be able to solve many recurrences quite easily, often without pencil and paper.

The recurrence (4.20) describes the running time of an algorithm that divides a problem of size n into a subproblems, each of size n/b, where a and b are positive constants. The a subproblems are solved recursively, each in time $T(n/b)$. The function $f(n)$ encompasses the cost of dividing the problem and combining the results of the subproblems. For example, the recurrence arising from Strassen's algorithm has $a = 7$, $b = 2$, and $f(n) = \Theta(n^2)$.

As a matter of technical correctness, the recurrence is not actually well defined, because n/b might not be an integer. Replacing each of the a terms $T(n/b)$ with either $T(\lfloor n/b \rfloor)$ or $T(\lceil n/b \rceil)$ will not affect the asymptotic behavior of the recurrence, however. (We will prove this assertion in the next section.) We normally find it convenient, therefore, to omit the floor and ceiling functions when writing divide-and-conquer recurrences of this form.

The master theorem

The master method depends on the following theorem.

Theorem 4.1 (Master theorem)
Let $a \geq 1$ and $b > 1$ be constants, let $f(n)$ be a function, and let $T(n)$ be defined on the nonnegative integers by the recurrence

$$T(n) = aT(n/b) + f(n) ,$$

where we interpret n/b to mean either $\lfloor n/b \rfloor$ or $\lceil n/b \rceil$. Then $T(n)$ has the following asymptotic bounds:

1. If $f(n) = O(n^{\log_b a - \epsilon})$ for some constant $\epsilon > 0$, then $T(n) = \Theta(n^{\log_b a})$.
2. If $f(n) = \Theta(n^{\log_b a})$, then $T(n) = \Theta(n^{\log_b a} \lg n)$.
3. If $f(n) = \Omega(n^{\log_b a + \epsilon})$ for some constant $\epsilon > 0$, and if $af(n/b) \leq cf(n)$ for some constant $c < 1$ and all sufficiently large n, then $T(n) = \Theta(f(n))$. ■

Before applying the master theorem to some examples, let's spend a moment trying to understand what it says. In each of the three cases, we compare the function $f(n)$ with the function $n^{\log_b a}$. Intuitively, the larger of the two functions determines the solution to the recurrence. If, as in case 1, the function $n^{\log_b a}$ is the larger, then the solution is $T(n) = \Theta(n^{\log_b a})$. If, as in case 3, the function $f(n)$ is the larger, then the solution is $T(n) = \Theta(f(n))$. If, as in case 2, the two functions are the same size, we multiply by a logarithmic factor, and the solution is $T(n) = \Theta(n^{\log_b a} \lg n) = \Theta(f(n) \lg n)$.

Beyond this intuition, you need to be aware of some technicalities. In the first case, not only must $f(n)$ be smaller than $n^{\log_b a}$, it must be *polynomially* smaller.

That is, $f(n)$ must be asymptotically smaller than $n^{\log_b a}$ by a factor of n^ϵ for some constant $\epsilon > 0$. In the third case, not only must $f(n)$ be larger than $n^{\log_b a}$, it also must be polynomially larger and in addition satisfy the "regularity" condition that $af(n/b) \le cf(n)$. This condition is satisfied by most of the polynomially bounded functions that we shall encounter.

Note that the three cases do not cover all the possibilities for $f(n)$. There is a gap between cases 1 and 2 when $f(n)$ is smaller than $n^{\log_b a}$ but not polynomially smaller. Similarly, there is a gap between cases 2 and 3 when $f(n)$ is larger than $n^{\log_b a}$ but not polynomially larger. If the function $f(n)$ falls into one of these gaps, or if the regularity condition in case 3 fails to hold, you cannot use the master method to solve the recurrence.

Using the master method

To use the master method, we simply determine which case (if any) of the master theorem applies and write down the answer.

As a first example, consider

$$T(n) = 9T(n/3) + n \ .$$

For this recurrence, we have $a = 9$, $b = 3$, $f(n) = n$, and thus we have that $n^{\log_b a} = n^{\log_3 9} = \Theta(n^2)$. Since $f(n) = O(n^{\log_3 9 - \epsilon})$, where $\epsilon = 1$, we can apply case 1 of the master theorem and conclude that the solution is $T(n) = \Theta(n^2)$.

Now consider

$$T(n) = T(2n/3) + 1,$$

in which $a = 1$, $b = 3/2$, $f(n) = 1$, and $n^{\log_b a} = n^{\log_{3/2} 1} = n^0 = 1$. Case 2 applies, since $f(n) = \Theta(n^{\log_b a}) = \Theta(1)$, and thus the solution to the recurrence is $T(n) = \Theta(\lg n)$.

For the recurrence

$$T(n) = 3T(n/4) + n \lg n \ ,$$

we have $a = 3$, $b = 4$, $f(n) = n \lg n$, and $n^{\log_b a} = n^{\log_4 3} = O(n^{0.793})$. Since $f(n) = \Omega(n^{\log_4 3 + \epsilon})$, where $\epsilon \approx 0.2$, case 3 applies if we can show that the regularity condition holds for $f(n)$. For sufficiently large n, we have that $af(n/b) = 3(n/4)\lg(n/4) \le (3/4)n \lg n = cf(n)$ for $c = 3/4$. Consequently, by case 3, the solution to the recurrence is $T(n) = \Theta(n \lg n)$.

The master method does not apply to the recurrence

$$T(n) = 2T(n/2) + n \lg n \ ,$$

even though it appears to have the proper form: $a = 2$, $b = 2$, $f(n) = n \lg n$, and $n^{\log_b a} = n$. You might mistakenly think that case 3 should apply, since

$f(n) = n \lg n$ is asymptotically larger than $n^{\log_b a} = n$. The problem is that it is not *polynomially* larger. The ratio $f(n)/n^{\log_b a} = (n \lg n)/n = \lg n$ is asymptotically less than n^ϵ for any positive constant ϵ. Consequently, the recurrence falls into the gap between case 2 and case 3. (See Exercise 4.6-2 for a solution.)

Let's use the master method to solve the recurrences we saw in Sections 4.1 and 4.2. Recurrence (4.7),

$$T(n) = 2T(n/2) + \Theta(n) ,$$

characterizes the running times of the divide-and-conquer algorithm for both the maximum-subarray problem and merge sort. (As is our practice, we omit stating the base case in the recurrence.) Here, we have $a = 2$, $b = 2$, $f(n) = \Theta(n)$, and thus we have that $n^{\log_b a} = n^{\log_2 2} = n$. Case 2 applies, since $f(n) = \Theta(n)$, and so we have the solution $T(n) = \Theta(n \lg n)$.

Recurrence (4.17),

$$T(n) = 8T(n/2) + \Theta(n^2) ,$$

describes the running time of the first divide-and-conquer algorithm that we saw for matrix multiplication. Now we have $a = 8$, $b = 2$, and $f(n) = \Theta(n^2)$, and so $n^{\log_b a} = n^{\log_2 8} = n^3$. Since n^3 is polynomially larger than $f(n)$ (that is, $f(n) = O(n^{3-\epsilon})$ for $\epsilon = 1$), case 1 applies, and $T(n) = \Theta(n^3)$.

Finally, consider recurrence (4.18),

$$T(n) = 7T(n/2) + \Theta(n^2) ,$$

which describes the running time of Strassen's algorithm. Here, we have $a = 7$, $b = 2$, $f(n) = \Theta(n^2)$, and thus $n^{\log_b a} = n^{\log_2 7}$. Rewriting $\log_2 7$ as $\lg 7$ and recalling that $2.80 < \lg 7 < 2.81$, we see that $f(n) = O(n^{\lg 7 - \epsilon})$ for $\epsilon = 0.8$. Again, case 1 applies, and we have the solution $T(n) = \Theta(n^{\lg 7})$.

Exercises

4.5-1

Use the master method to give tight asymptotic bounds for the following recurrences.

a. $T(n) = 2T(n/4) + 1$.

b. $T(n) = 2T(n/4) + \sqrt{n}$.

c. $T(n) = 2T(n/4) + n$.

d. $T(n) = 2T(n/4) + n^2$.

4.5-2
Professor Caesar wishes to develop a matrix-multiplication algorithm that is asymptotically faster than Strassen's algorithm. His algorithm will use the divide-and-conquer method, dividing each matrix into pieces of size $n/4 \times n/4$, and the divide and combine steps together will take $\Theta(n^2)$ time. He needs to determine how many subproblems his algorithm has to create in order to beat Strassen's algorithm. If his algorithm creates a subproblems, then the recurrence for the running time $T(n)$ becomes $T(n) = aT(n/4) + \Theta(n^2)$. What is the largest integer value of a for which Professor Caesar's algorithm would be asymptotically faster than Strassen's algorithm?

4.5-3
Use the master method to show that the solution to the binary-search recurrence $T(n) = T(n/2) + \Theta(1)$ is $T(n) = \Theta(\lg n)$. (See Exercise 2.3-5 for a description of binary search.)

4.5-4
Can the master method be applied to the recurrence $T(n) = 4T(n/2) + n^2 \lg n$? Why or why not? Give an asymptotic upper bound for this recurrence.

4.5-5 ⋆
Consider the regularity condition $af(n/b) \leq cf(n)$ for some constant $c < 1$, which is part of case 3 of the master theorem. Give an example of constants $a \geq 1$ and $b > 1$ and a function $f(n)$ that satisfies all the conditions in case 3 of the master theorem except the regularity condition.

⋆ 4.6 Proof of the master theorem

This section contains a proof of the master theorem (Theorem 4.1). You do not need to understand the proof in order to apply the master theorem.

The proof appears in two parts. The first part analyzes the master recurrence (4.20), under the simplifying assumption that $T(n)$ is defined only on exact powers of $b > 1$, that is, for $n = 1, b, b^2, \ldots$. This part gives all the intuition needed to understand why the master theorem is true. The second part shows how to extend the analysis to all positive integers n; it applies mathematical technique to the problem of handling floors and ceilings.

In this section, we shall sometimes abuse our asymptotic notation slightly by using it to describe the behavior of functions that are defined only over exact powers of b. Recall that the definitions of asymptotic notations require that

bounds be proved for all sufficiently large numbers, not just those that are powers of b. Since we could make new asymptotic notations that apply only to the set $\{b^i : i = 0, 1, 2, \ldots\}$, instead of to the nonnegative numbers, this abuse is minor.

Nevertheless, we must always be on guard when we use asymptotic notation over a limited domain lest we draw improper conclusions. For example, proving that $T(n) = O(n)$ when n is an exact power of 2 does not guarantee that $T(n) = O(n)$. The function $T(n)$ could be defined as

$$T(n) = \begin{cases} n & \text{if } n = 1, 2, 4, 8, \ldots , \\ n^2 & \text{otherwise} , \end{cases}$$

in which case the best upper bound that applies to all values of n is $T(n) = O(n^2)$. Because of this sort of drastic consequence, we shall never use asymptotic notation over a limited domain without making it absolutely clear from the context that we are doing so.

4.6.1 The proof for exact powers

The first part of the proof of the master theorem analyzes the recurrence (4.20)

$$T(n) = aT(n/b) + f(n) ,$$

for the master method, under the assumption that n is an exact power of $b > 1$, where b need not be an integer. We break the analysis into three lemmas. The first reduces the problem of solving the master recurrence to the problem of evaluating an expression that contains a summation. The second determines bounds on this summation. The third lemma puts the first two together to prove a version of the master theorem for the case in which n is an exact power of b.

Lemma 4.2

Let $a \geq 1$ and $b > 1$ be constants, and let $f(n)$ be a nonnegative function defined on exact powers of b. Define $T(n)$ on exact powers of b by the recurrence

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 , \\ aT(n/b) + f(n) & \text{if } n = b^i , \end{cases}$$

where i is a positive integer. Then

$$T(n) = \Theta(n^{\log_b a}) + \sum_{j=0}^{\log_b n - 1} a^j f(n/b^j) . \tag{4.21}$$

Proof We use the recursion tree in Figure 4.7. The root of the tree has cost $f(n)$, and it has a children, each with cost $f(n/b)$. (It is convenient to think of a as being

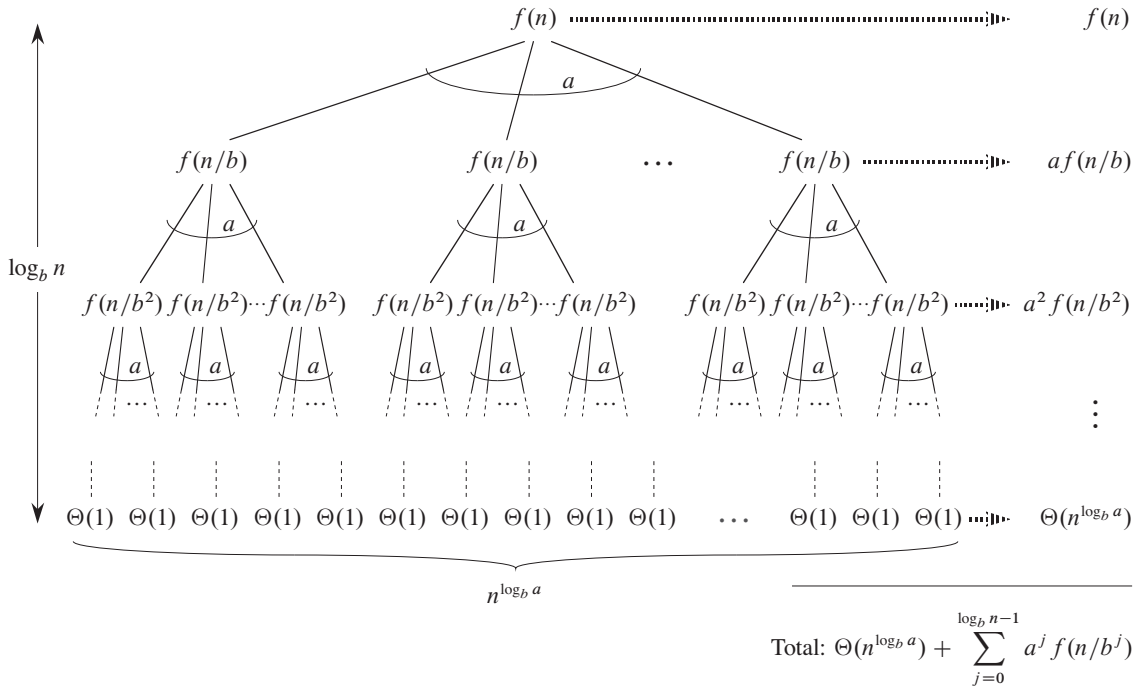


Figure 4.7 The recursion tree generated by $T(n) = aT(n/b) + f(n)$. The tree is a complete a-ary tree with $n^{\log_b a}$ leaves and height $\log_b n$. The cost of the nodes at each depth is shown at the right, and their sum is given in equation (4.21).

an integer, especially when visualizing the recursion tree, but the mathematics does not require it.) Each of these children has a children, making a^2 nodes at depth 2, and each of the a children has cost $f(n/b^2)$. In general, there are a^j nodes at depth j, and each has cost $f(n/b^j)$. The cost of each leaf is $T(1) = \Theta(1)$, and each leaf is at depth $\log_b n$, since $n/b^{\log_b n} = 1$. There are $a^{\log_b n} = n^{\log_b a}$ leaves in the tree.

We can obtain equation (4.21) by summing the costs of the nodes at each depth in the tree, as shown in the figure. The cost for all internal nodes at depth j is $a^j f(n/b^j)$, and so the total cost of all internal nodes is

$$\sum_{j=0}^{\log_b n - 1} a^j f(n/b^j) \; .$$

In the underlying divide-and-conquer algorithm, this sum represents the costs of dividing problems into subproblems and then recombining the subproblems. The

cost of all the leaves, which is the cost of doing all $n^{\log_b a}$ subproblems of size 1, is $\Theta(n^{\log_b a})$. ■

In terms of the recursion tree, the three cases of the master theorem correspond to cases in which the total cost of the tree is (1) dominated by the costs in the leaves, (2) evenly distributed among the levels of the tree, or (3) dominated by the cost of the root.

The summation in equation (4.21) describes the cost of the dividing and combining steps in the underlying divide-and-conquer algorithm. The next lemma provides asymptotic bounds on the summation's growth.

Lemma 4.3

Let $a \geq 1$ and $b > 1$ be constants, and let $f(n)$ be a nonnegative function defined on exact powers of b. A function $g(n)$ defined over exact powers of b by

$$g(n) = \sum_{j=0}^{\log_b n - 1} a^j f(n/b^j) \tag{4.22}$$

has the following asymptotic bounds for exact powers of b:

1. If $f(n) = O(n^{\log_b a - \epsilon})$ for some constant $\epsilon > 0$, then $g(n) = O(n^{\log_b a})$.
2. If $f(n) = \Theta(n^{\log_b a})$, then $g(n) = \Theta(n^{\log_b a} \lg n)$.
3. If $af(n/b) \leq cf(n)$ for some constant $c < 1$ and for all sufficiently large n, then $g(n) = \Theta(f(n))$.

Proof For case 1, we have $f(n) = O(n^{\log_b a - \epsilon})$, which implies that $f(n/b^j) = O((n/b^j)^{\log_b a - \epsilon})$. Substituting into equation (4.22) yields

$$g(n) = O\left(\sum_{j=0}^{\log_b n - 1} a^j \left(\frac{n}{b^j}\right)^{\log_b a - \epsilon}\right) . \tag{4.23}$$

We bound the summation within the O-notation by factoring out terms and simplifying, which leaves an increasing geometric series:

$$\begin{aligned}
\sum_{j=0}^{\log_b n - 1} a^j \left(\frac{n}{b^j}\right)^{\log_b a - \epsilon} &= n^{\log_b a - \epsilon} \sum_{j=0}^{\log_b n - 1} \left(\frac{ab^\epsilon}{b^{\log_b a}}\right)^j \\
&= n^{\log_b a - \epsilon} \sum_{j=0}^{\log_b n - 1} (b^\epsilon)^j \\
&= n^{\log_b a - \epsilon} \left(\frac{b^{\epsilon \log_b n} - 1}{b^\epsilon - 1}\right)
\end{aligned}$$

$$= \quad n^{\log_b a-\epsilon}\left(\frac{n^\epsilon-1}{b^\epsilon-1}\right) .$$

Since b and ϵ are constants, we can rewrite the last expression as $n^{\log_b a-\epsilon}O(n^\epsilon) = O(n^{\log_b a})$. Substituting this expression for the summation in equation (4.23) yields

$$g(n) = O(n^{\log_b a}) ,$$

thereby proving case 1.

Because case 2 assumes that $f(n) = \Theta(n^{\log_b a})$, we have that $f(n/b^j) = \Theta((n/b^j)^{\log_b a})$. Substituting into equation (4.22) yields

$$g(n) = \Theta\left(\sum_{j=0}^{\log_b n-1} a^j\left(\frac{n}{b^j}\right)^{\log_b a}\right) . \tag{4.24}$$

We bound the summation within the Θ-notation as in case 1, but this time we do not obtain a geometric series. Instead, we discover that every term of the summation is the same:

$$\begin{aligned}\sum_{j=0}^{\log_b n-1} a^j\left(\frac{n}{b^j}\right)^{\log_b a} &= n^{\log_b a}\sum_{j=0}^{\log_b n-1}\left(\frac{a}{b^{\log_b a}}\right)^j \\ &= n^{\log_b a}\sum_{j=0}^{\log_b n-1} 1 \\ &= n^{\log_b a}\log_b n .\end{aligned}$$

Substituting this expression for the summation in equation (4.24) yields

$$\begin{aligned}g(n) &= \Theta(n^{\log_b a}\log_b n) \\ &= \Theta(n^{\log_b a}\lg n) ,\end{aligned}$$

proving case 2.

We prove case 3 similarly. Since $f(n)$ appears in the definition (4.22) of $g(n)$ and all terms of $g(n)$ are nonnegative, we can conclude that $g(n) = \Omega(f(n))$ for exact powers of b. We assume in the statement of the lemma that $af(n/b) \le cf(n)$ for some constant $c < 1$ and all sufficiently large n. We rewrite this assumption as $f(n/b) \le (c/a)f(n)$ and iterate j times, yielding $f(n/b^j) \le (c/a)^j f(n)$ or, equivalently, $a^j f(n/b^j) \le c^j f(n)$, where we assume that the values we iterate on are sufficiently large. Since the last, and smallest, such value is n/b^{j-1}, it is enough to assume that n/b^{j-1} is sufficiently large.

Substituting into equation (4.22) and simplifying yields a geometric series, but unlike the series in case 1, this one has decreasing terms. We use an $O(1)$ term to

capture the terms that are not covered by our assumption that n is sufficiently large:

$$\begin{aligned} g(n) &= \sum_{j=0}^{\log_b n-1} a^j f(n/b^j) \\ &\le \sum_{j=0}^{\log_b n-1} c^j f(n) + O(1) \\ &\le f(n) \sum_{j=0}^{\infty} c^j + O(1) \\ &= f(n) \left(\frac{1}{1-c} \right) + O(1) \\ &= O(f(n)) , \end{aligned}$$

since c is a constant. Thus, we can conclude that $g(n) = \Theta(f(n))$ for exact powers of b. With case 3 proved, the proof of the lemma is complete. ■

We can now prove a version of the master theorem for the case in which n is an exact power of b.

Lemma 4.4
Let $a \ge 1$ and $b > 1$ be constants, and let $f(n)$ be a nonnegative function defined on exact powers of b. Define $T(n)$ on exact powers of b by the recurrence

$$T(n) = \begin{cases} \Theta(1) & \text{if } n = 1 , \\ aT(n/b) + f(n) & \text{if } n = b^i , \end{cases}$$

where i is a positive integer. Then $T(n)$ has the following asymptotic bounds for exact powers of b:

1. If $f(n) = O(n^{\log_b a - \epsilon})$ for some constant $\epsilon > 0$, then $T(n) = \Theta(n^{\log_b a})$.
2. If $f(n) = \Theta(n^{\log_b a})$, then $T(n) = \Theta(n^{\log_b a} \lg n)$.
3. If $f(n) = \Omega(n^{\log_b a + \epsilon})$ for some constant $\epsilon > 0$, and if $af(n/b) \le cf(n)$ for some constant $c < 1$ and all sufficiently large n, then $T(n) = \Theta(f(n))$.

Proof We use the bounds in Lemma 4.3 to evaluate the summation (4.21) from Lemma 4.2. For case 1, we have

$$\begin{aligned} T(n) &= \Theta(n^{\log_b a}) + O(n^{\log_b a}) \\ &= \Theta(n^{\log_b a}) , \end{aligned}$$

and for case 2,

$$\begin{aligned} T(n) &= \Theta(n^{\log_b a}) + \Theta(n^{\log_b a} \lg n) \\ &= \Theta(n^{\log_b a} \lg n) \ . \end{aligned}$$

For case 3,

$$\begin{aligned} T(n) &= \Theta(n^{\log_b a}) + \Theta(f(n)) \\ &= \Theta(f(n)) \ , \end{aligned}$$

because $f(n) = \Omega(n^{\log_b a + \epsilon})$. ■

4.6.2 Floors and ceilings

To complete the proof of the master theorem, we must now extend our analysis to the situation in which floors and ceilings appear in the master recurrence, so that the recurrence is defined for all integers, not for just exact powers of b. Obtaining a lower bound on

$$T(n) = aT(\lceil n/b \rceil) + f(n) \tag{4.25}$$

and an upper bound on

$$T(n) = aT(\lfloor n/b \rfloor) + f(n) \tag{4.26}$$

is routine, since we can push through the bound $\lceil n/b \rceil \geq n/b$ in the first case to yield the desired result, and we can push through the bound $\lfloor n/b \rfloor \leq n/b$ in the second case. We use much the same technique to lower-bound the recurrence (4.26) as to upper-bound the recurrence (4.25), and so we shall present only this latter bound.

We modify the recursion tree of Figure 4.7 to produce the recursion tree in Figure 4.8. As we go down in the recursion tree, we obtain a sequence of recursive invocations on the arguments

$$\begin{aligned} &n \ , \\ &\lceil n/b \rceil \ , \\ &\lceil \lceil n/b \rceil /b \rceil \ , \\ &\lceil \lceil \lceil n/b \rceil /b \rceil /b \rceil \ , \\ &\qquad \vdots \end{aligned}$$

Let us denote the jth element in the sequence by n_j, where

$$n_j = \begin{cases} n & \text{if } j = 0 \ , \\ \lceil n_{j-1}/b \rceil & \text{if } j > 0 \ . \end{cases} \tag{4.27}$$

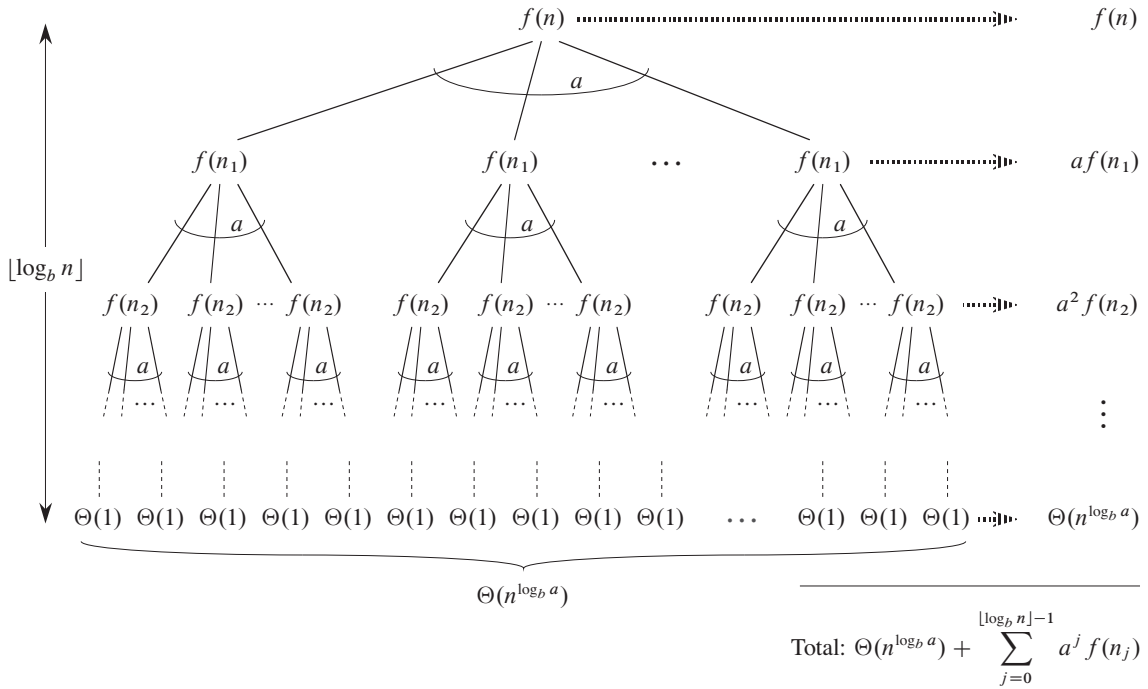


Figure 4.8 The recursion tree generated by $T(n) = aT(\lceil n/b \rceil) + f(n)$. The recursive argument n_j is given by equation (4.27).

Our first goal is to determine the depth k such that n_k is a constant. Using the inequality $\lceil x \rceil \leq x + 1$, we obtain

$$\begin{aligned} n_0 &\leq n \,, \\ n_1 &\leq \frac{n}{b} + 1 \,, \\ n_2 &\leq \frac{n}{b^2} + \frac{1}{b} + 1 \,, \\ n_3 &\leq \frac{n}{b^3} + \frac{1}{b^2} + \frac{1}{b} + 1 \,, \\ &\vdots \end{aligned}$$

In general, we have

$$\begin{aligned} n_j &\le \frac{n}{b^j} + \sum_{i=0}^{j-1} \frac{1}{b^i} \\ &< \frac{n}{b^j} + \sum_{i=0}^{\infty} \frac{1}{b^i} \\ &= \frac{n}{b^j} + \frac{b}{b-1} \,. \end{aligned}$$

Letting $j = \lfloor \log_b n \rfloor$, we obtain

$$\begin{aligned} n_{\lfloor \log_b n \rfloor} &< \frac{n}{b^{\lfloor \log_b n \rfloor}} + \frac{b}{b-1} \\ &< \frac{n}{b^{\log_b n - 1}} + \frac{b}{b-1} \\ &= \frac{n}{n/b} + \frac{b}{b-1} \\ &= b + \frac{b}{b-1} \\ &= O(1) \,, \end{aligned}$$

and thus we see that at depth $\lfloor \log_b n \rfloor$, the problem size is at most a constant.

From Figure 4.8, we see that

$$T(n) = \Theta(n^{\log_b a}) + \sum_{j=0}^{\lfloor \log_b n \rfloor - 1} a^j f(n_j) \,, \tag{4.28}$$

which is much the same as equation (4.21), except that n is an arbitrary integer and not restricted to be an exact power of b.

We can now evaluate the summation

$$g(n) = \sum_{j=0}^{\lfloor \log_b n \rfloor - 1} a^j f(n_j) \tag{4.29}$$

from equation (4.28) in a manner analogous to the proof of Lemma 4.3. Beginning with case 3, if $af(\lceil n/b \rceil) \le cf(n)$ for $n > b + b/(b-1)$, where $c < 1$ is a constant, then it follows that $a^j f(n_j) \le c^j f(n)$. Therefore, we can evaluate the sum in equation (4.29) just as in Lemma 4.3. For case 2, we have $f(n) = \Theta(n^{\log_b a})$. If we can show that $f(n_j) = O(n^{\log_b a}/a^j) = O((n/b^j)^{\log_b a})$, then the proof for case 2 of Lemma 4.3 will go through. Observe that $j \le \lfloor \log_b n \rfloor$ implies $b^j/n \le 1$. The bound $f(n) = O(n^{\log_b a})$ implies that there exists a constant $c > 0$ such that for all sufficiently large n_j,

$$
\begin{aligned}
f(n_j) &\le c\left(\frac{n}{b^j} + \frac{b}{b-1}\right)^{\log_b a} \\
&= c\left(\frac{n}{b^j}\left(1 + \frac{b^j}{n}\cdot\frac{b}{b-1}\right)\right)^{\log_b a} \\
&= c\left(\frac{n^{\log_b a}}{a^j}\right)\left(1 + \left(\frac{b^j}{n}\cdot\frac{b}{b-1}\right)\right)^{\log_b a} \\
&\le c\left(\frac{n^{\log_b a}}{a^j}\right)\left(1 + \frac{b}{b-1}\right)^{\log_b a} \\
&= O\left(\frac{n^{\log_b a}}{a^j}\right) ,
\end{aligned}
$$

since $c(1 + b/(b-1))^{\log_b a}$ is a constant. Thus, we have proved case 2. The proof of case 1 is almost identical. The key is to prove the bound $f(n_j) = O(n^{\log_b a - \epsilon})$, which is similar to the corresponding proof of case 2, though the algebra is more intricate.

We have now proved the upper bounds in the master theorem for all integers n. The proof of the lower bounds is similar.

Exercises

4.6-1 ⋆

Give a simple and exact expression for n_j in equation (4.27) for the case in which b is a positive integer instead of an arbitrary real number.

4.6-2 ⋆

Show that if $f(n) = \Theta(n^{\log_b a} \lg^k n)$, where $k \ge 0$, then the master recurrence has solution $T(n) = \Theta(n^{\log_b a} \lg^{k+1} n)$. For simplicity, confine your analysis to exact powers of b.

4.6-3 ⋆

Show that case 3 of the master theorem is overstated, in the sense that the regularity condition $af(n/b) \le cf(n)$ for some constant $c < 1$ implies that there exists a constant $\epsilon > 0$ such that $f(n) = \Omega(n^{\log_b a + \epsilon})$.

Problems

4-1 Recurrence examples

Give asymptotic upper and lower bounds for $T(n)$ in each of the following recurrences. Assume that $T(n)$ is constant for $n \leq 2$. Make your bounds as tight as possible, and justify your answers.

a. $T(n) = 2T(n/2) + n^4$.

b. $T(n) = T(7n/10) + n$.

c. $T(n) = 16T(n/4) + n^2$.

d. $T(n) = 7T(n/3) + n^2$.

e. $T(n) = 7T(n/2) + n^2$.

f. $T(n) = 2T(n/4) + \sqrt{n}$.

g. $T(n) = T(n-2) + n^2$.

4-2 Parameter-passing costs

Throughout this book, we assume that parameter passing during procedure calls takes constant time, even if an N-element array is being passed. This assumption is valid in most systems because a pointer to the array is passed, not the array itself. This problem examines the implications of three parameter-passing strategies:

1. An array is passed by pointer. Time $= \Theta(1)$.
2. An array is passed by copying. Time $= \Theta(N)$, where N is the size of the array.
3. An array is passed by copying only the subrange that might be accessed by the called procedure. Time $= \Theta(q - p + 1)$ if the subarray $A[p\,..\,q]$ is passed.

a. Consider the recursive binary search algorithm for finding a number in a sorted array (see Exercise 2.3-5). Give recurrences for the worst-case running times of binary search when arrays are passed using each of the three methods above, and give good upper bounds on the solutions of the recurrences. Let N be the size of the original problem and n be the size of a subproblem.

b. Redo part (a) for the MERGE-SORT algorithm from Section 2.3.1.

4-3 More recurrence examples

Give asymptotic upper and lower bounds for $T(n)$ in each of the following recurrences. Assume that $T(n)$ is constant for sufficiently small n. Make your bounds as tight as possible, and justify your answers.

a. $T(n) = 4T(n/3) + n \lg n$.

b. $T(n) = 3T(n/3) + n/\lg n$.

c. $T(n) = 4T(n/2) + n^2\sqrt{n}$.

d. $T(n) = 3T(n/3 - 2) + n/2$.

e. $T(n) = 2T(n/2) + n/\lg n$.

f. $T(n) = T(n/2) + T(n/4) + T(n/8) + n$.

g. $T(n) = T(n-1) + 1/n$.

h. $T(n) = T(n-1) + \lg n$.

i. $T(n) = T(n-2) + 1/\lg n$.

j. $T(n) = \sqrt{n}T(\sqrt{n}) + n$.

4-4 Fibonacci numbers

This problem develops properties of the Fibonacci numbers, which are defined by recurrence (3.22). We shall use the technique of generating functions to solve the Fibonacci recurrence. Define the ***generating function*** (or ***formal power series***) $\mathcal{F}$ as

$$\begin{aligned}\mathcal{F}(z) &= \sum_{i=0}^{\infty} F_i z^i \\ &= 0 + z + z^2 + 2z^3 + 3z^4 + 5z^5 + 8z^6 + 13z^7 + 21z^8 + \cdots ,\end{aligned}$$

where F_i is the ith Fibonacci number.

a. Show that $\mathcal{F}(z) = z + z\mathcal{F}(z) + z^2\mathcal{F}(z)$.

b. Show that

$$\begin{aligned}\mathcal{F}(z) &= \frac{z}{1-z-z^2} \\ &= \frac{z}{(1-\phi z)(1-\hat{\phi}z)} \\ &= \frac{1}{\sqrt{5}}\left(\frac{1}{1-\phi z} - \frac{1}{1-\hat{\phi}z}\right) ,\end{aligned}$$

where

$$\phi = \frac{1+\sqrt{5}}{2} = 1.61803\ldots$$

and

$$\hat{\phi} = \frac{1-\sqrt{5}}{2} = -0.61803\ldots .$$

c. Show that

$$\mathcal{F}(z) = \sum_{i=0}^{\infty} \frac{1}{\sqrt{5}}(\phi^i - \hat{\phi}^i)z^i .$$

d. Use part (c) to prove that $F_i = \phi^i/\sqrt{5}$ for $i > 0$, rounded to the nearest integer. (*Hint:* Observe that $|\hat{\phi}| < 1$.)

4-5 Chip testing

Professor Diogenes has n supposedly identical integrated-circuit chips that in principle are capable of testing each other. The professor's test jig accommodates two chips at a time. When the jig is loaded, each chip tests the other and reports whether it is good or bad. A good chip always reports accurately whether the other chip is good or bad, but the professor cannot trust the answer of a bad chip. Thus, the four possible outcomes of a test are as follows:

Chip A says	Chip B says	Conclusion
B is good	A is good	both are good, or both are bad
B is good	A is bad	at least one is bad
B is bad	A is good	at least one is bad
B is bad	A is bad	at least one is bad

a. Show that if more than $n/2$ chips are bad, the professor cannot necessarily determine which chips are good using any strategy based on this kind of pairwise test. Assume that the bad chips can conspire to fool the professor.

b. Consider the problem of finding a single good chip from among n chips, assuming that more than $n/2$ of the chips are good. Show that $\lfloor n/2 \rfloor$ pairwise tests are sufficient to reduce the problem to one of nearly half the size.

c. Show that the good chips can be identified with $\Theta(n)$ pairwise tests, assuming that more than $n/2$ of the chips are good. Give and solve the recurrence that describes the number of tests.

4-6 Monge arrays

An $m \times n$ array A of real numbers is a ***Monge array*** if for all i, j, k, and l such that $1 \le i < k \le m$ and $1 \le j < l \le n$, we have

$$A[i, j] + A[k, l] \le A[i, l] + A[k, j] .$$

In other words, whenever we pick two rows and two columns of a Monge array and consider the four elements at the intersections of the rows and the columns, the sum of the upper-left and lower-right elements is less than or equal to the sum of the lower-left and upper-right elements. For example, the following array is Monge:

10	17	13	28	23
17	22	16	29	23
24	28	22	34	24
11	13	6	17	7
45	44	32	37	23
36	33	19	21	6
75	66	51	53	34

a. Prove that an array is Monge if and only if for all $i = 1, 2, ..., m - 1$ and $j = 1, 2, ..., n - 1$, we have

$$A[i, j] + A[i + 1, j + 1] \le A[i, j + 1] + A[i + 1, j] .$$

(*Hint:* For the "if" part, use induction separately on rows and columns.)

b. The following array is not Monge. Change one element in order to make it Monge. (*Hint:* Use part (a).)

37	23	22	32
21	6	7	10
53	34	30	31
32	13	9	6
43	21	15	8

c. Let $f(i)$ be the index of the column containing the leftmost minimum element of row i. Prove that $f(1) \leq f(2) \leq \cdots \leq f(m)$ for any $m \times n$ Monge array.

d. Here is a description of a divide-and-conquer algorithm that computes the leftmost minimum element in each row of an $m \times n$ Monge array A:

> Construct a submatrix A' of A consisting of the even-numbered rows of A. Recursively determine the leftmost minimum for each row of A'. Then compute the leftmost minimum in the odd-numbered rows of A.

Explain how to compute the leftmost minimum in the odd-numbered rows of A (given that the leftmost minimum of the even-numbered rows is known) in $O(m + n)$ time.

e. Write the recurrence describing the running time of the algorithm described in part (d). Show that its solution is $O(m + n \log m)$.

Chapter notes

Divide-and-conquer as a technique for designing algorithms dates back to at least 1962 in an article by Karatsuba and Ofman [194]. It might have been used well before then, however; according to Heideman, Johnson, and Burrus [163], C. F. Gauss devised the first fast Fourier transform algorithm in 1805, and Gauss's formulation breaks the problem into smaller subproblems whose solutions are combined.

The maximum-subarray problem in Section 4.1 is a minor variation on a problem studied by Bentley [43, Chapter 7].

Strassen's algorithm [325] caused much excitement when it was published in 1969. Before then, few imagined the possibility of an algorithm asymptotically faster than the basic SQUARE-MATRIX-MULTIPLY procedure. The asymptotic upper bound for matrix multiplication has been improved since then. The most asymptotically efficient algorithm for multiplying $n \times n$ matrices to date, due to Coppersmith and Winograd [78], has a running time of $O(n^{2.376})$. The best lower bound known is just the obvious $\Omega(n^2)$ bound (obvious because we must fill in n^2 elements of the product matrix).

From a practical point of view, Strassen's algorithm is often not the method of choice for matrix multiplication, for four reasons:

1. The constant factor hidden in the $\Theta(n^{\lg 7})$ running time of Strassen's algorithm is larger than the constant factor in the $\Theta(n^3)$-time SQUARE-MATRIX-MULTIPLY procedure.
2. When the matrices are sparse, methods tailored for sparse matrices are faster.

3. Strassen's algorithm is not quite as numerically stable as SQUARE-MATRIX-MULTIPLY. In other words, because of the limited precision of computer arithmetic on noninteger values, larger errors accumulate in Strassen's algorithm than in SQUARE-MATRIX-MULTIPLY.
4. The submatrices formed at the levels of recursion consume space.

The latter two reasons were mitigated around 1990. Higham [167] demonstrated that the difference in numerical stability had been overemphasized; although Strassen's algorithm is too numerically unstable for some applications, it is within acceptable limits for others. Bailey, Lee, and Simon [32] discuss techniques for reducing the memory requirements for Strassen's algorithm.

In practice, fast matrix-multiplication implementations for dense matrices use Strassen's algorithm for matrix sizes above a "crossover point," and they switch to a simpler method once the subproblem size reduces to below the crossover point. The exact value of the crossover point is highly system dependent. Analyses that count operations but ignore effects from caches and pipelining have produced crossover points as low as $n = 8$ (by Higham [167]) or $n = 12$ (by Huss-Lederman et al. [186]). D'Alberto and Nicolau [81] developed an adaptive scheme, which determines the crossover point by benchmarking when their software package is installed. They found crossover points on various systems ranging from $n = 400$ to $n = 2150$, and they could not find a crossover point on a couple of systems.

Recurrences were studied as early as 1202 by L. Fibonacci, for whom the Fibonacci numbers are named. A. De Moivre introduced the method of generating functions (see Problem 4-4) for solving recurrences. The master method is adapted from Bentley, Haken, and Saxe [44], which provides the extended method justified by Exercise 4.6-2. Knuth [209] and Liu [237] show how to solve linear recurrences using the method of generating functions. Purdom and Brown [287] and Graham, Knuth, and Patashnik [152] contain extended discussions of recurrence solving.

Several researchers, including Akra and Bazzi [13], Roura [299], Verma [346], and Yap [360], have given methods for solving more general divide-and-conquer recurrences than are solved by the master method. We describe the result of Akra and Bazzi here, as modified by Leighton [228]. The Akra-Bazzi method works for recurrences of the form

$$T(x) = \begin{cases} \Theta(1) & \text{if } 1 \le x \le x_0 \,, \\ \sum_{i=1}^{k} a_i T(b_i x) + f(x) & \text{if } x > x_0 \,, \end{cases} \tag{4.30}$$

where

- $x \ge 1$ is a real number,
- x_0 is a constant such that $x_0 \ge 1/b_i$ and $x_0 \ge 1/(1 - b_i)$ for $i = 1, 2, \ldots, k$,
- a_i is a positive constant for $i = 1, 2, \ldots, k$,

- b_i is a constant in the range $0 < b_i < 1$ for $i = 1, 2, \ldots, k$,
- $k \geq 1$ is an integer constant, and
- $f(x)$ is a nonnegative function that satisfies the ***polynomial-growth condition***: there exist positive constants c_1 and c_2 such that for all $x \geq 1$, for $i = 1, 2, \ldots, k$, and for all u such that $b_i x \leq u \leq x$, we have $c_1 f(x) \leq f(u) \leq c_2 f(x)$. (If $|f'(x)|$ is upper-bounded by some polynomial in x, then $f(x)$ satisfies the polynomial-growth condition. For example, $f(x) = x^\alpha \lg^\beta x$ satisfies this condition for any real constants α and β.)

Although the master method does not apply to a recurrence such as $T(n) = T(\lfloor n/3 \rfloor) + T(\lfloor 2n/3 \rfloor) + O(n)$, the Akra-Bazzi method does. To solve the recurrence (4.30), we first find the unique real number p such that $\sum_{i=1}^{k} a_i b_i^p = 1$. (Such a p always exists.) The solution to the recurrence is then

$$T(n) = \Theta\left(x^p \left(1 + \int_1^x \frac{f(u)}{u^{p+1}}\, du\right)\right) .$$

The Akra-Bazzi method can be somewhat difficult to use, but it serves in solving recurrences that model division of the problem into substantially unequally sized subproblems. The master method is simpler to use, but it applies only when subproblem sizes are equal.

5 Probabilistic Analysis and Randomized Algorithms

This chapter introduces probabilistic analysis and randomized algorithms. If you are unfamiliar with the basics of probability theory, you should read Appendix C, which reviews this material. We shall revisit probabilistic analysis and randomized algorithms several times throughout this book.

5.1 The hiring problem

Suppose that you need to hire a new office assistant. Your previous attempts at hiring have been unsuccessful, and you decide to use an employment agency. The employment agency sends you one candidate each day. You interview that person and then decide either to hire that person or not. You must pay the employment agency a small fee to interview an applicant. To actually hire an applicant is more costly, however, since you must fire your current office assistant and pay a substantial hiring fee to the employment agency. You are committed to having, at all times, the best possible person for the job. Therefore, you decide that, after interviewing each applicant, if that applicant is better qualified than the current office assistant, you will fire the current office assistant and hire the new applicant. You are willing to pay the resulting price of this strategy, but you wish to estimate what that price will be.

The procedure HIRE-ASSISTANT, given below, expresses this strategy for hiring in pseudocode. It assumes that the candidates for the office assistant job are numbered 1 through n. The procedure assumes that you are able to, after interviewing candidate i, determine whether candidate i is the best candidate you have seen so far. To initialize, the procedure creates a dummy candidate, numbered 0, who is less qualified than each of the other candidates.

```
HIRE-ASSISTANT(n)
1  best = 0          // candidate 0 is a least-qualified dummy candidate
2  for i = 1 to n
3      interview candidate i
4      if candidate i is better than candidate best
5          best = i
6          hire candidate i
```

The cost model for this problem differs from the model described in Chapter 2. We focus not on the running time of HIRE-ASSISTANT, but instead on the costs incurred by interviewing and hiring. On the surface, analyzing the cost of this algorithm may seem very different from analyzing the running time of, say, merge sort. The analytical techniques used, however, are identical whether we are analyzing cost or running time. In either case, we are counting the number of times certain basic operations are executed.

Interviewing has a low cost, say c_i, whereas hiring is expensive, costing c_h. Letting m be the number of people hired, the total cost associated with this algorithm is $O(c_i n + c_h m)$. No matter how many people we hire, we always interview n candidates and thus always incur the cost $c_i n$ associated with interviewing. We therefore concentrate on analyzing $c_h m$, the hiring cost. This quantity varies with each run of the algorithm.

This scenario serves as a model for a common computational paradigm. We often need to find the maximum or minimum value in a sequence by examining each element of the sequence and maintaining a current "winner." The hiring problem models how often we update our notion of which element is currently winning.

Worst-case analysis

In the worst case, we actually hire every candidate that we interview. This situation occurs if the candidates come in strictly increasing order of quality, in which case we hire n times, for a total hiring cost of $O(c_h n)$.

Of course, the candidates do not always come in increasing order of quality. In fact, we have no idea about the order in which they arrive, nor do we have any control over this order. Therefore, it is natural to ask what we expect to happen in a typical or average case.

Probabilistic analysis

Probabilistic analysis is the use of probability in the analysis of problems. Most commonly, we use probabilistic analysis to analyze the running time of an algorithm. Sometimes we use it to analyze other quantities, such as the hiring cost

in procedure HIRE-ASSISTANT. In order to perform a probabilistic analysis, we must use knowledge of, or make assumptions about, the distribution of the inputs. Then we analyze our algorithm, computing an average-case running time, where we take the average over the distribution of the possible inputs. Thus we are, in effect, averaging the running time over all possible inputs. When reporting such a running time, we will refer to it as the ***average-case running time***.

We must be very careful in deciding on the distribution of inputs. For some problems, we may reasonably assume something about the set of all possible inputs, and then we can use probabilistic analysis as a technique for designing an efficient algorithm and as a means for gaining insight into a problem. For other problems, we cannot describe a reasonable input distribution, and in these cases we cannot use probabilistic analysis.

For the hiring problem, we can assume that the applicants come in a random order. What does that mean for this problem? We assume that we can compare any two candidates and decide which one is better qualified; that is, there is a total order on the candidates. (See Appendix B for the definition of a total order.) Thus, we can rank each candidate with a unique number from 1 through n, using $rank(i)$ to denote the rank of applicant i, and adopt the convention that a higher rank corresponds to a better qualified applicant. The ordered list $\langle rank(1), rank(2), \ldots, rank(n)\rangle$ is a permutation of the list $\langle 1, 2, \ldots, n\rangle$. Saying that the applicants come in a random order is equivalent to saying that this list of ranks is equally likely to be any one of the $n!$ permutations of the numbers 1 through n. Alternatively, we say that the ranks form a ***uniform random permutation***; that is, each of the possible $n!$ permutations appears with equal probability.

Section 5.2 contains a probabilistic analysis of the hiring problem.

Randomized algorithms

In order to use probabilistic analysis, we need to know something about the distribution of the inputs. In many cases, we know very little about the input distribution. Even if we do know something about the distribution, we may not be able to model this knowledge computationally. Yet we often can use probability and randomness as a tool for algorithm design and analysis, by making the behavior of part of the algorithm random.

In the hiring problem, it may seem as if the candidates are being presented to us in a random order, but we have no way of knowing whether or not they really are. Thus, in order to develop a randomized algorithm for the hiring problem, we must have greater control over the order in which we interview the candidates. We will, therefore, change the model slightly. We say that the employment agency has n candidates, and they send us a list of the candidates in advance. On each day, we choose, randomly, which candidate to interview. Although we know nothing about

the candidates (besides their names), we have made a significant change. Instead of relying on a guess that the candidates come to us in a random order, we have instead gained control of the process and enforced a random order.

More generally, we call an algorithm ***randomized*** if its behavior is determined not only by its input but also by values produced by a ***random-number generator***. We shall assume that we have at our disposal a random-number generator RANDOM. A call to RANDOM(a, b) returns an integer between a and b, inclusive, with each such integer being equally likely. For example, RANDOM$(0, 1)$ produces 0 with probability $1/2$, and it produces 1 with probability $1/2$. A call to RANDOM$(3, 7)$ returns either 3, 4, 5, 6, or 7, each with probability $1/5$. Each integer returned by RANDOM is independent of the integers returned on previous calls. You may imagine RANDOM as rolling a $(b - a + 1)$-sided die to obtain its output. (In practice, most programming environments offer a ***pseudorandom-number generator***: a deterministic algorithm returning numbers that "look" statistically random.)

When analyzing the running time of a randomized algorithm, we take the expectation of the running time over the distribution of values returned by the random number generator. We distinguish these algorithms from those in which the input is random by referring to the running time of a randomized algorithm as an ***expected running time***. In general, we discuss the average-case running time when the probability distribution is over the inputs to the algorithm, and we discuss the expected running time when the algorithm itself makes random choices.

Exercises

5.1-1

Show that the assumption that we are always able to determine which candidate is best, in line 4 of procedure HIRE-ASSISTANT, implies that we know a total order on the ranks of the candidates.

5.1-2 ⋆

Describe an implementation of the procedure RANDOM(a, b) that only makes calls to RANDOM$(0, 1)$. What is the expected running time of your procedure, as a function of a and b?

5.1-3 ⋆

Suppose that you want to output 0 with probability $1/2$ and 1 with probability $1/2$. At your disposal is a procedure BIASED-RANDOM, that outputs either 0 or 1. It outputs 1 with some probability p and 0 with probability $1 - p$, where $0 < p < 1$, but you do not know what p is. Give an algorithm that uses BIASED-RANDOM as a subroutine, and returns an unbiased answer, returning 0 with probability $1/2$

and 1 with probability $1/2$. What is the expected running time of your algorithm as a function of p?

5.2 Indicator random variables

In order to analyze many algorithms, including the hiring problem, we use indicator random variables. Indicator random variables provide a convenient method for converting between probabilities and expectations. Suppose we are given a sample space S and an event A. Then the ***indicator random variable*** $\mathrm{I}\{A\}$ associated with event A is defined as

$$\mathrm{I}\{A\} = \begin{cases} 1 & \text{if } A \text{ occurs ,} \\ 0 & \text{if } A \text{ does not occur .} \end{cases} \tag{5.1}$$

As a simple example, let us determine the expected number of heads that we obtain when flipping a fair coin. Our sample space is $S = \{H, T\}$, with $\Pr\{H\} = \Pr\{T\} = 1/2$. We can then define an indicator random variable X_H, associated with the coin coming up heads, which is the event H. This variable counts the number of heads obtained in this flip, and it is 1 if the coin comes up heads and 0 otherwise. We write

$$\begin{aligned} X_H &= \mathrm{I}\{H\} \\ &= \begin{cases} 1 & \text{if } H \text{ occurs ,} \\ 0 & \text{if } T \text{ occurs .} \end{cases} \end{aligned}$$

The expected number of heads obtained in one flip of the coin is simply the expected value of our indicator variable X_H:

$$\begin{aligned} \mathrm{E}[X_H] &= \mathrm{E}[\mathrm{I}\{H\}] \\ &= 1 \cdot \Pr\{H\} + 0 \cdot \Pr\{T\} \\ &= 1 \cdot (1/2) + 0 \cdot (1/2) \\ &= 1/2 . \end{aligned}$$

Thus the expected number of heads obtained by one flip of a fair coin is $1/2$. As the following lemma shows, the expected value of an indicator random variable associated with an event A is equal to the probability that A occurs.

Lemma 5.1
Given a sample space S and an event A in the sample space S, let $X_A = \mathrm{I}\{A\}$. Then $\mathrm{E}[X_A] = \Pr\{A\}$.

Proof By the definition of an indicator random variable from equation (5.1) and the definition of expected value, we have

$$\begin{aligned} \mathrm{E}[X_A] &= \mathrm{E}[\mathrm{I}\{A\}] \\ &= 1 \cdot \Pr\{A\} + 0 \cdot \Pr\{\overline{A}\} \\ &= \Pr\{A\} \ , \end{aligned}$$

where $\overline{A}$ denotes $S - A$, the complement of A. ■

Although indicator random variables may seem cumbersome for an application such as counting the expected number of heads on a flip of a single coin, they are useful for analyzing situations in which we perform repeated random trials. For example, indicator random variables give us a simple way to arrive at the result of equation (C.37). In this equation, we compute the number of heads in n coin flips by considering separately the probability of obtaining 0 heads, 1 head, 2 heads, etc. The simpler method proposed in equation (C.38) instead uses indicator random variables implicitly. Making this argument more explicit, we let X_i be the indicator random variable associated with the event in which the ith flip comes up heads: $X_i = \mathrm{I}\{\text{the } i\text{th flip results in the event } H\}$. Let X be the random variable denoting the total number of heads in the n coin flips, so that

$$X = \sum_{i=1}^{n} X_i \ .$$

We wish to compute the expected number of heads, and so we take the expectation of both sides of the above equation to obtain

$$\mathrm{E}[X] = \mathrm{E}\left[\sum_{i=1}^{n} X_i\right] \ .$$

The above equation gives the expectation of the sum of n indicator random variables. By Lemma 5.1, we can easily compute the expectation of each of the random variables. By equation (C.21)—linearity of expectation—it is easy to compute the expectation of the sum: it equals the sum of the expectations of the n random variables. Linearity of expectation makes the use of indicator random variables a powerful analytical technique; it applies even when there is dependence among the random variables. We now can easily compute the expected number of heads:

$$\begin{aligned}
\mathrm{E}[X] &= \mathrm{E}\left[\sum_{i=1}^{n} X_i\right] \\
&= \sum_{i=1}^{n} \mathrm{E}[X_i] \\
&= \sum_{i=1}^{n} 1/2 \\
&= n/2 \,.
\end{aligned}$$

Thus, compared to the method used in equation (C.37), indicator random variables greatly simplify the calculation. We shall use indicator random variables throughout this book.

Analysis of the hiring problem using indicator random variables

Returning to the hiring problem, we now wish to compute the expected number of times that we hire a new office assistant. In order to use a probabilistic analysis, we assume that the candidates arrive in a random order, as discussed in the previous section. (We shall see in Section 5.3 how to remove this assumption.) Let X be the random variable whose value equals the number of times we hire a new office assistant. We could then apply the definition of expected value from equation (C.20) to obtain

$$\mathrm{E}[X] = \sum_{x=1}^{n} x \Pr\{X = x\} \,,$$

but this calculation would be cumbersome. We shall instead use indicator random variables to greatly simplify the calculation.

To use indicator random variables, instead of computing $\mathrm{E}[X]$ by defining one variable associated with the number of times we hire a new office assistant, we define n variables related to whether or not each particular candidate is hired. In particular, we let X_i be the indicator random variable associated with the event in which the ith candidate is hired. Thus,

$$\begin{aligned}
X_i &= \mathrm{I}\{\text{candidate } i \text{ is hired}\} \\
&= \begin{cases} 1 & \text{if candidate } i \text{ is hired} \,, \\ 0 & \text{if candidate } i \text{ is not hired} \,, \end{cases}
\end{aligned}$$

and

$$X = X_1 + X_2 + \cdots + X_n \,. \tag{5.2}$$

By Lemma 5.1, we have that

$$\mathrm{E}[X_i] = \Pr\{\text{candidate } i \text{ is hired}\} ,$$

and we must therefore compute the probability that lines 5–6 of HIRE-ASSISTANT are executed.

Candidate i is hired, in line 6, exactly when candidate i is better than each of candidates 1 through $i-1$. Because we have assumed that the candidates arrive in a random order, the first i candidates have appeared in a random order. Any one of these first i candidates is equally likely to be the best-qualified so far. Candidate i has a probability of $1/i$ of being better qualified than candidates 1 through $i-1$ and thus a probability of $1/i$ of being hired. By Lemma 5.1, we conclude that

$$\mathrm{E}[X_i] = 1/i . \tag{5.3}$$

Now we can compute $\mathrm{E}[X]$:

$$\begin{aligned}
\mathrm{E}[X] &= \mathrm{E}\left[\sum_{i=1}^{n} X_i\right] && \text{(by equation (5.2))} \qquad (5.4)\\
&= \sum_{i=1}^{n} \mathrm{E}[X_i] && \text{(by linearity of expectation)}\\
&= \sum_{i=1}^{n} 1/i && \text{(by equation (5.3))}\\
&= \ln n + O(1) && \text{(by equation (A.7))} . \qquad (5.5)
\end{aligned}$$

Even though we interview n people, we actually hire only approximately $\ln n$ of them, on average. We summarize this result in the following lemma.

Lemma 5.2
Assuming that the candidates are presented in a random order, algorithm HIRE-ASSISTANT has an average-case total hiring cost of $O(c_h \ln n)$.

Proof The bound follows immediately from our definition of the hiring cost and equation (5.5), which shows that the expected number of hires is approximately $\ln n$. ■

The average-case hiring cost is a significant improvement over the worst-case hiring cost of $O(c_h n)$.

Exercises

5.2-1
In HIRE-ASSISTANT, assuming that the candidates are presented in a random order, what is the probability that you hire exactly one time? What is the probability that you hire exactly n times?

5.2-2
In HIRE-ASSISTANT, assuming that the candidates are presented in a random order, what is the probability that you hire exactly twice?

5.2-3
Use indicator random variables to compute the expected value of the sum of n dice.

5.2-4
Use indicator random variables to solve the following problem, which is known as the ***hat-check problem***. Each of n customers gives a hat to a hat-check person at a restaurant. The hat-check person gives the hats back to the customers in a random order. What is the expected number of customers who get back their own hat?

5.2-5
Let $A[1..n]$ be an array of n distinct numbers. If $i < j$ and $A[i] > A[j]$, then the pair (i, j) is called an ***inversion*** of A. (See Problem 2-4 for more on inversions.) Suppose that the elements of A form a uniform random permutation of $\langle 1, 2, \ldots, n \rangle$. Use indicator random variables to compute the expected number of inversions.

5.3 Randomized algorithms

In the previous section, we showed how knowing a distribution on the inputs can help us to analyze the average-case behavior of an algorithm. Many times, we do not have such knowledge, thus precluding an average-case analysis. As mentioned in Section 5.1, we may be able to use a randomized algorithm.

For a problem such as the hiring problem, in which it is helpful to assume that all permutations of the input are equally likely, a probabilistic analysis can guide the development of a randomized algorithm. Instead of assuming a distribution of inputs, we impose a distribution. In particular, before running the algorithm, we randomly permute the candidates in order to enforce the property that every permutation is equally likely. Although we have modified the algorithm, we still expect to hire a new office assistant approximately $\ln n$ times. But now we expect

this to be the case for *any* input, rather than for inputs drawn from a particular distribution.

Let us further explore the distinction between probabilistic analysis and randomized algorithms. In Section 5.2, we claimed that, assuming that the candidates arrive in a random order, the expected number of times we hire a new office assistant is about $\ln n$. Note that the algorithm here is deterministic; for any particular input, the number of times a new office assistant is hired is always the same. Furthermore, the number of times we hire a new office assistant differs for different inputs, and it depends on the ranks of the various candidates. Since this number depends only on the ranks of the candidates, we can represent a particular input by listing, in order, the ranks of the candidates, i.e., $\langle rank(1), rank(2), \ldots, rank(n)\rangle$. Given the rank list $A_1 = \langle 1, 2, 3, 4, 5, 6, 7, 8, 9, 10\rangle$, a new office assistant is always hired 10 times, since each successive candidate is better than the previous one, and lines 5–6 are executed in each iteration. Given the list of ranks $A_2 = \langle 10, 9, 8, 7, 6, 5, 4, 3, 2, 1\rangle$, a new office assistant is hired only once, in the first iteration. Given a list of ranks $A_3 = \langle 5, 2, 1, 8, 4, 7, 10, 9, 3, 6\rangle$, a new office assistant is hired three times, upon interviewing the candidates with ranks 5, 8, and 10. Recalling that the cost of our algorithm depends on how many times we hire a new office assistant, we see that there are expensive inputs such as A_1, inexpensive inputs such as A_2, and moderately expensive inputs such as A_3.

Consider, on the other hand, the randomized algorithm that first permutes the candidates and then determines the best candidate. In this case, we randomize in the algorithm, not in the input distribution. Given a particular input, say A_3 above, we cannot say how many times the maximum is updated, because this quantity differs with each run of the algorithm. The first time we run the algorithm on A_3, it may produce the permutation A_1 and perform 10 updates; but the second time we run the algorithm, we may produce the permutation A_2 and perform only one update. The third time we run it, we may perform some other number of updates. Each time we run the algorithm, the execution depends on the random choices made and is likely to differ from the previous execution of the algorithm. For this algorithm and many other randomized algorithms, *no particular input elicits its worst-case behavior*. Even your worst enemy cannot produce a bad input array, since the random permutation makes the input order irrelevant. The randomized algorithm performs badly only if the random-number generator produces an "unlucky" permutation.

For the hiring problem, the only change needed in the code is to randomly permute the array.

```
RANDOMIZED-HIRE-ASSISTANT(n)
1  randomly permute the list of candidates
2  best = 0            // candidate 0 is a least-qualified dummy candidate
3  for i = 1 to n
4      interview candidate i
5      if candidate i is better than candidate best
6          best = i
7          hire candidate i
```

With this simple change, we have created a randomized algorithm whose performance matches that obtained by assuming that the candidates were presented in a random order.

Lemma 5.3
The expected hiring cost of the procedure RANDOMIZED-HIRE-ASSISTANT is $O(c_h \ln n)$.

Proof After permuting the input array, we have achieved a situation identical to that of the probabilistic analysis of HIRE-ASSISTANT. ■

Comparing Lemmas 5.2 and 5.3 highlights the difference between probabilistic analysis and randomized algorithms. In Lemma 5.2, we make an assumption about the input. In Lemma 5.3, we make no such assumption, although randomizing the input takes some additional time. To remain consistent with our terminology, we couched Lemma 5.2 in terms of the average-case hiring cost and Lemma 5.3 in terms of the expected hiring cost. In the remainder of this section, we discuss some issues involved in randomly permuting inputs.

Randomly permuting arrays

Many randomized algorithms randomize the input by permuting the given input array. (There are other ways to use randomization.) Here, we shall discuss two methods for doing so. We assume that we are given an array A which, without loss of generality, contains the elements 1 through n. Our goal is to produce a random permutation of the array.

One common method is to assign each element $A[i]$ of the array a random priority $P[i]$, and then sort the elements of A according to these priorities. For example, if our initial array is $A = \langle 1, 2, 3, 4 \rangle$ and we choose random priorities $P = \langle 36, 3, 62, 19 \rangle$, we would produce an array $B = \langle 2, 4, 1, 3 \rangle$, since the second priority is the smallest, followed by the fourth, then the first, and finally the third. We call this procedure PERMUTE-BY-SORTING:

PERMUTE-BY-SORTING(A)

```
1  n = A.length
2  let P[1..n] be a new array
3  for i = 1 to n
4      P[i] = RANDOM(1, n^3)
5  sort A, using P as sort keys
```

Line 4 chooses a random number between 1 and n^3. We use a range of 1 to n^3 to make it likely that all the priorities in P are unique. (Exercise 5.3-5 asks you to prove that the probability that all entries are unique is at least $1 - 1/n$, and Exercise 5.3-6 asks how to implement the algorithm even if two or more priorities are identical.) Let us assume that all the priorities are unique.

The time-consuming step in this procedure is the sorting in line 5. As we shall see in Chapter 8, if we use a comparison sort, sorting takes $\Omega(n \lg n)$ time. We can achieve this lower bound, since we have seen that merge sort takes $\Theta(n \lg n)$ time. (We shall see other comparison sorts that take $\Theta(n \lg n)$ time in Part II. Exercise 8.3-4 asks you to solve the very similar problem of sorting numbers in the range 0 to $n^3 - 1$ in $O(n)$ time.) After sorting, if $P[i]$ is the jth smallest priority, then $A[i]$ lies in position j of the output. In this manner we obtain a permutation. It remains to prove that the procedure produces a ***uniform random permutation***, that is, that the procedure is equally likely to produce every permutation of the numbers 1 through n.

Lemma 5.4
Procedure PERMUTE-BY-SORTING produces a uniform random permutation of the input, assuming that all priorities are distinct.

Proof We start by considering the particular permutation in which each element $A[i]$ receives the ith smallest priority. We shall show that this permutation occurs with probability exactly $1/n!$. For $i = 1, 2, \ldots, n$, let E_i be the event that element $A[i]$ receives the ith smallest priority. Then we wish to compute the probability that for all i, event E_i occurs, which is

$$\Pr\{E_1 \cap E_2 \cap E_3 \cap \cdots \cap E_{n-1} \cap E_n\} \ .$$

Using Exercise C.2-5, this probability is equal to

$$\Pr\{E_1\} \cdot \Pr\{E_2 \mid E_1\} \cdot \Pr\{E_3 \mid E_2 \cap E_1\} \cdot \Pr\{E_4 \mid E_3 \cap E_2 \cap E_1\}$$
$$\cdots \Pr\{E_i \mid E_{i-1} \cap E_{i-2} \cap \cdots \cap E_1\} \cdots \Pr\{E_n \mid E_{n-1} \cap \cdots \cap E_1\} \ .$$

We have that $\Pr\{E_1\} = 1/n$ because it is the probability that one priority chosen randomly out of a set of n is the smallest priority. Next, we observe

that $\Pr\{E_2 \mid E_1\} = 1/(n-1)$ because given that element $A[1]$ has the smallest priority, each of the remaining $n-1$ elements has an equal chance of having the second smallest priority. In general, for $i = 2, 3, \ldots, n$, we have that $\Pr\{E_i \mid E_{i-1} \cap E_{i-2} \cap \cdots \cap E_1\} = 1/(n-i+1)$, since, given that elements $A[1]$ through $A[i-1]$ have the $i-1$ smallest priorities (in order), each of the remaining $n-(i-1)$ elements has an equal chance of having the ith smallest priority. Thus, we have

$$\begin{aligned}\Pr\{E_1 \cap E_2 \cap E_3 \cap \cdots \cap E_{n-1} \cap E_n\} &= \left(\frac{1}{n}\right)\left(\frac{1}{n-1}\right)\cdots\left(\frac{1}{2}\right)\left(\frac{1}{1}\right) \\ &= \frac{1}{n!}\,,\end{aligned}$$

and we have shown that the probability of obtaining the identity permutation is $1/n!$.

We can extend this proof to work for any permutation of priorities. Consider any fixed permutation $\sigma = \langle\sigma(1), \sigma(2), \ldots, \sigma(n)\rangle$ of the set $\{1, 2, \ldots, n\}$. Let us denote by r_i the rank of the priority assigned to element $A[i]$, where the element with the jth smallest priority has rank j. If we define E_i as the event in which element $A[i]$ receives the $\sigma(i)$th smallest priority, or $r_i = \sigma(i)$, the same proof still applies. Therefore, if we calculate the probability of obtaining any particular permutation, the calculation is identical to the one above, so that the probability of obtaining this permutation is also $1/n!$. ■

You might think that to prove that a permutation is a uniform random permutation, it suffices to show that, for each element $A[i]$, the probability that the element winds up in position j is $1/n$. Exercise 5.3-4 shows that this weaker condition is, in fact, insufficient.

A better method for generating a random permutation is to permute the given array in place. The procedure RANDOMIZE-IN-PLACE does so in $O(n)$ time. In its ith iteration, it chooses the element $A[i]$ randomly from among elements $A[i]$ through $A[n]$. Subsequent to the ith iteration, $A[i]$ is never altered.

```
RANDOMIZE-IN-PLACE(A)
1  n = A.length
2  for i = 1 to n
3      swap A[i] with A[RANDOM(i, n)]
```

We shall use a loop invariant to show that procedure RANDOMIZE-IN-PLACE produces a uniform random permutation. A ***k-permutation*** on a set of n elements is a sequence containing k of the n elements, with no repetitions. (See Appendix C.) There are $n!/(n-k)!$ such possible k-permutations.

Lemma 5.5
Procedure RANDOMIZE-IN-PLACE computes a uniform random permutation.

Proof We use the following loop invariant:

> Just prior to the ith iteration of the **for** loop of lines 2–3, for each possible $(i-1)$-permutation of the n elements, the subarray $A[1\,..\,i-1]$ contains this $(i-1)$-permutation with probability $(n-i+1)!/n!$.

We need to show that this invariant is true prior to the first loop iteration, that each iteration of the loop maintains the invariant, and that the invariant provides a useful property to show correctness when the loop terminates.

Initialization: Consider the situation just before the first loop iteration, so that $i = 1$. The loop invariant says that for each possible 0-permutation, the subarray $A[1\,..\,0]$ contains this 0-permutation with probability $(n-i+1)!/n! = n!/n! = 1$. The subarray $A[1\,..\,0]$ is an empty subarray, and a 0-permutation has no elements. Thus, $A[1\,..\,0]$ contains any 0-permutation with probability 1, and the loop invariant holds prior to the first iteration.

Maintenance: We assume that just before the ith iteration, each possible $(i-1)$-permutation appears in the subarray $A[1\,..\,i-1]$ with probability $(n-i+1)!/n!$, and we shall show that after the ith iteration, each possible i-permutation appears in the subarray $A[1\,..\,i]$ with probability $(n-i)!/n!$. Incrementing i for the next iteration then maintains the loop invariant.

Let us examine the ith iteration. Consider a particular i-permutation, and denote the elements in it by $\langle x_1, x_2, \ldots, x_i\rangle$. This permutation consists of an $(i-1)$-permutation $\langle x_1, \ldots, x_{i-1}\rangle$ followed by the value x_i that the algorithm places in $A[i]$. Let E_1 denote the event in which the first $i-1$ iterations have created the particular $(i-1)$-permutation $\langle x_1, \ldots, x_{i-1}\rangle$ in $A[1\,..\,i-1]$. By the loop invariant, $\Pr\{E_1\} = (n-i+1)!/n!$. Let E_2 be the event that ith iteration puts x_i in position $A[i]$. The i-permutation $\langle x_1, \ldots, x_i\rangle$ appears in $A[1\,..\,i]$ precisely when both E_1 and E_2 occur, and so we wish to compute $\Pr\{E_2 \cap E_1\}$. Using equation (C.14), we have

$$\Pr\{E_2 \cap E_1\} = \Pr\{E_2 \mid E_1\}\Pr\{E_1\}\ .$$

The probability $\Pr\{E_2 \mid E_1\}$ equals $1/(n-i+1)$ because in line 3 the algorithm chooses x_i randomly from the $n-i+1$ values in positions $A[i\,..\,n]$. Thus, we have

$$\begin{aligned}\Pr\{E_2 \cap E_1\} &= \Pr\{E_2 \mid E_1\}\Pr\{E_1\} \\ &= \frac{1}{n-i+1} \cdot \frac{(n-i+1)!}{n!} \\ &= \frac{(n-i)!}{n!} .\end{aligned}$$

Termination: At termination, $i = n + 1$, and we have that the subarray $A[1\,..\,n]$ is a given n-permutation with probability $(n-(n+1)+1)/n! = 0!/n! = 1/n!$.

Thus, RANDOMIZE-IN-PLACE produces a uniform random permutation. ■

A randomized algorithm is often the simplest and most efficient way to solve a problem. We shall use randomized algorithms occasionally throughout this book.

Exercises

5.3-1

Professor Marceau objects to the loop invariant used in the proof of Lemma 5.5. He questions whether it is true prior to the first iteration. He reasons that we could just as easily declare that an empty subarray contains no 0-permutations. Therefore, the probability that an empty subarray contains a 0-permutation should be 0, thus invalidating the loop invariant prior to the first iteration. Rewrite the procedure RANDOMIZE-IN-PLACE so that its associated loop invariant applies to a nonempty subarray prior to the first iteration, and modify the proof of Lemma 5.5 for your procedure.

5.3-2

Professor Kelp decides to write a procedure that produces at random any permutation besides the identity permutation. He proposes the following procedure:

```
PERMUTE-WITHOUT-IDENTITY(A)
1  n = A.length
2  for i = 1 to n - 1
3      swap A[i] with A[RANDOM(i + 1, n)]
```

Does this code do what Professor Kelp intends?

5.3-3

Suppose that instead of swapping element $A[i]$ with a random element from the subarray $A[i\,..\,n]$, we swapped it with a random element from anywhere in the array:

```
PERMUTE-WITH-ALL(A)
1  n = A.length
2  for i = 1 to n
3      swap A[i] with A[RANDOM(1, n)]
```

Does this code produce a uniform random permutation? Why or why not?

5.3-4
Professor Armstrong suggests the following procedure for generating a uniform random permutation:

```
PERMUTE-BY-CYCLIC(A)
1  n = A.length
2  let B[1..n] be a new array
3  offset = RANDOM(1, n)
4  for i = 1 to n
5      dest = i + offset
6      if dest > n
7          dest = dest − n
8      B[dest] = A[i]
9  return B
```

Show that each element $A[i]$ has a $1/n$ probability of winding up in any particular position in B. Then show that Professor Armstrong is mistaken by showing that the resulting permutation is not uniformly random.

5.3-5 ⋆
Prove that in the array P in procedure PERMUTE-BY-SORTING, the probability that all elements are unique is at least $1 - 1/n$.

5.3-6
Explain how to implement the algorithm PERMUTE-BY-SORTING to handle the case in which two or more priorities are identical. That is, your algorithm should produce a uniform random permutation, even if two or more priorities are identical.

5.3-7
Suppose we want to create a ***random sample*** of the set $\{1, 2, 3, \ldots, n\}$, that is, an m-element subset S, where $0 \le m \le n$, such that each m-subset is equally likely to be created. One way would be to set $A[i] = i$ for $i = 1, 2, 3, \ldots, n$, call RANDOMIZE-IN-PLACE(A), and then take just the first m array elements. This method would make n calls to the RANDOM procedure. If n is much larger than m, we can create a random sample with fewer calls to RANDOM. Show that

the following recursive procedure returns a random m-subset S of $\{1, 2, 3, \ldots, n\}$, in which each m-subset is equally likely, while making only m calls to RANDOM:

```
RANDOM-SAMPLE(m, n)
1  if m == 0
2      return ∅
3  else S = RANDOM-SAMPLE(m − 1, n − 1)
4      i = RANDOM(1, n)
5      if i ∈ S
6          S = S ∪ {n}
7      else S = S ∪ {i}
8      return S
```

⋆ 5.4 Probabilistic analysis and further uses of indicator random variables

This advanced section further illustrates probabilistic analysis by way of four examples. The first determines the probability that in a room of k people, two of them share the same birthday. The second example examines what happens when we randomly toss balls into bins. The third investigates "streaks" of consecutive heads when we flip coins. The final example analyzes a variant of the hiring problem in which you have to make decisions without actually interviewing all the candidates.

5.4.1 The birthday paradox

Our first example is the ***birthday paradox***. How many people must there be in a room before there is a 50% chance that two of them were born on the same day of the year? The answer is surprisingly few. The paradox is that it is in fact far fewer than the number of days in a year, or even half the number of days in a year, as we shall see.

To answer this question, we index the people in the room with the integers $1, 2, \ldots, k$, where k is the number of people in the room. We ignore the issue of leap years and assume that all years have $n = 365$ days. For $i = 1, 2, \ldots, k$, let b_i be the day of the year on which person i's birthday falls, where $1 \le b_i \le n$. We also assume that birthdays are uniformly distributed across the n days of the year, so that $\Pr\{b_i = r\} = 1/n$ for $i = 1, 2, \ldots, k$ and $r = 1, 2, \ldots, n$.

The probability that two given people, say i and j, have matching birthdays depends on whether the random selection of birthdays is independent. We assume from now on that birthdays are independent, so that the probability that i's birthday

and j's birthday both fall on day r is

$$\begin{aligned}\Pr\{b_i = r \text{ and } b_j = r\} &= \Pr\{b_i = r\}\Pr\{b_j = r\} \\ &= 1/n^2 .\end{aligned}$$

Thus, the probability that they both fall on the same day is

$$\begin{aligned}\Pr\{b_i = b_j\} &= \sum_{r=1}^{n} \Pr\{b_i = r \text{ and } b_j = r\} \\ &= \sum_{r=1}^{n} (1/n^2) \\ &= 1/n . \end{aligned} \tag{5.6}$$

More intuitively, once b_i is chosen, the probability that b_j is chosen to be the same day is $1/n$. Thus, the probability that i and j have the same birthday is the same as the probability that the birthday of one of them falls on a given day. Notice, however, that this coincidence depends on the assumption that the birthdays are independent.

We can analyze the probability of at least 2 out of k people having matching birthdays by looking at the complementary event. The probability that at least two of the birthdays match is 1 minus the probability that all the birthdays are different. The event that k people have distinct birthdays is

$$B_k = \bigcap_{i=1}^{k} A_i ,$$

where A_i is the event that person i's birthday is different from person j's for all $j < i$. Since we can write $B_k = A_k \cap B_{k-1}$, we obtain from equation (C.16) the recurrence

$$\Pr\{B_k\} = \Pr\{B_{k-1}\}\Pr\{A_k \mid B_{k-1}\} , \tag{5.7}$$

where we take $\Pr\{B_1\} = \Pr\{A_1\} = 1$ as an initial condition. In other words, the probability that $b_1, b_2, \ldots, b_k$ are distinct birthdays is the probability that $b_1, b_2, \ldots, b_{k-1}$ are distinct birthdays times the probability that $b_k \neq b_i$ for $i = 1, 2, \ldots, k-1$, given that $b_1, b_2, \ldots, b_{k-1}$ are distinct.

If $b_1, b_2, \ldots, b_{k-1}$ are distinct, the conditional probability that $b_k \neq b_i$ for $i = 1, 2, \ldots, k-1$ is $\Pr\{A_k \mid B_{k-1}\} = (n - k + 1)/n$, since out of the n days, $n - (k-1)$ days are not taken. We iteratively apply the recurrence (5.7) to obtain

$$\begin{aligned}
\Pr\{B_k\} &= \Pr\{B_{k-1}\}\Pr\{A_k \mid B_{k-1}\} \\
&= \Pr\{B_{k-2}\}\Pr\{A_{k-1} \mid B_{k-2}\}\Pr\{A_k \mid B_{k-1}\} \\
&\vdots \\
&= \Pr\{B_1\}\Pr\{A_2 \mid B_1\}\Pr\{A_3 \mid B_2\}\cdots\Pr\{A_k \mid B_{k-1}\} \\
&= 1 \cdot \left(\frac{n-1}{n}\right)\left(\frac{n-2}{n}\right)\cdots\left(\frac{n-k+1}{n}\right) \\
&= 1 \cdot \left(1-\frac{1}{n}\right)\left(1-\frac{2}{n}\right)\cdots\left(1-\frac{k-1}{n}\right) .
\end{aligned}$$

Inequality (3.12), $1 + x \le e^x$, gives us

$$\begin{aligned}
\Pr\{B_k\} &\le e^{-1/n}e^{-2/n}\cdots e^{-(k-1)/n} \\
&= e^{-\sum_{i=1}^{k-1} i/n} \\
&= e^{-k(k-1)/2n} \\
&\le 1/2
\end{aligned}$$

when $-k(k-1)/2n \le \ln(1/2)$. The probability that all k birthdays are distinct is at most $1/2$ when $k(k-1) \ge 2n\ln 2$ or, solving the quadratic equation, when $k \ge (1 + \sqrt{1 + (8\ln 2)n})/2$. For $n = 365$, we must have $k \ge 23$. Thus, if at least 23 people are in a room, the probability is at least $1/2$ that at least two people have the same birthday. On Mars, a year is 669 Martian days long; it therefore takes 31 Martians to get the same effect.

An analysis using indicator random variables

We can use indicator random variables to provide a simpler but approximate analysis of the birthday paradox. For each pair (i, j) of the k people in the room, we define the indicator random variable X_{ij}, for $1 \le i < j \le k$, by

$$\begin{aligned}
X_{ij} &= \mathrm{I}\{\text{person } i \text{ and person } j \text{ have the same birthday}\} \\
&= \begin{cases} 1 & \text{if person } i \text{ and person } j \text{ have the same birthday} , \\ 0 & \text{otherwise} . \end{cases}
\end{aligned}$$

By equation (5.6), the probability that two people have matching birthdays is $1/n$, and thus by Lemma 5.1, we have

$$\begin{aligned}
\mathrm{E}[X_{ij}] &= \Pr\{\text{person } i \text{ and person } j \text{ have the same birthday}\} \\
&= 1/n .
\end{aligned}$$

Letting X be the random variable that counts the number of pairs of individuals having the same birthday, we have

$$X = \sum_{i=1}^{k} \sum_{j=i+1}^{k} X_{ij} \ .$$

Taking expectations of both sides and applying linearity of expectation, we obtain

$$\begin{aligned} \mathrm{E}[X] &= \mathrm{E}\left[\sum_{i=1}^{k} \sum_{j=i+1}^{k} X_{ij}\right] \\ &= \sum_{i=1}^{k} \sum_{j=i+1}^{k} \mathrm{E}[X_{ij}] \\ &= \binom{k}{2}\frac{1}{n} \\ &= \frac{k(k-1)}{2n} \ . \end{aligned}$$

When $k(k-1) \geq 2n$, therefore, the expected number of pairs of people with the same birthday is at least 1. Thus, if we have at least $\sqrt{2n}+1$ individuals in a room, we can expect at least two to have the same birthday. For $n = 365$, if $k = 28$, the expected number of pairs with the same birthday is $(28 \cdot 27)/(2 \cdot 365) \approx 1.0356$. Thus, with at least 28 people, we expect to find at least one matching pair of birthdays. On Mars, where a year is 669 Martian days long, we need at least 38 Martians.

The first analysis, which used only probabilities, determined the number of people required for the probability to exceed $1/2$ that a matching pair of birthdays exists, and the second analysis, which used indicator random variables, determined the number such that the expected number of matching birthdays is 1. Although the exact numbers of people differ for the two situations, they are the same asymptotically: $\Theta(\sqrt{n})$.

5.4.2 Balls and bins

Consider a process in which we randomly toss identical balls into b bins, numbered $1, 2, \ldots, b$. The tosses are independent, and on each toss the ball is equally likely to end up in any bin. The probability that a tossed ball lands in any given bin is $1/b$. Thus, the ball-tossing process is a sequence of Bernoulli trials (see Appendix C.4) with a probability $1/b$ of success, where success means that the ball falls in the given bin. This model is particularly useful for analyzing hashing (see Chapter 11), and we can answer a variety of interesting questions about the ball-tossing process. (Problem C-1 asks additional questions about balls and bins.)

How many balls fall in a given bin? The number of balls that fall in a given bin follows the binomial distribution $b(k; n, 1/b)$. If we toss n balls, equation (C.37) tells us that the expected number of balls that fall in the given bin is n/b.

How many balls must we toss, on the average, until a given bin contains a ball? The number of tosses until the given bin receives a ball follows the geometric distribution with probability $1/b$ and, by equation (C.32), the expected number of tosses until success is $1/(1/b) = b$.

How many balls must we toss until every bin contains at least one ball? Let us call a toss in which a ball falls into an empty bin a "hit." We want to know the expected number n of tosses required to get b hits.

Using the hits, we can partition the n tosses into stages. The ith stage consists of the tosses after the $(i-1)$st hit until the ith hit. The first stage consists of the first toss, since we are guaranteed to have a hit when all bins are empty. For each toss during the ith stage, $i-1$ bins contain balls and $b-i+1$ bins are empty. Thus, for each toss in the ith stage, the probability of obtaining a hit is $(b-i+1)/b$.

Let n_i denote the number of tosses in the ith stage. Thus, the number of tosses required to get b hits is $n = \sum_{i=1}^{b} n_i$. Each random variable n_i has a geometric distribution with probability of success $(b-i+1)/b$ and thus, by equation (C.32), we have

$$\mathrm{E}[n_i] = \frac{b}{b-i+1} .$$

By linearity of expectation, we have

$$\begin{aligned}
\mathrm{E}[n] &= \mathrm{E}\left[\sum_{i=1}^{b} n_i\right] \\
&= \sum_{i=1}^{b} \mathrm{E}[n_i] \\
&= \sum_{i=1}^{b} \frac{b}{b-i+1} \\
&= b\sum_{i=1}^{b} \frac{1}{i} \\
&= b(\ln b + O(1)) \quad \text{(by equation (A.7))} .
\end{aligned}$$

It therefore takes approximately $b \ln b$ tosses before we can expect that every bin has a ball. This problem is also known as the ***coupon collector's problem***, which says that a person trying to collect each of b different coupons expects to acquire approximately $b \ln b$ randomly obtained coupons in order to succeed.

5.4.3 Streaks

Suppose you flip a fair coin n times. What is the longest streak of consecutive heads that you expect to see? The answer is $\Theta(\lg n)$, as the following analysis shows.

We first prove that the expected length of the longest streak of heads is $O(\lg n)$. The probability that each coin flip is a head is $1/2$. Let A_{ik} be the event that a streak of heads of length at least k begins with the ith coin flip or, more precisely, the event that the k consecutive coin flips $i, i+1, \ldots, i+k-1$ yield only heads, where $1 \le k \le n$ and $1 \le i \le n-k+1$. Since coin flips are mutually independent, for any given event A_{ik}, the probability that all k flips are heads is

$$\Pr\{A_{ik}\} = 1/2^k \ . \tag{5.8}$$

For $k = 2\lceil \lg n \rceil$,

$$\begin{aligned} \Pr\{A_{i,2\lceil \lg n \rceil}\} &= 1/2^{2\lceil \lg n \rceil} \\ &\le 1/2^{2 \lg n} \\ &= 1/n^2 \ , \end{aligned}$$

and thus the probability that a streak of heads of length at least $2\lceil \lg n \rceil$ begins in position i is quite small. There are at most $n - 2\lceil \lg n \rceil + 1$ positions where such a streak can begin. The probability that a streak of heads of length at least $2\lceil \lg n \rceil$ begins anywhere is therefore

$$\begin{aligned} \Pr\left\{ \bigcup_{i=1}^{n-2\lceil \lg n \rceil+1} A_{i,2\lceil \lg n \rceil} \right\} &\le \sum_{i=1}^{n-2\lceil \lg n \rceil+1} 1/n^2 \\ &< \sum_{i=1}^{n} 1/n^2 \\ &= 1/n \ , \end{aligned} \tag{5.9}$$

since by Boole's inequality (C.19), the probability of a union of events is at most the sum of the probabilities of the individual events. (Note that Boole's inequality holds even for events such as these that are not independent.)

We now use inequality (5.9) to bound the length of the longest streak. For $j = 0, 1, 2, \ldots, n$, let L_j be the event that the longest streak of heads has length exactly j, and let L be the length of the longest streak. By the definition of expected value, we have

$$\mathrm{E}[L] = \sum_{j=0}^{n} j \Pr\{L_j\} \ . \tag{5.10}$$

We could try to evaluate this sum using upper bounds on each $\Pr\{L_j\}$ similar to those computed in inequality (5.9). Unfortunately, this method would yield weak bounds. We can use some intuition gained by the above analysis to obtain a good bound, however. Informally, we observe that for no individual term in the summation in equation (5.10) are both the factors j and $\Pr\{L_j\}$ large. Why? When $j \geq 2\lceil \lg n \rceil$, then $\Pr\{L_j\}$ is very small, and when $j < 2\lceil \lg n \rceil$, then j is fairly small. More formally, we note that the events L_j for $j = 0, 1, \ldots, n$ are disjoint, and so the probability that a streak of heads of length at least $2\lceil \lg n \rceil$ begins anywhere is $\sum_{j=2\lceil \lg n \rceil}^{n} \Pr\{L_j\}$. By inequality (5.9), we have $\sum_{j=2\lceil \lg n \rceil}^{n} \Pr\{L_j\} < 1/n$. Also, noting that $\sum_{j=0}^{n} \Pr\{L_j\} = 1$, we have that $\sum_{j=0}^{2\lceil \lg n \rceil - 1} \Pr\{L_j\} \leq 1$. Thus, we obtain

$$\begin{aligned}
\mathrm{E}[L] &= \sum_{j=0}^{n} j \Pr\{L_j\} \\
&= \sum_{j=0}^{2\lceil \lg n \rceil - 1} j \Pr\{L_j\} + \sum_{j=2\lceil \lg n \rceil}^{n} j \Pr\{L_j\} \\
&< \sum_{j=0}^{2\lceil \lg n \rceil - 1} (2\lceil \lg n \rceil) \Pr\{L_j\} + \sum_{j=2\lceil \lg n \rceil}^{n} n \Pr\{L_j\} \\
&= 2\lceil \lg n \rceil \sum_{j=0}^{2\lceil \lg n \rceil - 1} \Pr\{L_j\} + n \sum_{j=2\lceil \lg n \rceil}^{n} \Pr\{L_j\} \\
&< 2\lceil \lg n \rceil \cdot 1 + n \cdot (1/n) \\
&= O(\lg n) \, .
\end{aligned}$$

The probability that a streak of heads exceeds $r\lceil \lg n \rceil$ flips diminishes quickly with r. For $r \geq 1$, the probability that a streak of at least $r\lceil \lg n \rceil$ heads starts in position i is

$$\begin{aligned}
\Pr\{A_{i, r\lceil \lg n \rceil}\} &= 1/2^{r\lceil \lg n \rceil} \\
&\leq 1/n^r \, .
\end{aligned}$$

Thus, the probability is at most $n/n^r = 1/n^{r-1}$ that the longest streak is at least $r\lceil \lg n \rceil$, or equivalently, the probability is at least $1 - 1/n^{r-1}$ that the longest streak has length less than $r\lceil \lg n \rceil$.

As an example, for $n = 1000$ coin flips, the probability of having a streak of at least $2\lceil \lg n \rceil = 20$ heads is at most $1/n = 1/1000$. The chance of having a streak longer than $3\lceil \lg n \rceil = 30$ heads is at most $1/n^2 = 1/1{,}000{,}000$.

We now prove a complementary lower bound: the expected length of the longest streak of heads in n coin flips is $\Omega(\lg n)$. To prove this bound, we look for streaks

of length s by partitioning the n flips into approximately n/s groups of s flips each. If we choose $s = \lfloor (\lg n)/2 \rfloor$, we can show that it is likely that at least one of these groups comes up all heads, and hence it is likely that the longest streak has length at least $s = \Omega(\lg n)$. We then show that the longest streak has expected length $\Omega(\lg n)$.

We partition the n coin flips into at least $\lfloor n/\lfloor (\lg n)/2 \rfloor \rfloor$ groups of $\lfloor (\lg n)/2 \rfloor$ consecutive flips, and we bound the probability that no group comes up all heads. By equation (5.8), the probability that the group starting in position i comes up all heads is

$$\begin{aligned} \Pr\{A_{i,\lfloor (\lg n)/2 \rfloor}\} &= 1/2^{\lfloor (\lg n)/2 \rfloor} \\ &\geq 1/\sqrt{n} \, . \end{aligned}$$

The probability that a streak of heads of length at least $\lfloor (\lg n)/2 \rfloor$ does not begin in position i is therefore at most $1 - 1/\sqrt{n}$. Since the $\lfloor n/\lfloor (\lg n)/2 \rfloor \rfloor$ groups are formed from mutually exclusive, independent coin flips, the probability that every one of these groups *fails* to be a streak of length $\lfloor (\lg n)/2 \rfloor$ is at most

$$\begin{aligned} \left(1 - 1/\sqrt{n}\right)^{\lfloor n/\lfloor (\lg n)/2 \rfloor \rfloor} &\leq \left(1 - 1/\sqrt{n}\right)^{n/\lfloor (\lg n)/2 \rfloor - 1} \\ &\leq \left(1 - 1/\sqrt{n}\right)^{2n/\lg n - 1} \\ &\leq e^{-(2n/\lg n - 1)/\sqrt{n}} \\ &= O(e^{-\lg n}) \\ &= O(1/n) \, . \end{aligned}$$

For this argument, we used inequality (3.12), $1 + x \leq e^x$, and the fact, which you might want to verify, that $(2n/\lg n - 1)/\sqrt{n} \geq \lg n$ for sufficiently large n.

Thus, the probability that the longest streak exceeds $\lfloor (\lg n)/2 \rfloor$ is

$$\sum_{j=\lfloor (\lg n)/2 \rfloor + 1}^{n} \Pr\{L_j\} \geq 1 - O(1/n) \, . \tag{5.11}$$

We can now calculate a lower bound on the expected length of the longest streak, beginning with equation (5.10) and proceeding in a manner similar to our analysis of the upper bound:

$$
\begin{aligned}
\mathrm{E}[L] &= \sum_{j=0}^{n} j \Pr\{L_j\} \\
&= \sum_{j=0}^{\lfloor (\lg n)/2 \rfloor} j \Pr\{L_j\} + \sum_{j=\lfloor (\lg n)/2 \rfloor + 1}^{n} j \Pr\{L_j\} \\
&\geq \sum_{j=0}^{\lfloor (\lg n)/2 \rfloor} 0 \cdot \Pr\{L_j\} + \sum_{j=\lfloor (\lg n)/2 \rfloor + 1}^{n} \lfloor (\lg n)/2 \rfloor \Pr\{L_j\} \\
&= 0 \cdot \sum_{j=0}^{\lfloor (\lg n)/2 \rfloor} \Pr\{L_j\} + \lfloor (\lg n)/2 \rfloor \sum_{j=\lfloor (\lg n)/2 \rfloor + 1}^{n} \Pr\{L_j\} \\
&\geq 0 + \lfloor (\lg n)/2 \rfloor \, (1 - O(1/n)) \qquad \text{(by inequality (5.11))} \\
&= \Omega(\lg n) \, .
\end{aligned}
$$

As with the birthday paradox, we can obtain a simpler but approximate analysis using indicator random variables. We let $X_{ik} = \mathrm{I}\{A_{ik}\}$ be the indicator random variable associated with a streak of heads of length at least k beginning with the ith coin flip. To count the total number of such streaks, we define

$$
X = \sum_{i=1}^{n-k+1} X_{ik} \, .
$$

Taking expectations and using linearity of expectation, we have

$$
\begin{aligned}
\mathrm{E}[X] &= \mathrm{E}\left[\sum_{i=1}^{n-k+1} X_{ik} \right] \\
&= \sum_{i=1}^{n-k+1} \mathrm{E}[X_{ik}] \\
&= \sum_{i=1}^{n-k+1} \Pr\{A_{ik}\} \\
&= \sum_{i=1}^{n-k+1} 1/2^k \\
&= \frac{n-k+1}{2^k} \, .
\end{aligned}
$$

By plugging in various values for k, we can calculate the expected number of streaks of length k. If this number is large (much greater than 1), then we expect many streaks of length k to occur and the probability that one occurs is high. If

this number is small (much less than 1), then we expect few streaks of length k to occur and the probability that one occurs is low. If $k = c \lg n$, for some positive constant c, we obtain

$$\begin{aligned} \mathrm{E}[X] &= \frac{n - c\lg n + 1}{2^{c \lg n}} \\ &= \frac{n - c\lg n + 1}{n^c} \\ &= \frac{1}{n^{c-1}} - \frac{(c\lg n - 1)/n}{n^{c-1}} \\ &= \Theta(1/n^{c-1}) \ . \end{aligned}$$

If c is large, the expected number of streaks of length $c \lg n$ is small, and we conclude that they are unlikely to occur. On the other hand, if $c = 1/2$, then we obtain $\mathrm{E}[X] = \Theta(1/n^{1/2-1}) = \Theta(n^{1/2})$, and we expect that there are a large number of streaks of length $(1/2)\lg n$. Therefore, one streak of such a length is likely to occur. From these rough estimates alone, we can conclude that the expected length of the longest streak is $\Theta(\lg n)$.

5.4.4 The on-line hiring problem

As a final example, we consider a variant of the hiring problem. Suppose now that we do not wish to interview all the candidates in order to find the best one. We also do not wish to hire and fire as we find better and better applicants. Instead, we are willing to settle for a candidate who is close to the best, in exchange for hiring exactly once. We must obey one company requirement: after each interview we must either immediately offer the position to the applicant or immediately reject the applicant. What is the trade-off between minimizing the amount of interviewing and maximizing the quality of the candidate hired?

We can model this problem in the following way. After meeting an applicant, we are able to give each one a score; let $score(i)$ denote the score we give to the ith applicant, and assume that no two applicants receive the same score. After we have seen j applicants, we know which of the j has the highest score, but we do not know whether any of the remaining $n - j$ applicants will receive a higher score. We decide to adopt the strategy of selecting a positive integer $k < n$, interviewing and then rejecting the first k applicants, and hiring the first applicant thereafter who has a higher score than all preceding applicants. If it turns out that the best-qualified applicant was among the first k interviewed, then we hire the nth applicant. We formalize this strategy in the procedure ON-LINE-MAXIMUM(k, n), which returns the index of the candidate we wish to hire.

```
ON-LINE-MAXIMUM(k, n)
1  bestscore = −∞
2  for i = 1 to k
3      if score(i) > bestscore
4          bestscore = score(i)
5  for i = k + 1 to n
6      if score(i) > bestscore
7          return i
8  return n
```

We wish to determine, for each possible value of k, the probability that we hire the most qualified applicant. We then choose the best possible k, and implement the strategy with that value. For the moment, assume that k is fixed. Let $M(j) = \max_{1 \le i \le j} \{score(i)\}$ denote the maximum score among applicants 1 through j. Let S be the event that we succeed in choosing the best-qualified applicant, and let S_i be the event that we succeed when the best-qualified applicant is the ith one interviewed. Since the various S_i are disjoint, we have that $\Pr\{S\} = \sum_{i=1}^{n} \Pr\{S_i\}$. Noting that we never succeed when the best-qualified applicant is one of the first k, we have that $\Pr\{S_i\} = 0$ for $i = 1, 2, \ldots, k$. Thus, we obtain

$$\Pr\{S\} = \sum_{i=k+1}^{n} \Pr\{S_i\} \ . \tag{5.12}$$

We now compute $\Pr\{S_i\}$. In order to succeed when the best-qualified applicant is the ith one, two things must happen. First, the best-qualified applicant must be in position i, an event which we denote by B_i. Second, the algorithm must not select any of the applicants in positions $k+1$ through $i-1$, which happens only if, for each j such that $k+1 \le j \le i-1$, we find that $score(j) < bestscore$ in line 6. (Because scores are unique, we can ignore the possibility of $score(j) = bestscore$.) In other words, all of the values $score(k+1)$ through $score(i-1)$ must be less than $M(k)$; if any are greater than $M(k)$, we instead return the index of the first one that is greater. We use O_i to denote the event that none of the applicants in position $k+1$ through $i-1$ are chosen. Fortunately, the two events B_i and O_i are independent. The event O_i depends only on the relative ordering of the values in positions 1 through $i-1$, whereas B_i depends only on whether the value in position i is greater than the values in all other positions. The ordering of the values in positions 1 through $i-1$ does not affect whether the value in position i is greater than all of them, and the value in position i does not affect the ordering of the values in positions 1 through $i-1$. Thus we can apply equation (C.15) to obtain

$$\Pr\{S_i\} = \Pr\{B_i \cap O_i\} = \Pr\{B_i\}\Pr\{O_i\} \ .$$

The probability $\Pr\{B_i\}$ is clearly $1/n$, since the maximum is equally likely to be in any one of the n positions. For event O_i to occur, the maximum value in positions 1 through $i-1$, which is equally likely to be in any of these $i-1$ positions, must be in one of the first k positions. Consequently, $\Pr\{O_i\} = k/(i-1)$ and $\Pr\{S_i\} = k/(n(i-1))$. Using equation (5.12), we have

$$\begin{aligned}
\Pr\{S\} &= \sum_{i=k+1}^{n} \Pr\{S_i\} \\
&= \sum_{i=k+1}^{n} \frac{k}{n(i-1)} \\
&= \frac{k}{n} \sum_{i=k+1}^{n} \frac{1}{i-1} \\
&= \frac{k}{n} \sum_{i=k}^{n-1} \frac{1}{i} \ .
\end{aligned}$$

We approximate by integrals to bound this summation from above and below. By the inequalities (A.12), we have

$$\int_k^n \frac{1}{x}\,dx \le \sum_{i=k}^{n-1} \frac{1}{i} \le \int_{k-1}^{n-1} \frac{1}{x}\,dx \ .$$

Evaluating these definite integrals gives us the bounds

$$\frac{k}{n}(\ln n - \ln k) \le \Pr\{S\} \le \frac{k}{n}(\ln(n-1) - \ln(k-1)) \ ,$$

which provide a rather tight bound for $\Pr\{S\}$. Because we wish to maximize our probability of success, let us focus on choosing the value of k that maximizes the lower bound on $\Pr\{S\}$. (Besides, the lower-bound expression is easier to maximize than the upper-bound expression.) Differentiating the expression $(k/n)(\ln n - \ln k)$ with respect to k, we obtain

$$\frac{1}{n}(\ln n - \ln k - 1) \ .$$

Setting this derivative equal to 0, we see that we maximize the lower bound on the probability when $\ln k = \ln n - 1 = \ln(n/e)$ or, equivalently, when $k = n/e$. Thus, if we implement our strategy with $k = n/e$, we succeed in hiring our best-qualified applicant with probability at least $1/e$.

Exercises

5.4-1

How many people must there be in a room before the probability that someone has the same birthday as you do is at least $1/2$? How many people must there be before the probability that at least two people have a birthday on July 4 is greater than $1/2$?

5.4-2

Suppose that we toss balls into b bins until some bin contains two balls. Each toss is independent, and each ball is equally likely to end up in any bin. What is the expected number of ball tosses?

5.4-3 ⋆

For the analysis of the birthday paradox, is it important that the birthdays be mutually independent, or is pairwise independence sufficient? Justify your answer.

5.4-4 ⋆

How many people should be invited to a party in order to make it likely that there are *three* people with the same birthday?

5.4-5 ⋆

What is the probability that a k-string over a set of size n forms a k-permutation? How does this question relate to the birthday paradox?

5.4-6 ⋆

Suppose that n balls are tossed into n bins, where each toss is independent and the ball is equally likely to end up in any bin. What is the expected number of empty bins? What is the expected number of bins with exactly one ball?

5.4-7 ⋆

Sharpen the lower bound on streak length by showing that in n flips of a fair coin, the probability is less than $1/n$ that no streak longer than $\lg n - 2\lg\lg n$ consecutive heads occurs.

Problems

5-1 Probabilistic counting

With a b-bit counter, we can ordinarily only count up to $2^b - 1$. With R. Morris's ***probabilistic counting***, we can count up to a much larger value at the expense of some loss of precision.

We let a counter value of i represent a count of n_i for $i = 0, 1, \ldots, 2^b - 1$, where the n_i form an increasing sequence of nonnegative values. We assume that the initial value of the counter is 0, representing a count of $n_0 = 0$. The INCREMENT operation works on a counter containing the value i in a probabilistic manner. If $i = 2^b - 1$, then the operation reports an overflow error. Otherwise, the INCREMENT operation increases the counter by 1 with probability $1/(n_{i+1} - n_i)$, and it leaves the counter unchanged with probability $1 - 1/(n_{i+1} - n_i)$.

If we select $n_i = i$ for all $i \geq 0$, then the counter is an ordinary one. More interesting situations arise if we select, say, $n_i = 2^{i-1}$ for $i > 0$ or $n_i = F_i$ (the ith Fibonacci number—see Section 3.2).

For this problem, assume that n_{2^b-1} is large enough that the probability of an overflow error is negligible.

a. Show that the expected value represented by the counter after n INCREMENT operations have been performed is exactly n.

b. The analysis of the variance of the count represented by the counter depends on the sequence of the n_i. Let us consider a simple case: $n_i = 100i$ for all $i \geq 0$. Estimate the variance in the value represented by the register after n INCREMENT operations have been performed.

5-2 Searching an unsorted array

This problem examines three algorithms for searching for a value x in an unsorted array A consisting of n elements.

Consider the following randomized strategy: pick a random index i into A. If $A[i] = x$, then we terminate; otherwise, we continue the search by picking a new random index into A. We continue picking random indices into A until we find an index j such that $A[j] = x$ or until we have checked every element of A. Note that we pick from the whole set of indices each time, so that we may examine a given element more than once.

a. Write pseudocode for a procedure RANDOM-SEARCH to implement the strategy above. Be sure that your algorithm terminates when all indices into A have been picked.

b. Suppose that there is exactly one index i such that $A[i] = x$. What is the expected number of indices into A that we must pick before we find x and RANDOM-SEARCH terminates?

c. Generalizing your solution to part (b), suppose that there are $k \geq 1$ indices i such that $A[i] = x$. What is the expected number of indices into A that we must pick before we find x and RANDOM-SEARCH terminates? Your answer should be a function of n and k.

d. Suppose that there are no indices i such that $A[i] = x$. What is the expected number of indices into A that we must pick before we have checked all elements of A and RANDOM-SEARCH terminates?

Now consider a deterministic linear search algorithm, which we refer to as DETERMINISTIC-SEARCH. Specifically, the algorithm searches A for x in order, considering $A[1], A[2], A[3], \ldots, A[n]$ until either it finds $A[i] = x$ or it reaches the end of the array. Assume that all possible permutations of the input array are equally likely.

e. Suppose that there is exactly one index i such that $A[i] = x$. What is the average-case running time of DETERMINISTIC-SEARCH? What is the worst-case running time of DETERMINISTIC-SEARCH?

f. Generalizing your solution to part (e), suppose that there are $k \geq 1$ indices i such that $A[i] = x$. What is the average-case running time of DETERMINISTIC-SEARCH? What is the worst-case running time of DETERMINISTIC-SEARCH? Your answer should be a function of n and k.

g. Suppose that there are no indices i such that $A[i] = x$. What is the average-case running time of DETERMINISTIC-SEARCH? What is the worst-case running time of DETERMINISTIC-SEARCH?

Finally, consider a randomized algorithm SCRAMBLE-SEARCH that works by first randomly permuting the input array and then running the deterministic linear search given above on the resulting permuted array.

h. Letting k be the number of indices i such that $A[i] = x$, give the worst-case and expected running times of SCRAMBLE-SEARCH for the cases in which $k = 0$ and $k = 1$. Generalize your solution to handle the case in which $k \geq 1$.

i. Which of the three searching algorithms would you use? Explain your answer.

Chapter notes

Bollobás [53], Hofri [174], and Spencer [321] contain a wealth of advanced probabilistic techniques. The advantages of randomized algorithms are discussed and surveyed by Karp [200] and Rabin [288]. The textbook by Motwani and Raghavan [262] gives an extensive treatment of randomized algorithms.

Several variants of the hiring problem have been widely studied. These problems are more commonly referred to as "secretary problems." An example of work in this area is the paper by Ajtai, Meggido, and Waarts [11].

II Sorting and Order Statistics

Introduction

This part presents several algorithms that solve the following ***sorting problem***:

Input: A sequence of n numbers $\langle a_1, a_2, \ldots, a_n \rangle$.

Output: A permutation (reordering) $\langle a'_1, a'_2, \ldots, a'_n \rangle$ of the input sequence such that $a'_1 \leq a'_2 \leq \cdots \leq a'_n$.

The input sequence is usually an n-element array, although it may be represented in some other fashion, such as a linked list.

The structure of the data

In practice, the numbers to be sorted are rarely isolated values. Each is usually part of a collection of data called a ***record***. Each record contains a ***key***, which is the value to be sorted. The remainder of the record consists of ***satellite data***, which are usually carried around with the key. In practice, when a sorting algorithm permutes the keys, it must permute the satellite data as well. If each record includes a large amount of satellite data, we often permute an array of pointers to the records rather than the records themselves in order to minimize data movement.

In a sense, it is these implementation details that distinguish an algorithm from a full-blown program. A sorting algorithm describes the *method* by which we determine the sorted order, regardless of whether we are sorting individual numbers or large records containing many bytes of satellite data. Thus, when focusing on the problem of sorting, we typically assume that the input consists only of numbers. Translating an algorithm for sorting numbers into a program for sorting records

is conceptually straightforward, although in a given engineering situation other subtleties may make the actual programming task a challenge.

Why sorting?

Many computer scientists consider sorting to be the most fundamental problem in the study of algorithms. There are several reasons:

- Sometimes an application inherently needs to sort information. For example, in order to prepare customer statements, banks need to sort checks by check number.
- Algorithms often use sorting as a key subroutine. For example, a program that renders graphical objects which are layered on top of each other might have to sort the objects according to an "above" relation so that it can draw these objects from bottom to top. We shall see numerous algorithms in this text that use sorting as a subroutine.
- We can draw from among a wide variety of sorting algorithms, and they employ a rich set of techniques. In fact, many important techniques used throughout algorithm design appear in the body of sorting algorithms that have been developed over the years. In this way, sorting is also a problem of historical interest.
- We can prove a nontrivial lower bound for sorting (as we shall do in Chapter 8). Our best upper bounds match the lower bound asymptotically, and so we know that our sorting algorithms are asymptotically optimal. Moreover, we can use the lower bound for sorting to prove lower bounds for certain other problems.
- Many engineering issues come to the fore when implementing sorting algorithms. The fastest sorting program for a particular situation may depend on many factors, such as prior knowledge about the keys and satellite data, the memory hierarchy (caches and virtual memory) of the host computer, and the software environment. Many of these issues are best dealt with at the algorithmic level, rather than by "tweaking" the code.

Sorting algorithms

We introduced two algorithms that sort n real numbers in Chapter 2. Insertion sort takes $\Theta(n^2)$ time in the worst case. Because its inner loops are tight, however, it is a fast in-place sorting algorithm for small input sizes. (Recall that a sorting algorithm sorts ***in place*** if only a constant number of elements of the input array are ever stored outside the array.) Merge sort has a better asymptotic running time, $\Theta(n \lg n)$, but the MERGE procedure it uses does not operate in place.

In this part, we shall introduce two more algorithms that sort arbitrary real numbers. Heapsort, presented in Chapter 6, sorts n numbers in place in $O(n \lg n)$ time. It uses an important data structure, called a heap, with which we can also implement a priority queue.

Quicksort, in Chapter 7, also sorts n numbers in place, but its worst-case running time is $\Theta(n^2)$. Its expected running time is $\Theta(n \lg n)$, however, and it generally outperforms heapsort in practice. Like insertion sort, quicksort has tight code, and so the hidden constant factor in its running time is small. It is a popular algorithm for sorting large input arrays.

Insertion sort, merge sort, heapsort, and quicksort are all comparison sorts: they determine the sorted order of an input array by comparing elements. Chapter 8 begins by introducing the decision-tree model in order to study the performance limitations of comparison sorts. Using this model, we prove a lower bound of $\Omega(n \lg n)$ on the worst-case running time of any comparison sort on n inputs, thus showing that heapsort and merge sort are asymptotically optimal comparison sorts.

Chapter 8 then goes on to show that we can beat this lower bound of $\Omega(n \lg n)$ if we can gather information about the sorted order of the input by means other than comparing elements. The counting sort algorithm, for example, assumes that the input numbers are in the set $\{0, 1, \ldots, k\}$. By using array indexing as a tool for determining relative order, counting sort can sort n numbers in $\Theta(k + n)$ time. Thus, when $k = O(n)$, counting sort runs in time that is linear in the size of the input array. A related algorithm, radix sort, can be used to extend the range of counting sort. If there are n integers to sort, each integer has d digits, and each digit can take on up to k possible values, then radix sort can sort the numbers in $\Theta(d(n + k))$ time. When d is a constant and k is $O(n)$, radix sort runs in linear time. A third algorithm, bucket sort, requires knowledge of the probabilistic distribution of numbers in the input array. It can sort n real numbers uniformly distributed in the half-open interval $[0, 1)$ in average-case $O(n)$ time.

The following table summarizes the running times of the sorting algorithms from Chapters 2 and 6–8. As usual, n denotes the number of items to sort. For counting sort, the items to sort are integers in the set $\{0, 1, \ldots, k\}$. For radix sort, each item is a d-digit number, where each digit takes on k possible values. For bucket sort, we assume that the keys are real numbers uniformly distributed in the half-open interval $[0, 1)$. The rightmost column gives the average-case or expected running time, indicating which it gives when it differs from the worst-case running time. We omit the average-case running time of heapsort because we do not analyze it in this book.

Algorithm	Worst-case running time	Average-case/expected running time
Insertion sort	$\Theta(n^2)$	$\Theta(n^2)$
Merge sort	$\Theta(n \lg n)$	$\Theta(n \lg n)$
Heapsort	$O(n \lg n)$	—
Quicksort	$\Theta(n^2)$	$\Theta(n \lg n)$ (expected)
Counting sort	$\Theta(k + n)$	$\Theta(k + n)$
Radix sort	$\Theta(d(n + k))$	$\Theta(d(n + k))$
Bucket sort	$\Theta(n^2)$	$\Theta(n)$ (average-case)

Order statistics

The ith order statistic of a set of n numbers is the ith smallest number in the set. We can, of course, select the ith order statistic by sorting the input and indexing the ith element of the output. With no assumptions about the input distribution, this method runs in $\Omega(n \lg n)$ time, as the lower bound proved in Chapter 8 shows.

In Chapter 9, we show that we can find the ith smallest element in $O(n)$ time, even when the elements are arbitrary real numbers. We present a randomized algorithm with tight pseudocode that runs in $\Theta(n^2)$ time in the worst case, but whose expected running time is $O(n)$. We also give a more complicated algorithm that runs in $O(n)$ worst-case time.

Background

Although most of this part does not rely on difficult mathematics, some sections do require mathematical sophistication. In particular, analyses of quicksort, bucket sort, and the order-statistic algorithm use probability, which is reviewed in Appendix C, and the material on probabilistic analysis and randomized algorithms in Chapter 5. The analysis of the worst-case linear-time algorithm for order statistics involves somewhat more sophisticated mathematics than the other worst-case analyses in this part.

6 Heapsort

In this chapter, we introduce another sorting algorithm: heapsort. Like merge sort, but unlike insertion sort, heapsort's running time is $O(n \lg n)$. Like insertion sort, but unlike merge sort, heapsort sorts in place: only a constant number of array elements are stored outside the input array at any time. Thus, heapsort combines the better attributes of the two sorting algorithms we have already discussed.

Heapsort also introduces another algorithm design technique: using a data structure, in this case one we call a "heap," to manage information. Not only is the heap data structure useful for heapsort, but it also makes an efficient priority queue. The heap data structure will reappear in algorithms in later chapters.

The term "heap" was originally coined in the context of heapsort, but it has since come to refer to "garbage-collected storage," such as the programming languages Java and Lisp provide. Our heap data structure is *not* garbage-collected storage, and whenever we refer to heaps in this book, we shall mean a data structure rather than an aspect of garbage collection.

6.1 Heaps

The ***(binary) heap*** data structure is an array object that we can view as a nearly complete binary tree (see Section B.5.3), as shown in Figure 6.1. Each node of the tree corresponds to an element of the array. The tree is completely filled on all levels except possibly the lowest, which is filled from the left up to a point. An array A that represents a heap is an object with two attributes: $A.length$, which (as usual) gives the number of elements in the array, and $A.heap\text{-}size$, which represents how many elements in the heap are stored within array A. That is, although $A[1 \ldots A.length]$ may contain numbers, only the elements in $A[1 \ldots A.heap\text{-}size]$, where $0 \leq A.heap\text{-}size \leq A.length$, are valid elements of the heap. The root of the tree is $A[1]$, and given the index i of a node, we can easily compute the indices of its parent, left child, and right child:

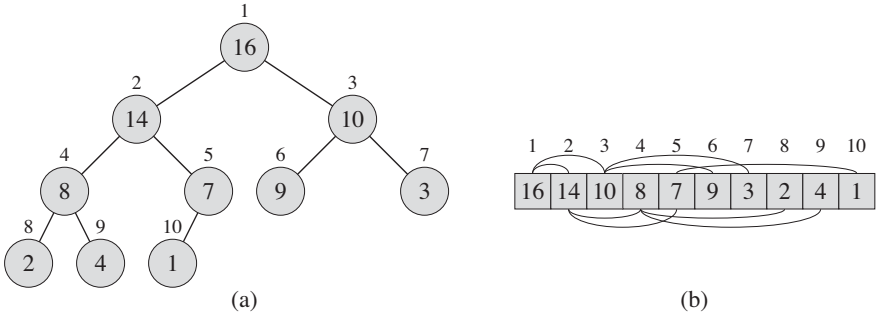


Figure 6.1 A max-heap viewed as **(a)** a binary tree and **(b)** an array. The number within the circle at each node in the tree is the value stored at that node. The number above a node is the corresponding index in the array. Above and below the array are lines showing parent-child relationships; parents are always to the left of their children. The tree has height three; the node at index 4 (with value 8) has height one.

PARENT(i)
1 **return** $\lfloor i/2 \rfloor$

LEFT(i)
1 **return** $2i$

RIGHT(i)
1 **return** $2i + 1$

On most computers, the LEFT procedure can compute $2i$ in one instruction by simply shifting the binary representation of i left by one bit position. Similarly, the RIGHT procedure can quickly compute $2i + 1$ by shifting the binary representation of i left by one bit position and then adding in a 1 as the low-order bit. The PARENT procedure can compute $\lfloor i/2 \rfloor$ by shifting i right one bit position. Good implementations of heapsort often implement these procedures as "macros" or "in-line" procedures.

There are two kinds of binary heaps: max-heaps and min-heaps. In both kinds, the values in the nodes satisfy a ***heap property***, the specifics of which depend on the kind of heap. In a ***max-heap***, the ***max-heap property*** is that for every node i other than the root,

$$A[\text{PARENT}(i)] \geq A[i] ,$$

that is, the value of a node is at most the value of its parent. Thus, the largest element in a max-heap is stored at the root, and the subtree rooted at a node contains

values no larger than that contained at the node itself. A ***min-heap*** is organized in the opposite way; the ***min-heap property*** is that for every node i other than the root,

$$A[\text{PARENT}(i)] \leq A[i] .$$

The smallest element in a min-heap is at the root.

For the heapsort algorithm, we use max-heaps. Min-heaps commonly implement priority queues, which we discuss in Section 6.5. We shall be precise in specifying whether we need a max-heap or a min-heap for any particular application, and when properties apply to either max-heaps or min-heaps, we just use the term "heap."

Viewing a heap as a tree, we define the ***height*** of a node in a heap to be the number of edges on the longest simple downward path from the node to a leaf, and we define the height of the heap to be the height of its root. Since a heap of n elements is based on a complete binary tree, its height is $\Theta(\lg n)$ (see Exercise 6.1-2). We shall see that the basic operations on heaps run in time at most proportional to the height of the tree and thus take $O(\lg n)$ time. The remainder of this chapter presents some basic procedures and shows how they are used in a sorting algorithm and a priority-queue data structure.

- The MAX-HEAPIFY procedure, which runs in $O(\lg n)$ time, is the key to maintaining the max-heap property.
- The BUILD-MAX-HEAP procedure, which runs in linear time, produces a max-heap from an unordered input array.
- The HEAPSORT procedure, which runs in $O(n \lg n)$ time, sorts an array in place.
- The MAX-HEAP-INSERT, HEAP-EXTRACT-MAX, HEAP-INCREASE-KEY, and HEAP-MAXIMUM procedures, which run in $O(\lg n)$ time, allow the heap data structure to implement a priority queue.

Exercises

6.1-1

What are the minimum and maximum numbers of elements in a heap of height h?

6.1-2

Show that an n-element heap has height $\lfloor \lg n \rfloor$.

6.1-3

Show that in any subtree of a max-heap, the root of the subtree contains the largest value occurring anywhere in that subtree.

6.1-4
Where in a max-heap might the smallest element reside, assuming that all elements are distinct?

6.1-5
Is an array that is in sorted order a min-heap?

6.1-6
Is the array with values $\langle 23, 17, 14, 6, 13, 10, 1, 5, 7, 12\rangle$ a max-heap?

6.1-7
Show that, with the array representation for storing an n-element heap, the leaves are the nodes indexed by $\lfloor n/2\rfloor + 1, \lfloor n/2\rfloor + 2, \ldots, n$.

6.2 Maintaining the heap property

In order to maintain the max-heap property, we call the procedure MAX-HEAPIFY. Its inputs are an array A and an index i into the array. When it is called, MAX-HEAPIFY assumes that the binary trees rooted at LEFT(i) and RIGHT(i) are max-heaps, but that $A[i]$ might be smaller than its children, thus violating the max-heap property. MAX-HEAPIFY lets the value at $A[i]$ "float down" in the max-heap so that the subtree rooted at index i obeys the max-heap property.

```
MAX-HEAPIFY(A, i)
 1  l = LEFT(i)
 2  r = RIGHT(i)
 3  if l ≤ A.heap-size and A[l] > A[i]
 4      largest = l
 5  else largest = i
 6  if r ≤ A.heap-size and A[r] > A[largest]
 7      largest = r
 8  if largest ≠ i
 9      exchange A[i] with A[largest]
10      MAX-HEAPIFY(A, largest)
```

Figure 6.2 illustrates the action of MAX-HEAPIFY. At each step, the largest of the elements $A[i]$, $A[\text{LEFT}(i)]$, and $A[\text{RIGHT}(i)]$ is determined, and its index is stored in *largest*. If $A[i]$ is largest, then the subtree rooted at node i is already a max-heap and the procedure terminates. Otherwise, one of the two children has the largest element, and $A[i]$ is swapped with $A[largest]$, which causes node i and its

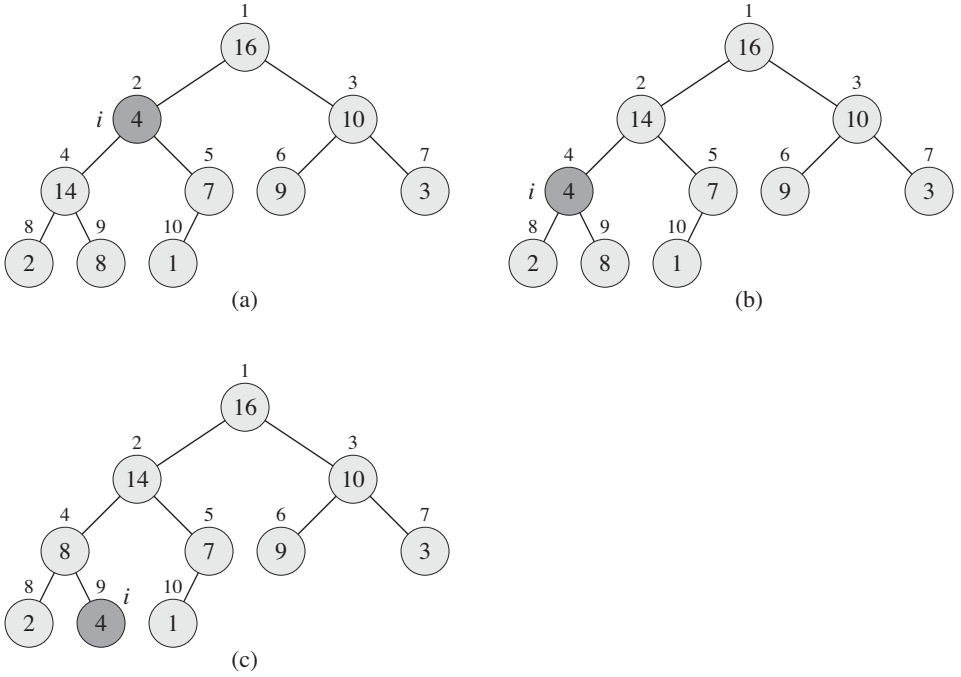


Figure 6.2 The action of MAX-HEAPIFY$(A, 2)$, where $A.heap\text{-}size = 10$. **(a)** The initial configuration, with $A[2]$ at node $i = 2$ violating the max-heap property since it is not larger than both children. The max-heap property is restored for node 2 in **(b)** by exchanging $A[2]$ with $A[4]$, which destroys the max-heap property for node 4. The recursive call MAX-HEAPIFY$(A, 4)$ now has $i = 4$. After swapping $A[4]$ with $A[9]$, as shown in **(c)**, node 4 is fixed up, and the recursive call MAX-HEAPIFY$(A, 9)$ yields no further change to the data structure.

children to satisfy the max-heap property. The node indexed by *largest*, however, now has the original value $A[i]$, and thus the subtree rooted at *largest* might violate the max-heap property. Consequently, we call MAX-HEAPIFY recursively on that subtree.

The running time of MAX-HEAPIFY on a subtree of size n rooted at a given node i is the $\Theta(1)$ time to fix up the relationships among the elements $A[i]$, $A[\text{LEFT}(i)]$, and $A[\text{RIGHT}(i)]$, plus the time to run MAX-HEAPIFY on a subtree rooted at one of the children of node i (assuming that the recursive call occurs). The children's subtrees each have size at most $2n/3$—the worst case occurs when the bottom level of the tree is exactly half full—and therefore we can describe the running time of MAX-HEAPIFY by the recurrence

$$T(n) \leq T(2n/3) + \Theta(1) .$$

The solution to this recurrence, by case 2 of the master theorem (Theorem 4.1), is $T(n) = O(\lg n)$. Alternatively, we can characterize the running time of MAX-HEAPIFY on a node of height h as $O(h)$.

Exercises

6.2-1
Using Figure 6.2 as a model, illustrate the operation of MAX-HEAPIFY$(A, 3)$ on the array $A = \langle 27, 17, 3, 16, 13, 10, 1, 5, 7, 12, 4, 8, 9, 0\rangle$.

6.2-2
Starting with the procedure MAX-HEAPIFY, write pseudocode for the procedure MIN-HEAPIFY(A, i), which performs the corresponding manipulation on a min-heap. How does the running time of MIN-HEAPIFY compare to that of MAX-HEAPIFY?

6.2-3
What is the effect of calling MAX-HEAPIFY(A, i) when the element $A[i]$ is larger than its children?

6.2-4
What is the effect of calling MAX-HEAPIFY(A, i) for $i > A.\mathit{heap\text{-}size}/2$?

6.2-5
The code for MAX-HEAPIFY is quite efficient in terms of constant factors, except possibly for the recursive call in line 10, which might cause some compilers to produce inefficient code. Write an efficient MAX-HEAPIFY that uses an iterative control construct (a loop) instead of recursion.

6.2-6
Show that the worst-case running time of MAX-HEAPIFY on a heap of size n is $\Omega(\lg n)$. (*Hint:* For a heap with n nodes, give node values that cause MAX-HEAPIFY to be called recursively at every node on a simple path from the root down to a leaf.)

6.3 Building a heap

We can use the procedure MAX-HEAPIFY in a bottom-up manner to convert an array $A[1\,..\,n]$, where $n = A.\mathit{length}$, into a max-heap. By Exercise 6.1-7, the elements in the subarray $A[(\lfloor n/2\rfloor + 1)\,..\,n]$ are all leaves of the tree, and so each is

a 1-element heap to begin with. The procedure BUILD-MAX-HEAP goes through the remaining nodes of the tree and runs MAX-HEAPIFY on each one.

```
BUILD-MAX-HEAP(A)
1  A.heap-size = A.length
2  for i = ⌊A.length/2⌋ downto 1
3      MAX-HEAPIFY(A, i)
```

Figure 6.3 shows an example of the action of BUILD-MAX-HEAP.

To show why BUILD-MAX-HEAP works correctly, we use the following loop invariant:

> At the start of each iteration of the **for** loop of lines 2–3, each node $i + 1$, $i + 2, \ldots, n$ is the root of a max-heap.

We need to show that this invariant is true prior to the first loop iteration, that each iteration of the loop maintains the invariant, and that the invariant provides a useful property to show correctness when the loop terminates.

Initialization: Prior to the first iteration of the loop, $i = \lfloor n/2 \rfloor$. Each node $\lfloor n/2 \rfloor + 1, \lfloor n/2 \rfloor + 2, \ldots, n$ is a leaf and is thus the root of a trivial max-heap.

Maintenance: To see that each iteration maintains the loop invariant, observe that the children of node i are numbered higher than i. By the loop invariant, therefore, they are both roots of max-heaps. This is precisely the condition required for the call MAX-HEAPIFY(A, i) to make node i a max-heap root. Moreover, the MAX-HEAPIFY call preserves the property that nodes $i + 1, i + 2, \ldots, n$ are all roots of max-heaps. Decrementing i in the **for** loop update reestablishes the loop invariant for the next iteration.

Termination: At termination, $i = 0$. By the loop invariant, each node $1, 2, \ldots, n$ is the root of a max-heap. In particular, node 1 is.

We can compute a simple upper bound on the running time of BUILD-MAX-HEAP as follows. Each call to MAX-HEAPIFY costs $O(\lg n)$ time, and BUILD-MAX-HEAP makes $O(n)$ such calls. Thus, the running time is $O(n \lg n)$. This upper bound, though correct, is not asymptotically tight.

We can derive a tighter bound by observing that the time for MAX-HEAPIFY to run at a node varies with the height of the node in the tree, and the heights of most nodes are small. Our tighter analysis relies on the properties that an n-element heap has height $\lfloor \lg n \rfloor$ (see Exercise 6.1-2) and at most $\lceil n/2^{h+1} \rceil$ nodes of any height h (see Exercise 6.3-3).

The time required by MAX-HEAPIFY when called on a node of height h is $O(h)$, and so we can express the total cost of BUILD-MAX-HEAP as being bounded from above by

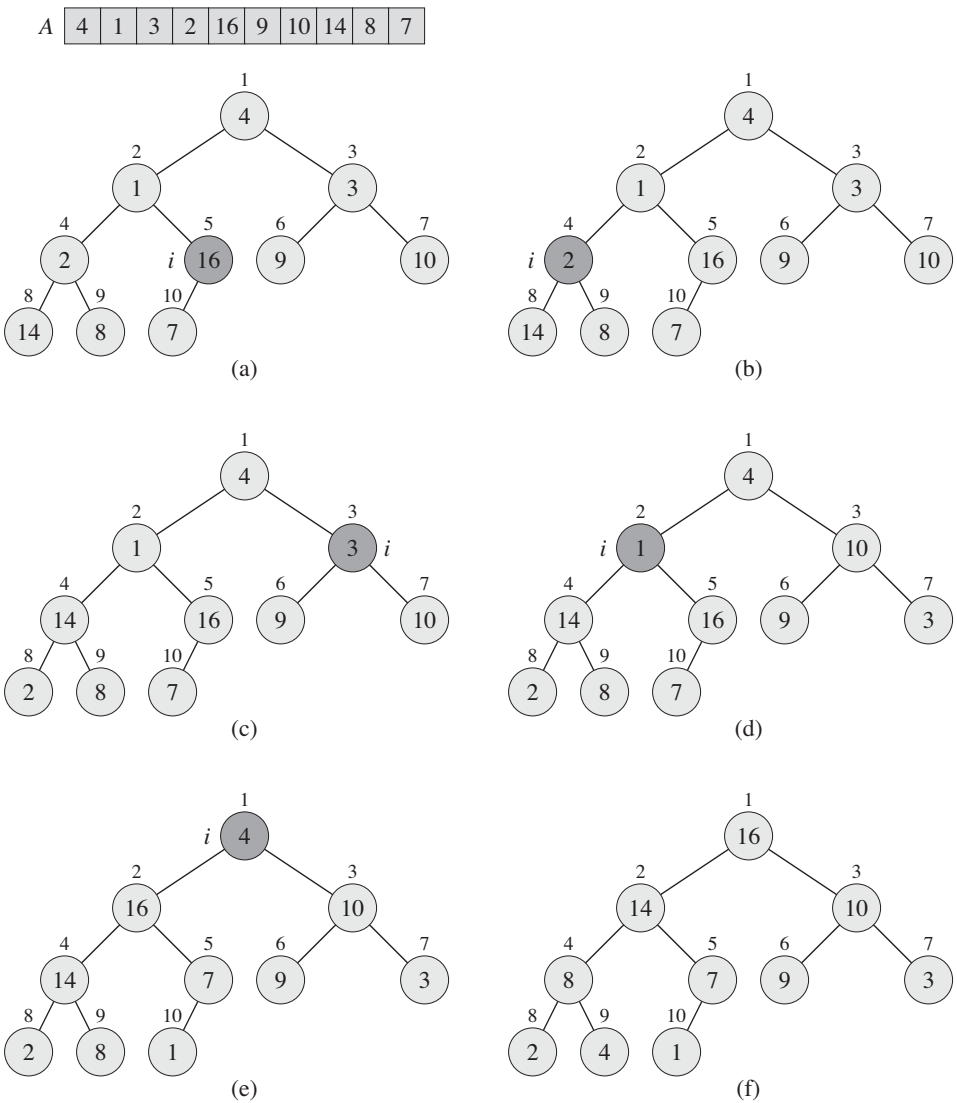


Figure 6.3 The operation of BUILD-MAX-HEAP, showing the data structure before the call to MAX-HEAPIFY in line 3 of BUILD-MAX-HEAP. **(a)** A 10-element input array A and the binary tree it represents. The figure shows that the loop index i refers to node 5 before the call MAX-HEAPIFY(A, i). **(b)** The data structure that results. The loop index i for the next iteration refers to node 4. **(c)–(e)** Subsequent iterations of the **for** loop in BUILD-MAX-HEAP. Observe that whenever MAX-HEAPIFY is called on a node, the two subtrees of that node are both max-heaps. **(f)** The max-heap after BUILD-MAX-HEAP finishes.

$$\sum_{h=0}^{\lfloor \lg n \rfloor} \left\lceil \frac{n}{2^{h+1}} \right\rceil O(h) = O\left(n \sum_{h=0}^{\lfloor \lg n \rfloor} \frac{h}{2^h} \right) .$$

We evalaute the last summation by substituting $x = 1/2$ in the formula (A.8), yielding

$$\begin{aligned} \sum_{h=0}^{\infty} \frac{h}{2^h} &= \frac{1/2}{(1-1/2)^2} \\ &= 2 . \end{aligned}$$

Thus, we can bound the running time of BUILD-MAX-HEAP as

$$\begin{aligned} O\left(n \sum_{h=0}^{\lfloor \lg n \rfloor} \frac{h}{2^h} \right) &= O\left(n \sum_{h=0}^{\infty} \frac{h}{2^h} \right) \\ &= O(n) . \end{aligned}$$

Hence, we can build a max-heap from an unordered array in linear time.

We can build a min-heap by the procedure BUILD-MIN-HEAP, which is the same as BUILD-MAX-HEAP but with the call to MAX-HEAPIFY in line 3 replaced by a call to MIN-HEAPIFY (see Exercise 6.2-2). BUILD-MIN-HEAP produces a min-heap from an unordered linear array in linear time.

Exercises

6.3-1
Using Figure 6.3 as a model, illustrate the operation of BUILD-MAX-HEAP on the array $A = \langle 5, 3, 17, 10, 84, 19, 6, 22, 9 \rangle$.

6.3-2
Why do we want the loop index i in line 2 of BUILD-MAX-HEAP to decrease from $\lfloor A.length/2 \rfloor$ to 1 rather than increase from 1 to $\lfloor A.length/2 \rfloor$?

6.3-3
Show that there are at most $\lceil n/2^{h+1} \rceil$ nodes of height h in any n-element heap.

6.4 The heapsort algorithm

The heapsort algorithm starts by using BUILD-MAX-HEAP to build a max-heap on the input array $A[1..n]$, where $n = A.length$. Since the maximum element of the array is stored at the root $A[1]$, we can put it into its correct final position

by exchanging it with $A[n]$. If we now discard node n from the heap—and we can do so by simply decrementing $A.heap\text{-}size$—we observe that the children of the root remain max-heaps, but the new root element might violate the max-heap property. All we need to do to restore the max-heap property, however, is call MAX-HEAPIFY$(A, 1)$, which leaves a max-heap in $A[1\,..\,n-1]$. The heapsort algorithm then repeats this process for the max-heap of size $n-1$ down to a heap of size 2. (See Exercise 6.4-2 for a precise loop invariant.)

```
HEAPSORT(A)
1  BUILD-MAX-HEAP(A)
2  for i = A.length downto 2
3      exchange A[1] with A[i]
4      A.heap-size = A.heap-size − 1
5      MAX-HEAPIFY(A, 1)
```

Figure 6.4 shows an example of the operation of HEAPSORT after line 1 has built the initial max-heap. The figure shows the max-heap before the first iteration of the **for** loop of lines 2–5 and after each iteration.

The HEAPSORT procedure takes time $O(n \lg n)$, since the call to BUILD-MAX-HEAP takes time $O(n)$ and each of the $n-1$ calls to MAX-HEAPIFY takes time $O(\lg n)$.

Exercises

6.4-1
Using Figure 6.4 as a model, illustrate the operation of HEAPSORT on the array $A = \langle 5, 13, 2, 25, 7, 17, 20, 8, 4\rangle$.

6.4-2
Argue the correctness of HEAPSORT using the following loop invariant:

> At the start of each iteration of the **for** loop of lines 2–5, the subarray $A[1\,..\,i]$ is a max-heap containing the i smallest elements of $A[1\,..\,n]$, and the subarray $A[i+1\,..\,n]$ contains the $n-i$ largest elements of $A[1\,..\,n]$, sorted.

6.4-3
What is the running time of HEAPSORT on an array A of length n that is already sorted in increasing order? What about decreasing order?

6.4-4
Show that the worst-case running time of HEAPSORT is $\Omega(n \lg n)$.

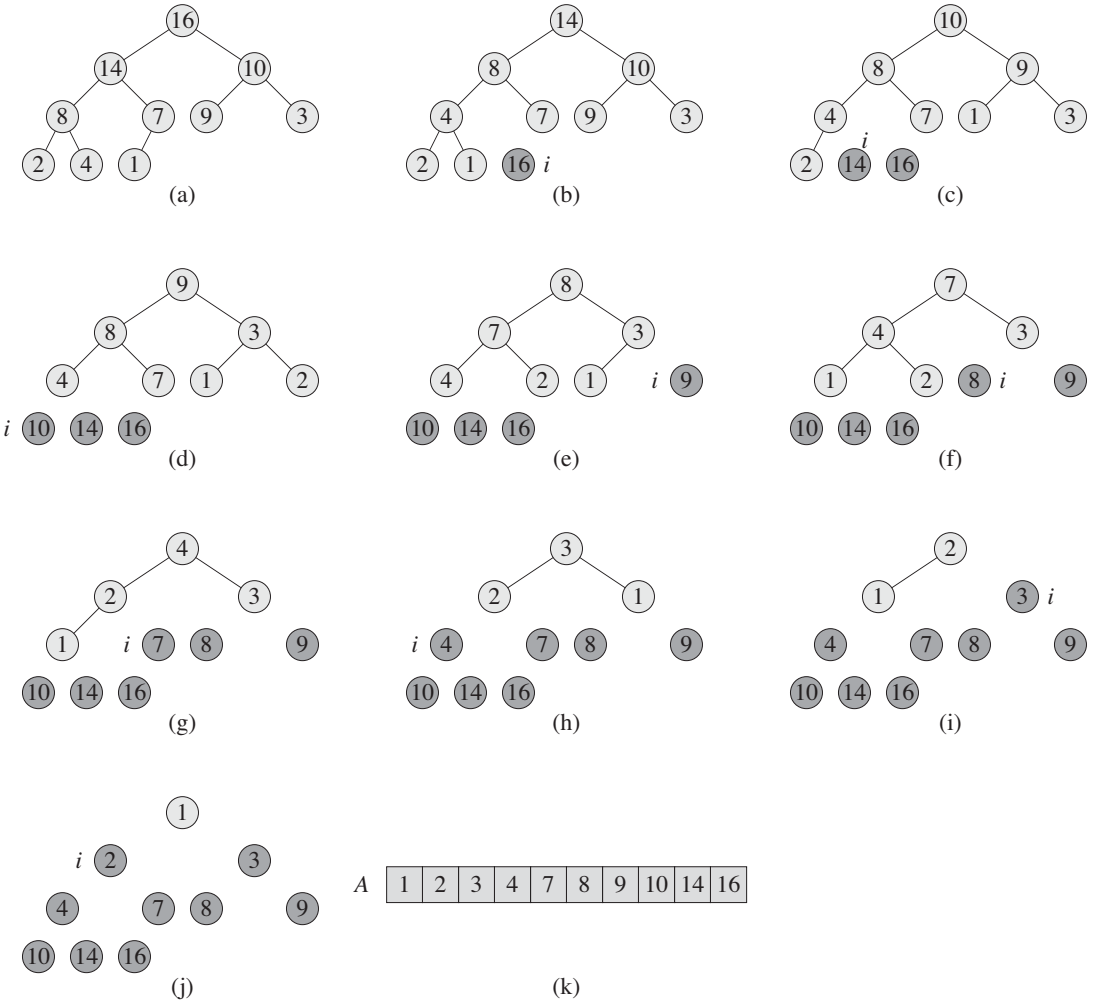


Figure 6.4 The operation of HEAPSORT. **(a)** The max-heap data structure just after BUILD-MAX-HEAP has built it in line 1. **(b)–(j)** The max-heap just after each call of MAX-HEAPIFY in line 5, showing the value of i at that time. Only lightly shaded nodes remain in the heap. **(k)** The resulting sorted array A.

6.4-5 ⋆

Show that when all elements are distinct, the best-case running time of HEAPSORT is $\Omega(n \lg n)$.

6.5 Priority queues

Heapsort is an excellent algorithm, but a good implementation of quicksort, presented in Chapter 7, usually beats it in practice. Nevertheless, the heap data structure itself has many uses. In this section, we present one of the most popular applications of a heap: as an efficient priority queue. As with heaps, priority queues come in two forms: max-priority queues and min-priority queues. We will focus here on how to implement max-priority queues, which are in turn based on max-heaps; Exercise 6.5-3 asks you to write the procedures for min-priority queues.

A ***priority queue*** is a data structure for maintaining a set S of elements, each with an associated value called a ***key***. A ***max-priority queue*** supports the following operations:

INSERT(S, x) inserts the element x into the set S, which is equivalent to the operation $S = S \cup \{x\}$.

MAXIMUM(S) returns the element of S with the largest key.

EXTRACT-MAX(S) removes and returns the element of S with the largest key.

INCREASE-KEY(S, x, k) increases the value of element x's key to the new value k, which is assumed to be at least as large as x's current key value.

Among their other applications, we can use max-priority queues to schedule jobs on a shared computer. The max-priority queue keeps track of the jobs to be performed and their relative priorities. When a job is finished or interrupted, the scheduler selects the highest-priority job from among those pending by calling EXTRACT-MAX. The scheduler can add a new job to the queue at any time by calling INSERT.

Alternatively, a ***min-priority queue*** supports the operations INSERT, MINIMUM, EXTRACT-MIN, and DECREASE-KEY. A min-priority queue can be used in an event-driven simulator. The items in the queue are events to be simulated, each with an associated time of occurrence that serves as its key. The events must be simulated in order of their time of occurrence, because the simulation of an event can cause other events to be simulated in the future. The simulation program calls EXTRACT-MIN at each step to choose the next event to simulate. As new events are produced, the simulator inserts them into the min-priority queue by calling INSERT.

We shall see other uses for min-priority queues, highlighting the DECREASE-KEY operation, in Chapters 23 and 24.

Not surprisingly, we can use a heap to implement a priority queue. In a given application, such as job scheduling or event-driven simulation, elements of a priority queue correspond to objects in the application. We often need to determine which application object corresponds to a given priority-queue element, and vice versa. When we use a heap to implement a priority queue, therefore, we often need to store a ***handle*** to the corresponding application object in each heap element. The exact makeup of the handle (such as a pointer or an integer) depends on the application. Similarly, we need to store a handle to the corresponding heap element in each application object. Here, the handle would typically be an array index. Because heap elements change locations within the array during heap operations, an actual implementation, upon relocating a heap element, would also have to update the array index in the corresponding application object. Because the details of accessing application objects depend heavily on the application and its implementation, we shall not pursue them here, other than noting that in practice, these handles do need to be correctly maintained.

Now we discuss how to implement the operations of a max-priority queue. The procedure HEAP-MAXIMUM implements the MAXIMUM operation in $\Theta(1)$ time.

```
HEAP-MAXIMUM(A)
1  return A[1]
```

The procedure HEAP-EXTRACT-MAX implements the EXTRACT-MAX operation. It is similar to the **for** loop body (lines 3–5) of the HEAPSORT procedure.

```
HEAP-EXTRACT-MAX(A)
1  if A.heap-size < 1
2       error "heap underflow"
3  max = A[1]
4  A[1] = A[A.heap-size]
5  A.heap-size = A.heap-size − 1
6  MAX-HEAPIFY(A, 1)
7  return max
```

The running time of HEAP-EXTRACT-MAX is $O(\lg n)$, since it performs only a constant amount of work on top of the $O(\lg n)$ time for MAX-HEAPIFY.

The procedure HEAP-INCREASE-KEY implements the INCREASE-KEY operation. An index i into the array identifies the priority-queue element whose key we wish to increase. The procedure first updates the key of element $A[i]$ to its new value. Because increasing the key of $A[i]$ might violate the max-heap property,

the procedure then, in a manner reminiscent of the insertion loop (lines 5–7) of INSERTION-SORT from Section 2.1, traverses a simple path from this node toward the root to find a proper place for the newly increased key. As HEAP-INCREASE-KEY traverses this path, it repeatedly compares an element to its parent, exchanging their keys and continuing if the element's key is larger, and terminating if the element's key is smaller, since the max-heap property now holds. (See Exercise 6.5-5 for a precise loop invariant.)

```
HEAP-INCREASE-KEY(A, i, key)
1  if key < A[i]
2       error "new key is smaller than current key"
3  A[i] = key
4  while i > 1 and A[PARENT(i)] < A[i]
5       exchange A[i] with A[PARENT(i)]
6       i = PARENT(i)
```

Figure 6.5 shows an example of a HEAP-INCREASE-KEY operation. The running time of HEAP-INCREASE-KEY on an n-element heap is $O(\lg n)$, since the path traced from the node updated in line 3 to the root has length $O(\lg n)$.

The procedure MAX-HEAP-INSERT implements the INSERT operation. It takes as an input the key of the new element to be inserted into max-heap A. The procedure first expands the max-heap by adding to the tree a new leaf whose key is $-\infty$. Then it calls HEAP-INCREASE-KEY to set the key of this new node to its correct value and maintain the max-heap property.

```
MAX-HEAP-INSERT(A, key)
1  A.heap-size = A.heap-size + 1
2  A[A.heap-size] = −∞
3  HEAP-INCREASE-KEY(A, A.heap-size, key)
```

The running time of MAX-HEAP-INSERT on an n-element heap is $O(\lg n)$.

In summary, a heap can support any priority-queue operation on a set of size n in $O(\lg n)$ time.

Exercises

6.5-1

Illustrate the operation of HEAP-EXTRACT-MAX on the heap $A = \langle 15, 13, 9, 5, 12, 8, 7, 4, 0, 6, 2, 1 \rangle$.

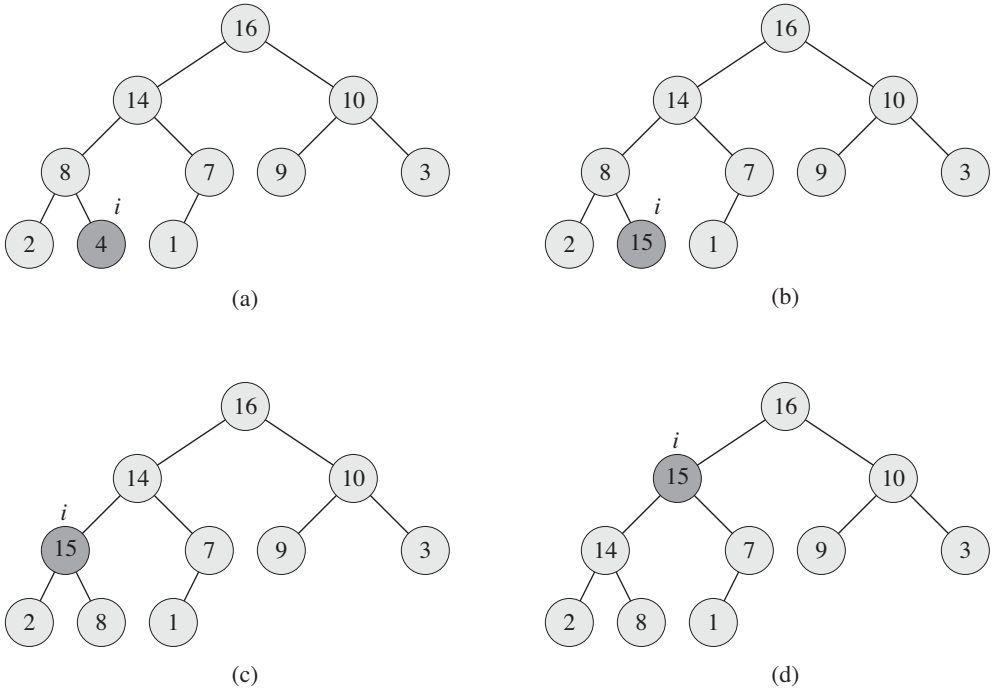


Figure 6.5 The operation of HEAP-INCREASE-KEY. **(a)** The max-heap of Figure 6.4(a) with a node whose index is i heavily shaded. **(b)** This node has its key increased to 15. **(c)** After one iteration of the **while** loop of lines 4–6, the node and its parent have exchanged keys, and the index i moves up to the parent. **(d)** The max-heap after one more iteration of the **while** loop. At this point, $A[\text{PARENT}(i)] \geq A[i]$. The max-heap property now holds and the procedure terminates.

6.5-2

Illustrate the operation of MAX-HEAP-INSERT$(A, 10)$ on the heap $A = \langle 15, 13, 9, 5, 12, 8, 7, 4, 0, 6, 2, 1 \rangle$.

6.5-3

Write pseudocode for the procedures HEAP-MINIMUM, HEAP-EXTRACT-MIN, HEAP-DECREASE-KEY, and MIN-HEAP-INSERT that implement a min-priority queue with a min-heap.

6.5-4

Why do we bother setting the key of the inserted node to $-\infty$ in line 2 of MAX-HEAP-INSERT when the next thing we do is increase its key to the desired value?

6.5-5
Argue the correctness of HEAP-INCREASE-KEY using the following loop invariant:

> At the start of each iteration of the **while** loop of lines 4–6, the subarray $A[1 \,..\, A.heap\text{-}size]$ satisfies the max-heap property, except that there may be one violation: $A[i]$ may be larger than $A[\text{PARENT}(i)]$.

You may assume that the subarray $A[1 \,..\, A.heap\text{-}size]$ satisfies the max-heap property at the time HEAP-INCREASE-KEY is called.

6.5-6
Each exchange operation on line 5 of HEAP-INCREASE-KEY typically requires three assignments. Show how to use the idea of the inner loop of INSERTION-SORT to reduce the three assignments down to just one assignment.

6.5-7
Show how to implement a first-in, first-out queue with a priority queue. Show how to implement a stack with a priority queue. (Queues and stacks are defined in Section 10.1.)

6.5-8
The operation HEAP-DELETE(A, i) deletes the item in node i from heap A. Give an implementation of HEAP-DELETE that runs in $O(\lg n)$ time for an n-element max-heap.

6.5-9
Give an $O(n \lg k)$-time algorithm to merge k sorted lists into one sorted list, where n is the total number of elements in all the input lists. (*Hint:* Use a min-heap for k-way merging.)

Problems

6-1 Building a heap using insertion
We can build a heap by repeatedly calling MAX-HEAP-INSERT to insert the elements into the heap. Consider the following variation on the BUILD-MAX-HEAP procedure:

```
BUILD-MAX-HEAP′(A)
1  A.heap-size = 1
2  for i = 2 to A.length
3      MAX-HEAP-INSERT(A, A[i])
```

a. Do the procedures BUILD-MAX-HEAP and BUILD-MAX-HEAP′ always create the same heap when run on the same input array? Prove that they do, or provide a counterexample.

b. Show that in the worst case, BUILD-MAX-HEAP′ requires $\Theta(n \lg n)$ time to build an n-element heap.

6-2 Analysis of d-ary heaps

A ***d-ary heap*** is like a binary heap, but (with one possible exception) non-leaf nodes have d children instead of 2 children.

a. How would you represent a d-ary heap in an array?

b. What is the height of a d-ary heap of n elements in terms of n and d?

c. Give an efficient implementation of EXTRACT-MAX in a d-ary max-heap. Analyze its running time in terms of d and n.

d. Give an efficient implementation of INSERT in a d-ary max-heap. Analyze its running time in terms of d and n.

e. Give an efficient implementation of INCREASE-KEY(A, i, k), which flags an error if $k < A[i]$, but otherwise sets $A[i] = k$ and then updates the d-ary max-heap structure appropriately. Analyze its running time in terms of d and n.

6-3 Young tableaus

An $m \times n$ ***Young tableau*** is an $m \times n$ matrix such that the entries of each row are in sorted order from left to right and the entries of each column are in sorted order from top to bottom. Some of the entries of a Young tableau may be ∞, which we treat as nonexistent elements. Thus, a Young tableau can be used to hold $r \le mn$ finite numbers.

a. Draw a 4×4 Young tableau containing the elements $\{9, 16, 3, 2, 4, 8, 5, 14, 12\}$.

b. Argue that an $m \times n$ Young tableau Y is empty if $Y[1, 1] = \infty$. Argue that Y is full (contains mn elements) if $Y[m, n] < \infty$.

c. Give an algorithm to implement EXTRACT-MIN on a nonempty $m \times n$ Young tableau that runs in $O(m + n)$ time. Your algorithm should use a recursive subroutine that solves an $m \times n$ problem by recursively solving either an $(m-1) \times n$ or an $m \times (n-1)$ subproblem. (*Hint:* Think about MAX-HEAPIFY.) Define $T(p)$, where $p = m + n$, to be the maximum running time of EXTRACT-MIN on any $m \times n$ Young tableau. Give and solve a recurrence for $T(p)$ that yields the $O(m + n)$ time bound.

d. Show how to insert a new element into a nonfull $m \times n$ Young tableau in $O(m + n)$ time.

e. Using no other sorting method as a subroutine, show how to use an $n \times n$ Young tableau to sort n^2 numbers in $O(n^3)$ time.

f. Give an $O(m + n)$-time algorithm to determine whether a given number is stored in a given $m \times n$ Young tableau.

Chapter notes

The heapsort algorithm was invented by Williams [357], who also described how to implement a priority queue with a heap. The BUILD-MAX-HEAP procedure was suggested by Floyd [106].

We use min-heaps to implement min-priority queues in Chapters 16, 23, and 24. We also give an implementation with improved time bounds for certain operations in Chapter 19 and, assuming that the keys are drawn from a bounded set of nonnegative integers, Chapter 20.

If the data are b-bit integers, and the computer memory consists of addressable b-bit words, Fredman and Willard [115] showed how to implement MINIMUM in $O(1)$ time and INSERT and EXTRACT-MIN in $O(\sqrt{\lg n})$ time. Thorup [337] has improved the $O(\sqrt{\lg n})$ bound to $O(\lg \lg n)$ time. This bound uses an amount of space unbounded in n, but it can be implemented in linear space by using randomized hashing.

An important special case of priority queues occurs when the sequence of EXTRACT-MIN operations is ***monotone***, that is, the values returned by successive EXTRACT-MIN operations are monotonically increasing over time. This case arises in several important applications, such as Dijkstra's single-source shortest-paths algorithm, which we discuss in Chapter 24, and in discrete-event simulation. For Dijkstra's algorithm it is particularly important that the DECREASE-KEY operation be implemented efficiently. For the monotone case, if the data are integers in the range $1, 2, \ldots, C$, Ahuja, Mehlhorn, Orlin, and Tarjan [8] describe

how to implement EXTRACT-MIN and INSERT in $O(\lg C)$ amortized time (see Chapter 17 for more on amortized analysis) and DECREASE-KEY in $O(1)$ time, using a data structure called a radix heap. The $O(\lg C)$ bound can be improved to $O(\sqrt{\lg C})$ using Fibonacci heaps (see Chapter 19) in conjunction with radix heaps. Cherkassky, Goldberg, and Silverstein [65] further improved the bound to $O(\lg^{1/3+\epsilon} C)$ expected time by combining the multilevel bucketing structure of Denardo and Fox [85] with the heap of Thorup mentioned earlier. Raman [291] further improved these results to obtain a bound of $O(\min(\lg^{1/4+\epsilon} C, \lg^{1/3+\epsilon} n))$, for any fixed $\epsilon > 0$.

7 Quicksort

The quicksort algorithm has a worst-case running time of $\Theta(n^2)$ on an input array of n numbers. Despite this slow worst-case running time, quicksort is often the best practical choice for sorting because it is remarkably efficient on the average: its expected running time is $\Theta(n \lg n)$, and the constant factors hidden in the $\Theta(n \lg n)$ notation are quite small. It also has the advantage of sorting in place (see page 17), and it works well even in virtual-memory environments.

Section 7.1 describes the algorithm and an important subroutine used by quicksort for partitioning. Because the behavior of quicksort is complex, we start with an intuitive discussion of its performance in Section 7.2 and postpone its precise analysis to the end of the chapter. Section 7.3 presents a version of quicksort that uses random sampling. This algorithm has a good expected running time, and no particular input elicits its worst-case behavior. Section 7.4 analyzes the randomized algorithm, showing that it runs in $\Theta(n^2)$ time in the worst case and, assuming distinct elements, in expected $O(n \lg n)$ time.

7.1 Description of quicksort

Quicksort, like merge sort, applies the divide-and-conquer paradigm introduced in Section 2.3.1. Here is the three-step divide-and-conquer process for sorting a typical subarray $A[p \,..\, r]$:

Divide: Partition (rearrange) the array $A[p \,..\, r]$ into two (possibly empty) subarrays $A[p \,..\, q-1]$ and $A[q+1 \,..\, r]$ such that each element of $A[p \,..\, q-1]$ is less than or equal to $A[q]$, which is, in turn, less than or equal to each element of $A[q+1 \,..\, r]$. Compute the index q as part of this partitioning procedure.

Conquer: Sort the two subarrays $A[p \,..\, q-1]$ and $A[q+1 \,..\, r]$ by recursive calls to quicksort.

Combine: Because the subarrays are already sorted, no work is needed to combine them: the entire array $A[p\,..\,r]$ is now sorted.

The following procedure implements quicksort:

```
QUICKSORT(A, p, r)
1  if p < r
2      q = PARTITION(A, p, r)
3      QUICKSORT(A, p, q − 1)
4      QUICKSORT(A, q + 1, r)
```

To sort an entire array A, the initial call is QUICKSORT$(A, 1, A.length)$.

Partitioning the array

The key to the algorithm is the PARTITION procedure, which rearranges the subarray $A[p\,..\,r]$ in place.

```
PARTITION(A, p, r)
1  x = A[r]
2  i = p − 1
3  for j = p to r − 1
4      if A[j] ≤ x
5          i = i + 1
6          exchange A[i] with A[j]
7  exchange A[i + 1] with A[r]
8  return i + 1
```

Figure 7.1 shows how PARTITION works on an 8-element array. PARTITION always selects an element $x = A[r]$ as a ***pivot*** element around which to partition the subarray $A[p\,..\,r]$. As the procedure runs, it partitions the array into four (possibly empty) regions. At the start of each iteration of the **for** loop in lines 3–6, the regions satisfy certain properties, shown in Figure 7.2. We state these properties as a loop invariant:

> At the beginning of each iteration of the loop of lines 3–6, for any array index k,
>
> 1. If $p \le k \le i$, then $A[k] \le x$.
> 2. If $i + 1 \le k \le j - 1$, then $A[k] > x$.
> 3. If $k = r$, then $A[k] = x$.

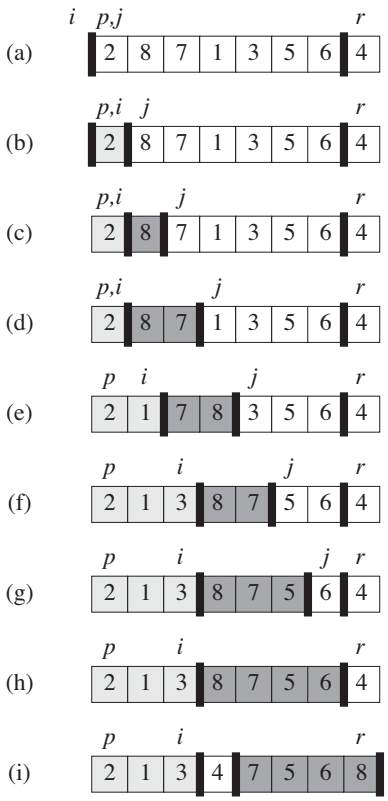


Figure 7.1 The operation of PARTITION on a sample array. Array entry $A[r]$ becomes the pivot element x. Lightly shaded array elements are all in the first partition with values no greater than x. Heavily shaded elements are in the second partition with values greater than x. The unshaded elements have not yet been put in one of the first two partitions, and the final white element is the pivot x. **(a)** The initial array and variable settings. None of the elements have been placed in either of the first two partitions. **(b)** The value 2 is "swapped with itself" and put in the partition of smaller values. **(c)–(d)** The values 8 and 7 are added to the partition of larger values. **(e)** The values 1 and 8 are swapped, and the smaller partition grows. **(f)** The values 3 and 7 are swapped, and the smaller partition grows. **(g)–(h)** The larger partition grows to include 5 and 6, and the loop terminates. **(i)** In lines 7–8, the pivot element is swapped so that it lies between the two partitions.

The indices between j and $r - 1$ are not covered by any of the three cases, and the values in these entries have no particular relationship to the pivot x.

We need to show that this loop invariant is true prior to the first iteration, that each iteration of the loop maintains the invariant, and that the invariant provides a useful property to show correctness when the loop terminates.

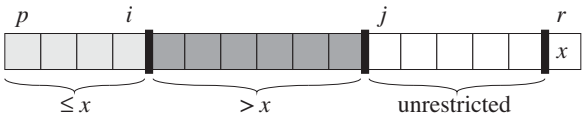


Figure 7.2 The four regions maintained by the procedure PARTITION on a subarray $A[p\,..\,r]$. The values in $A[p\,..\,i]$ are all less than or equal to x, the values in $A[i+1\,..\,j-1]$ are all greater than x, and $A[r] = x$. The subarray $A[j\,..\,r-1]$ can take on any values.

Initialization: Prior to the first iteration of the loop, $i = p-1$ and $j = p$. Because no values lie between p and i and no values lie between $i+1$ and $j-1$, the first two conditions of the loop invariant are trivially satisfied. The assignment in line 1 satisfies the third condition.

Maintenance: As Figure 7.3 shows, we consider two cases, depending on the outcome of the test in line 4. Figure 7.3(a) shows what happens when $A[j] > x$; the only action in the loop is to increment j. After j is incremented, condition 2 holds for $A[j-1]$ and all other entries remain unchanged. Figure 7.3(b) shows what happens when $A[j] \le x$; the loop increments i, swaps $A[i]$ and $A[j]$, and then increments j. Because of the swap, we now have that $A[i] \le x$, and condition 1 is satisfied. Similarly, we also have that $A[j-1] > x$, since the item that was swapped into $A[j-1]$ is, by the loop invariant, greater than x.

Termination: At termination, $j = r$. Therefore, every entry in the array is in one of the three sets described by the invariant, and we have partitioned the values in the array into three sets: those less than or equal to x, those greater than x, and a singleton set containing x.

The final two lines of PARTITION finish up by swapping the pivot element with the leftmost element greater than x, thereby moving the pivot into its correct place in the partitioned array, and then returning the pivot's new index. The output of PARTITION now satisfies the specifications given for the divide step. In fact, it satisfies a slightly stronger condition: after line 2 of QUICKSORT, $A[q]$ is strictly less than every element of $A[q+1\,..\,r]$.

The running time of PARTITION on the subarray $A[p\,..\,r]$ is $\Theta(n)$, where $n = r - p + 1$ (see Exercise 7.1-3).

Exercises

7.1-1

Using Figure 7.1 as a model, illustrate the operation of PARTITION on the array $A = \langle 13, 19, 9, 5, 12, 8, 7, 4, 21, 2, 6, 11 \rangle$.

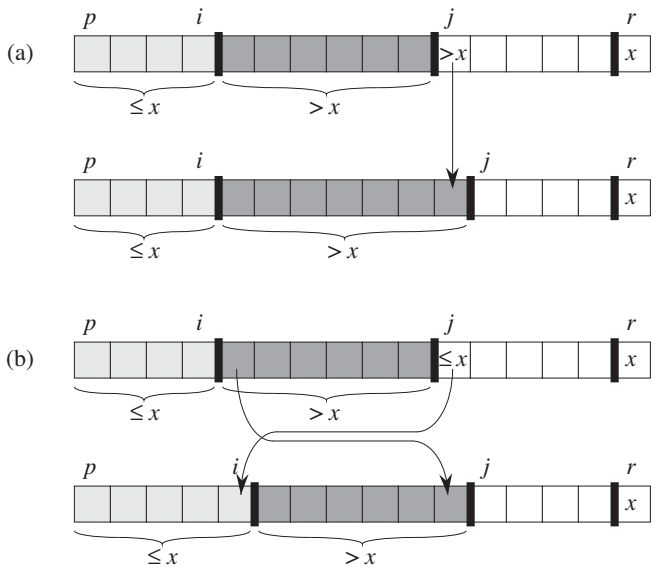


Figure 7.3 The two cases for one iteration of procedure PARTITION. **(a)** If $A[j] > x$, the only action is to increment j, which maintains the loop invariant. **(b)** If $A[j] \le x$, index i is incremented, $A[i]$ and $A[j]$ are swapped, and then j is incremented. Again, the loop invariant is maintained.

7.1-2

What value of q does PARTITION return when all elements in the array $A[p..r]$ have the same value? Modify PARTITION so that $q = \lfloor (p + r)/2 \rfloor$ when all elements in the array $A[p..r]$ have the same value.

7.1-3

Give a brief argument that the running time of PARTITION on a subarray of size n is $\Theta(n)$.

7.1-4

How would you modify QUICKSORT to sort into nonincreasing order?

7.2 Performance of quicksort

The running time of quicksort depends on whether the partitioning is balanced or unbalanced, which in turn depends on which elements are used for partitioning. If the partitioning is balanced, the algorithm runs asymptotically as fast as merge

sort. If the partitioning is unbalanced, however, it can run asymptotically as slowly as insertion sort. In this section, we shall informally investigate how quicksort performs under the assumptions of balanced versus unbalanced partitioning.

Worst-case partitioning

The worst-case behavior for quicksort occurs when the partitioning routine produces one subproblem with $n - 1$ elements and one with 0 elements. (We prove this claim in Section 7.4.1.) Let us assume that this unbalanced partitioning arises in each recursive call. The partitioning costs $\Theta(n)$ time. Since the recursive call on an array of size 0 just returns, $T(0) = \Theta(1)$, and the recurrence for the running time is

$$\begin{aligned} T(n) &= T(n-1) + T(0) + \Theta(n) \\ &= T(n-1) + \Theta(n) \,. \end{aligned}$$

Intuitively, if we sum the costs incurred at each level of the recursion, we get an arithmetic series (equation (A.2)), which evaluates to $\Theta(n^2)$. Indeed, it is straightforward to use the substitution method to prove that the recurrence $T(n) = T(n-1) + \Theta(n)$ has the solution $T(n) = \Theta(n^2)$. (See Exercise 7.2-1.)

Thus, if the partitioning is maximally unbalanced at every recursive level of the algorithm, the running time is $\Theta(n^2)$. Therefore the worst-case running time of quicksort is no better than that of insertion sort. Moreover, the $\Theta(n^2)$ running time occurs when the input array is already completely sorted—a common situation in which insertion sort runs in $O(n)$ time.

Best-case partitioning

In the most even possible split, PARTITION produces two subproblems, each of size no more than $n/2$, since one is of size $\lfloor n/2 \rfloor$ and one of size $\lceil n/2 \rceil - 1$. In this case, quicksort runs much faster. The recurrence for the running time is then

$$T(n) = 2T(n/2) + \Theta(n) \,,$$

where we tolerate the sloppiness from ignoring the floor and ceiling and from subtracting 1. By case 2 of the master theorem (Theorem 4.1), this recurrence has the solution $T(n) = \Theta(n \lg n)$. By equally balancing the two sides of the partition at every level of the recursion, we get an asymptotically faster algorithm.

Balanced partitioning

The average-case running time of quicksort is much closer to the best case than to the worst case, as the analyses in Section 7.4 will show. The key to understand-

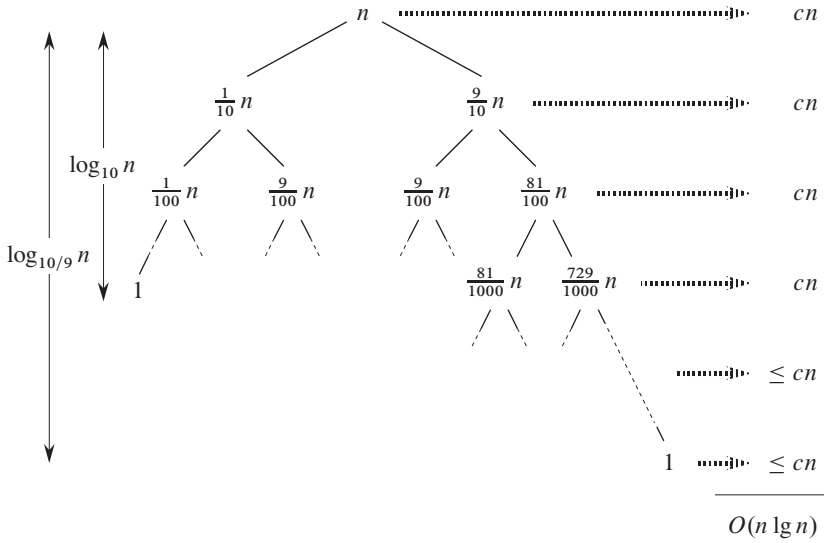


Figure 7.4 A recursion tree for QUICKSORT in which PARTITION always produces a 9-to-1 split, yielding a running time of $O(n \lg n)$. Nodes show subproblem sizes, with per-level costs on the right. The per-level costs include the constant c implicit in the $\Theta(n)$ term.

ing why is to understand how the balance of the partitioning is reflected in the recurrence that describes the running time.

Suppose, for example, that the partitioning algorithm always produces a 9-to-1 proportional split, which at first blush seems quite unbalanced. We then obtain the recurrence

$$T(n) = T(9n/10) + T(n/10) + cn \ ,$$

on the running time of quicksort, where we have explicitly included the constant c hidden in the $\Theta(n)$ term. Figure 7.4 shows the recursion tree for this recurrence. Notice that every level of the tree has cost cn, until the recursion reaches a boundary condition at depth $\log_{10} n = \Theta(\lg n)$, and then the levels have cost at most cn. The recursion terminates at depth $\log_{10/9} n = \Theta(\lg n)$. The total cost of quicksort is therefore $O(n \lg n)$. Thus, with a 9-to-1 proportional split at every level of recursion, which intuitively seems quite unbalanced, quicksort runs in $O(n \lg n)$ time—asymptotically the same as if the split were right down the middle. Indeed, even a 99-to-1 split yields an $O(n \lg n)$ running time. In fact, any split of *constant* proportionality yields a recursion tree of depth $\Theta(\lg n)$, where the cost at each level is $O(n)$. The running time is therefore $O(n \lg n)$ whenever the split has constant proportionality.

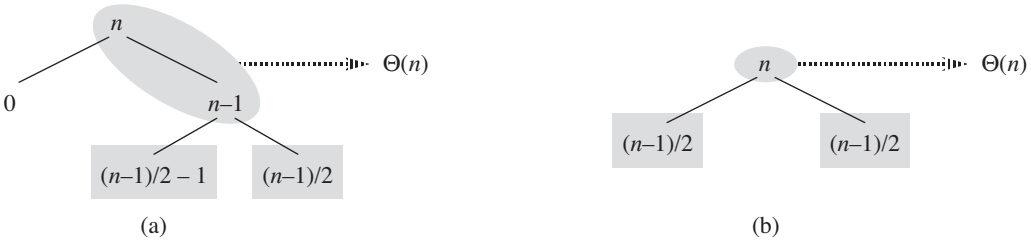


Figure 7.5 **(a)** Two levels of a recursion tree for quicksort. The partitioning at the root costs n and produces a "bad" split: two subarrays of sizes 0 and $n-1$. The partitioning of the subarray of size $n-1$ costs $n-1$ and produces a "good" split: subarrays of size $(n-1)/2-1$ and $(n-1)/2$. **(b)** A single level of a recursion tree that is very well balanced. In both parts, the partitioning cost for the subproblems shown with elliptical shading is $\Theta(n)$. Yet the subproblems remaining to be solved in (a), shown with square shading, are no larger than the corresponding subproblems remaining to be solved in (b).

Intuition for the average case

To develop a clear notion of the randomized behavior of quicksort, we must make an assumption about how frequently we expect to encounter the various inputs. The behavior of quicksort depends on the relative ordering of the values in the array elements given as the input, and not by the particular values in the array. As in our probabilistic analysis of the hiring problem in Section 5.2, we will assume for now that all permutations of the input numbers are equally likely.

When we run quicksort on a random input array, the partitioning is highly unlikely to happen in the same way at every level, as our informal analysis has assumed. We expect that some of the splits will be reasonably well balanced and that some will be fairly unbalanced. For example, Exercise 7.2-6 asks you to show that about 80 percent of the time PARTITION produces a split that is more balanced than 9 to 1, and about 20 percent of the time it produces a split that is less balanced than 9 to 1.

In the average case, PARTITION produces a mix of "good" and "bad" splits. In a recursion tree for an average-case execution of PARTITION, the good and bad splits are distributed randomly throughout the tree. Suppose, for the sake of intuition, that the good and bad splits alternate levels in the tree, and that the good splits are best-case splits and the bad splits are worst-case splits. Figure 7.5(a) shows the splits at two consecutive levels in the recursion tree. At the root of the tree, the cost is n for partitioning, and the subarrays produced have sizes $n-1$ and 0: the worst case. At the next level, the subarray of size $n-1$ undergoes best-case partitioning into subarrays of size $(n-1)/2-1$ and $(n-1)/2$. Let's assume that the boundary-condition cost is 1 for the subarray of size 0.

The combination of the bad split followed by the good split produces three subarrays of sizes 0, $(n-1)/2-1$, and $(n-1)/2$ at a combined partitioning cost of $\Theta(n)+\Theta(n-1)=\Theta(n)$. Certainly, this situation is no worse than that in Figure 7.5(b), namely a single level of partitioning that produces two subarrays of size $(n-1)/2$, at a cost of $\Theta(n)$. Yet this latter situation is balanced! Intuitively, the $\Theta(n-1)$ cost of the bad split can be absorbed into the $\Theta(n)$ cost of the good split, and the resulting split is good. Thus, the running time of quicksort, when levels alternate between good and bad splits, is like the running time for good splits alone: still $O(n \lg n)$, but with a slightly larger constant hidden by the O-notation. We shall give a rigorous analysis of the expected running time of a randomized version of quicksort in Section 7.4.2.

Exercises

7.2-1
Use the substitution method to prove that the recurrence $T(n) = T(n-1) + \Theta(n)$ has the solution $T(n) = \Theta(n^2)$, as claimed at the beginning of Section 7.2.

7.2-2
What is the running time of QUICKSORT when all elements of array A have the same value?

7.2-3
Show that the running time of QUICKSORT is $\Theta(n^2)$ when the array A contains distinct elements and is sorted in decreasing order.

7.2-4
Banks often record transactions on an account in order of the times of the transactions, but many people like to receive their bank statements with checks listed in order by check number. People usually write checks in order by check number, and merchants usually cash them with reasonable dispatch. The problem of converting time-of-transaction ordering to check-number ordering is therefore the problem of sorting almost-sorted input. Argue that the procedure INSERTION-SORT would tend to beat the procedure QUICKSORT on this problem.

7.2-5
Suppose that the splits at every level of quicksort are in the proportion $1-\alpha$ to α, where $0 < \alpha \leq 1/2$ is a constant. Show that the minimum depth of a leaf in the recursion tree is approximately $-\lg n / \lg \alpha$ and the maximum depth is approximately $-\lg n / \lg(1-\alpha)$. (Don't worry about integer round-off.)

7.2-6 ⋆

Argue that for any constant $0 < \alpha \leq 1/2$, the probability is approximately $1 - 2\alpha$ that on a random input array, PARTITION produces a split more balanced than $1-\alpha$ to α.

7.3 A randomized version of quicksort

In exploring the average-case behavior of quicksort, we have made an assumption that all permutations of the input numbers are equally likely. In an engineering situation, however, we cannot always expect this assumption to hold. (See Exercise 7.2-4.) As we saw in Section 5.3, we can sometimes add randomization to an algorithm in order to obtain good expected performance over all inputs. Many people regard the resulting randomized version of quicksort as the sorting algorithm of choice for large enough inputs.

In Section 5.3, we randomized our algorithm by explicitly permuting the input. We could do so for quicksort also, but a different randomization technique, called ***random sampling***, yields a simpler analysis. Instead of always using $A[r]$ as the pivot, we will select a randomly chosen element from the subarray $A[p\,..\,r]$. We do so by first exchanging element $A[r]$ with an element chosen at random from $A[p\,..\,r]$. By randomly sampling the range $p, \ldots, r$, we ensure that the pivot element $x = A[r]$ is equally likely to be any of the $r - p + 1$ elements in the subarray. Because we randomly choose the pivot element, we expect the split of the input array to be reasonably well balanced on average.

The changes to PARTITION and QUICKSORT are small. In the new partition procedure, we simply implement the swap before actually partitioning:

```
RANDOMIZED-PARTITION(A, p, r)
1  i = RANDOM(p, r)
2  exchange A[r] with A[i]
3  return PARTITION(A, p, r)
```

The new quicksort calls RANDOMIZED-PARTITION in place of PARTITION:

```
RANDOMIZED-QUICKSORT(A, p, r)
1  if p < r
2       q = RANDOMIZED-PARTITION(A, p, r)
3       RANDOMIZED-QUICKSORT(A, p, q − 1)
4       RANDOMIZED-QUICKSORT(A, q + 1, r)
```

We analyze this algorithm in the next section.

Exercises

7.3-1
Why do we analyze the expected running time of a randomized algorithm and not its worst-case running time?

7.3-2
When RANDOMIZED-QUICKSORT runs, how many calls are made to the random-number generator RANDOM in the worst case? How about in the best case? Give your answer in terms of Θ-notation.

7.4 Analysis of quicksort

Section 7.2 gave some intuition for the worst-case behavior of quicksort and for why we expect it to run quickly. In this section, we analyze the behavior of quicksort more rigorously. We begin with a worst-case analysis, which applies to either QUICKSORT or RANDOMIZED-QUICKSORT, and conclude with an analysis of the expected running time of RANDOMIZED-QUICKSORT.

7.4.1 Worst-case analysis

We saw in Section 7.2 that a worst-case split at every level of recursion in quicksort produces a $\Theta(n^2)$ running time, which, intuitively, is the worst-case running time of the algorithm. We now prove this assertion.

Using the substitution method (see Section 4.3), we can show that the running time of quicksort is $O(n^2)$. Let $T(n)$ be the worst-case time for the procedure QUICKSORT on an input of size n. We have the recurrence

$$T(n) = \max_{0 \le q \le n-1} (T(q) + T(n-q-1)) + \Theta(n) , \tag{7.1}$$

where the parameter q ranges from 0 to $n-1$ because the procedure PARTITION produces two subproblems with total size $n-1$. We guess that $T(n) \le cn^2$ for some constant c. Substituting this guess into recurrence (7.1), we obtain

$$\begin{aligned} T(n) &\le \max_{0 \le q \le n-1} (cq^2 + c(n-q-1)^2) + \Theta(n) \\ &= c \cdot \max_{0 \le q \le n-1} (q^2 + (n-q-1)^2) + \Theta(n) . \end{aligned}$$

The expression $q^2 + (n-q-1)^2$ achieves a maximum over the parameter's range $0 \le q \le n-1$ at either endpoint. To verify this claim, note that the second derivative of the expression with respect to q is positive (see Exercise 7.4-3). This

observation gives us the bound $\max_{0 \le q \le n-1}(q^2 + (n-q-1)^2) \le (n-1)^2 = n^2 - 2n + 1$. Continuing with our bounding of $T(n)$, we obtain

$$\begin{aligned} T(n) &\le cn^2 - c(2n-1) + \Theta(n) \\ &\le cn^2 , \end{aligned}$$

since we can pick the constant c large enough so that the $c(2n-1)$ term dominates the $\Theta(n)$ term. Thus, $T(n) = O(n^2)$. We saw in Section 7.2 a specific case in which quicksort takes $\Omega(n^2)$ time: when partitioning is unbalanced. Alternatively, Exercise 7.4-1 asks you to show that recurrence (7.1) has a solution of $T(n) = \Omega(n^2)$. Thus, the (worst-case) running time of quicksort is $\Theta(n^2)$.

7.4.2 Expected running time

We have already seen the intuition behind why the expected running time of RANDOMIZED-QUICKSORT is $O(n \lg n)$: if, in each level of recursion, the split induced by RANDOMIZED-PARTITION puts any constant fraction of the elements on one side of the partition, then the recursion tree has depth $\Theta(\lg n)$, and $O(n)$ work is performed at each level. Even if we add a few new levels with the most unbalanced split possible between these levels, the total time remains $O(n \lg n)$. We can analyze the expected running time of RANDOMIZED-QUICKSORT precisely by first understanding how the partitioning procedure operates and then using this understanding to derive an $O(n \lg n)$ bound on the expected running time. This upper bound on the expected running time, combined with the $\Theta(n \lg n)$ best-case bound we saw in Section 7.2, yields a $\Theta(n \lg n)$ expected running time. We assume throughout that the values of the elements being sorted are distinct.

Running time and comparisons

The QUICKSORT and RANDOMIZED-QUICKSORT procedures differ only in how they select pivot elements; they are the same in all other respects. We can therefore couch our analysis of RANDOMIZED-QUICKSORT by discussing the QUICKSORT and PARTITION procedures, but with the assumption that pivot elements are selected randomly from the subarray passed to RANDOMIZED-PARTITION.

The running time of QUICKSORT is dominated by the time spent in the PARTITION procedure. Each time the PARTITION procedure is called, it selects a pivot element, and this element is never included in any future recursive calls to QUICKSORT and PARTITION. Thus, there can be at most n calls to PARTITION over the entire execution of the quicksort algorithm. One call to PARTITION takes $O(1)$ time plus an amount of time that is proportional to the number of iterations of the **for** loop in lines 3–6. Each iteration of this **for** loop performs a comparison in line 4, comparing the pivot element to another element of the array A. Therefore,

if we can count the total number of times that line 4 is executed, we can bound the total time spent in the **for** loop during the entire execution of QUICKSORT.

Lemma 7.1
Let X be the number of comparisons performed in line 4 of PARTITION over the entire execution of QUICKSORT on an n-element array. Then the running time of QUICKSORT is $O(n + X)$.

Proof By the discussion above, the algorithm makes at most n calls to PARTITION, each of which does a constant amount of work and then executes the **for** loop some number of times. Each iteration of the **for** loop executes line 4. ■

Our goal, therefore, is to compute X, the total number of comparisons performed in all calls to PARTITION. We will not attempt to analyze how many comparisons are made in *each* call to PARTITION. Rather, we will derive an overall bound on the total number of comparisons. To do so, we must understand when the algorithm compares two elements of the array and when it does not. For ease of analysis, we rename the elements of the array A as $z_1, z_2, \ldots, z_n$, with z_i being the ith smallest element. We also define the set $Z_{ij} = \{z_i, z_{i+1}, \ldots, z_j\}$ to be the set of elements between z_i and z_j, inclusive.

When does the algorithm compare z_i and z_j? To answer this question, we first observe that each pair of elements is compared at most once. Why? Elements are compared only to the pivot element and, after a particular call of PARTITION finishes, the pivot element used in that call is never again compared to any other elements.

Our analysis uses indicator random variables (see Section 5.2). We define

$$X_{ij} = \mathrm{I}\{z_i \text{ is compared to } z_j\} ,$$

where we are considering whether the comparison takes place at any time during the execution of the algorithm, not just during one iteration or one call of PARTITION. Since each pair is compared at most once, we can easily characterize the total number of comparisons performed by the algorithm:

$$X = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} X_{ij} .$$

Taking expectations of both sides, and then using linearity of expectation and Lemma 5.1, we obtain

$$\mathrm{E}[X] = \mathrm{E}\left[\sum_{i=1}^{n-1} \sum_{j=i+1}^{n} X_{ij}\right]$$

$$
\begin{aligned}
&= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \mathrm{E}[X_{ij}] \\
&= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \Pr\{z_i \text{ is compared to } z_j\} \ . \qquad (7.2)
\end{aligned}
$$

It remains to compute $\Pr\{z_i \text{ is compared to } z_j\}$. Our analysis assumes that the RANDOMIZED-PARTITION procedure chooses each pivot randomly and independently.

Let us think about when two items are *not* compared. Consider an input to quicksort of the numbers 1 through 10 (in any order), and suppose that the first pivot element is 7. Then the first call to PARTITION separates the numbers into two sets: $\{1, 2, 3, 4, 5, 6\}$ and $\{8, 9, 10\}$. In doing so, the pivot element 7 is compared to all other elements, but no number from the first set (e.g., 2) is or ever will be compared to any number from the second set (e.g., 9).

In general, because we assume that element values are distinct, once a pivot x is chosen with $z_i < x < z_j$, we know that z_i and z_j cannot be compared at any subsequent time. If, on the other hand, z_i is chosen as a pivot before any other item in Z_{ij}, then z_i will be compared to each item in Z_{ij}, except for itself. Similarly, if z_j is chosen as a pivot before any other item in Z_{ij}, then z_j will be compared to each item in Z_{ij}, except for itself. In our example, the values 7 and 9 are compared because 7 is the first item from $Z_{7,9}$ to be chosen as a pivot. In contrast, 2 and 9 will never be compared because the first pivot element chosen from $Z_{2,9}$ is 7. Thus, z_i and z_j are compared if and only if the first element to be chosen as a pivot from Z_{ij} is either z_i or z_j.

We now compute the probability that this event occurs. Prior to the point at which an element from Z_{ij} has been chosen as a pivot, the whole set Z_{ij} is together in the same partition. Therefore, any element of Z_{ij} is equally likely to be the first one chosen as a pivot. Because the set Z_{ij} has $j-i+1$ elements, and because pivots are chosen randomly and independently, the probability that any given element is the first one chosen as a pivot is $1/(j-i+1)$. Thus, we have

$$
\begin{aligned}
\Pr\{z_i \text{ is compared to } z_j\} &= \Pr\{z_i \text{ or } z_j \text{ is first pivot chosen from } Z_{ij}\} \\
&= \Pr\{z_i \text{ is first pivot chosen from } Z_{ij}\} \\
&\quad + \Pr\{z_j \text{ is first pivot chosen from } Z_{ij}\} \\
&= \frac{1}{j-i+1} + \frac{1}{j-i+1} \\
&= \frac{2}{j-i+1} \ . \qquad (7.3)
\end{aligned}
$$

The second line follows because the two events are mutually exclusive. Combining equations (7.2) and (7.3), we get that

$$\mathrm{E}[X] = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \frac{2}{j-i+1} .$$

We can evaluate this sum using a change of variables ($k = j - i$) and the bound on the harmonic series in equation (A.7):

$$\begin{aligned}
\mathrm{E}[X] &= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \frac{2}{j-i+1} \\
&= \sum_{i=1}^{n-1} \sum_{k=1}^{n-i} \frac{2}{k+1} \\
&< \sum_{i=1}^{n-1} \sum_{k=1}^{n} \frac{2}{k} \\
&= \sum_{i=1}^{n-1} O(\lg n) \\
&= O(n \lg n) . \qquad (7.4)
\end{aligned}$$

Thus we conclude that, using RANDOMIZED-PARTITION, the expected running time of quicksort is $O(n \lg n)$ when element values are distinct.

Exercises

7.4-1
Show that in the recurrence

$$T(n) = \max_{0 \le q \le n-1} (T(q) + T(n-q-1)) + \Theta(n) ,$$

$T(n) = \Omega(n^2)$.

7.4-2
Show that quicksort's best-case running time is $\Omega(n \lg n)$.

7.4-3
Show that the expression $q^2 + (n-q-1)^2$ achieves a maximum over $q = 0, 1, \ldots, n-1$ when $q = 0$ or $q = n-1$.

7.4-4
Show that RANDOMIZED-QUICKSORT's expected running time is $\Omega(n \lg n)$.

7.4-5
We can improve the running time of quicksort in practice by taking advantage of the fast running time of insertion sort when its input is "nearly" sorted. Upon calling quicksort on a subarray with fewer than k elements, let it simply return without sorting the subarray. After the top-level call to quicksort returns, run insertion sort on the entire array to finish the sorting process. Argue that this sorting algorithm runs in $O(nk + n \lg(n/k))$ expected time. How should we pick k, both in theory and in practice?

7.4-6 ⋆
Consider modifying the PARTITION procedure by randomly picking three elements from array A and partitioning about their median (the middle value of the three elements). Approximate the probability of getting at worst an α-to-$(1-\alpha)$ split, as a function of α in the range $0 < \alpha < 1$.

Problems

7-1 Hoare partition correctness
The version of PARTITION given in this chapter is not the original partitioning algorithm. Here is the original partition algorithm, which is due to C. A. R. Hoare:

```
HOARE-PARTITION(A, p, r)
 1  x = A[p]
 2  i = p − 1
 3  j = r + 1
 4  while TRUE
 5      repeat
 6          j = j − 1
 7      until A[j] ≤ x
 8      repeat
 9          i = i + 1
10      until A[i] ≥ x
11      if i < j
12          exchange A[i] with A[j]
13      else return j
```

a. Demonstrate the operation of HOARE-PARTITION on the array $A = \langle 13, 19, 9, 5, 12, 8, 7, 4, 11, 2, 6, 21 \rangle$, showing the values of the array and auxiliary values after each iteration of the **while** loop in lines 4–13.

The next three questions ask you to give a careful argument that the procedure HOARE-PARTITION is correct. Assuming that the subarray $A[p..r]$ contains at least two elements, prove the following:

b. The indices i and j are such that we never access an element of A outside the subarray $A[p..r]$.

c. When HOARE-PARTITION terminates, it returns a value j such that $p \le j < r$.

d. Every element of $A[p..j]$ is less than or equal to every element of $A[j+1..r]$ when HOARE-PARTITION terminates.

The PARTITION procedure in Section 7.1 separates the pivot value (originally in $A[r]$) from the two partitions it forms. The HOARE-PARTITION procedure, on the other hand, always places the pivot value (originally in $A[p]$) into one of the two partitions $A[p..j]$ and $A[j+1..r]$. Since $p \le j < r$, this split is always nontrivial.

e. Rewrite the QUICKSORT procedure to use HOARE-PARTITION.

7-2 Quicksort with equal element values

The analysis of the expected running time of randomized quicksort in Section 7.4.2 assumes that all element values are distinct. In this problem, we examine what happens when they are not.

a. Suppose that all element values are equal. What would be randomized quicksort's running time in this case?

b. The PARTITION procedure returns an index q such that each element of $A[p..q-1]$ is less than or equal to $A[q]$ and each element of $A[q+1..r]$ is greater than $A[q]$. Modify the PARTITION procedure to produce a procedure PARTITION$'(A, p, r)$, which permutes the elements of $A[p..r]$ and returns two indices q and t, where $p \le q \le t \le r$, such that

- all elements of $A[q..t]$ are equal,
- each element of $A[p..q-1]$ is less than $A[q]$, and
- each element of $A[t+1..r]$ is greater than $A[q]$.

Like PARTITION, your PARTITION$'$ procedure should take $\Theta(r-p)$ time.

c. Modify the RANDOMIZED-QUICKSORT procedure to call PARTITION$'$, and name the new procedure RANDOMIZED-QUICKSORT$'$. Then modify the QUICKSORT procedure to produce a procedure QUICKSORT$'(p, r)$ that calls

RANDOMIZED-PARTITION′ and recurses only on partitions of elements not known to be equal to each other.

d. Using QUICKSORT′, how would you adjust the analysis in Section 7.4.2 to avoid the assumption that all elements are distinct?

7-3 Alternative quicksort analysis

An alternative analysis of the running time of randomized quicksort focuses on the expected running time of each individual recursive call to RANDOMIZED-QUICKSORT, rather than on the number of comparisons performed.

a. Argue that, given an array of size n, the probability that any particular element is chosen as the pivot is $1/n$. Use this to define indicator random variables $X_i = \mathrm{I}\{i\text{th smallest element is chosen as the pivot}\}$. What is $\mathrm{E}[X_i]$?

b. Let $T(n)$ be a random variable denoting the running time of quicksort on an array of size n. Argue that

$$\mathrm{E}[T(n)] = \mathrm{E}\left[\sum_{q=1}^{n} X_q \left(T(q-1) + T(n-q) + \Theta(n)\right)\right] . \tag{7.5}$$

c. Show that we can rewrite equation (7.5) as

$$\mathrm{E}[T(n)] = \frac{2}{n}\sum_{q=2}^{n-1} \mathrm{E}[T(q)] + \Theta(n) . \tag{7.6}$$

d. Show that

$$\sum_{k=2}^{n-1} k \lg k \le \frac{1}{2}n^2 \lg n - \frac{1}{8}n^2 . \tag{7.7}$$

(*Hint:* Split the summation into two parts, one for $k = 2, 3, \ldots, \lceil n/2 \rceil - 1$ and one for $k = \lceil n/2 \rceil, \ldots, n-1$.)

e. Using the bound from equation (7.7), show that the recurrence in equation (7.6) has the solution $\mathrm{E}[T(n)] = \Theta(n \lg n)$. (*Hint:* Show, by substitution, that $\mathrm{E}[T(n)] \le an \lg n$ for sufficiently large n and for some positive constant a.)

7-4 Stack depth for quicksort

The QUICKSORT algorithm of Section 7.1 contains two recursive calls to itself. After QUICKSORT calls PARTITION, it recursively sorts the left subarray and then it recursively sorts the right subarray. The second recursive call in QUICKSORT is not really necessary; we can avoid it by using an iterative control structure. This technique, called ***tail recursion***, is provided automatically by good compilers. Consider the following version of quicksort, which simulates tail recursion:

```
TAIL-RECURSIVE-QUICKSORT(A, p, r)
1  while p < r
2      // Partition and sort left subarray.
3      q = PARTITION(A, p, r)
4      TAIL-RECURSIVE-QUICKSORT(A, p, q − 1)
5      p = q + 1
```

a. Argue that TAIL-RECURSIVE-QUICKSORT$(A, 1, A.length)$ correctly sorts the array A.

Compilers usually execute recursive procedures by using a ***stack*** that contains pertinent information, including the parameter values, for each recursive call. The information for the most recent call is at the top of the stack, and the information for the initial call is at the bottom. Upon calling a procedure, its information is ***pushed*** onto the stack; when it terminates, its information is ***popped***. Since we assume that array parameters are represented by pointers, the information for each procedure call on the stack requires $O(1)$ stack space. The ***stack depth*** is the maximum amount of stack space used at any time during a computation.

b. Describe a scenario in which TAIL-RECURSIVE-QUICKSORT's stack depth is $\Theta(n)$ on an n-element input array.

c. Modify the code for TAIL-RECURSIVE-QUICKSORT so that the worst-case stack depth is $\Theta(\lg n)$. Maintain the $O(n \lg n)$ expected running time of the algorithm.

7-5 Median-of-3 partition

One way to improve the RANDOMIZED-QUICKSORT procedure is to partition around a pivot that is chosen more carefully than by picking a random element from the subarray. One common approach is the ***median-of-3*** method: choose the pivot as the median (middle element) of a set of 3 elements randomly selected from the subarray. (See Exercise 7.4-6.) For this problem, let us assume that the elements in the input array $A[1..n]$ are distinct and that $n \geq 3$. We denote the

sorted output array by $A'[1..n]$. Using the median-of-3 method to choose the pivot element x, define $p_i = \Pr\{x = A'[i]\}$.

a. Give an exact formula for p_i as a function of n and i for $i = 2, 3, \ldots, n-1$. (Note that $p_1 = p_n = 0$.)

b. By what amount have we increased the likelihood of choosing the pivot as $x = A'[\lfloor (n+1)/2 \rfloor]$, the median of $A[1..n]$, compared with the ordinary implementation? Assume that $n \to \infty$, and give the limiting ratio of these probabilities.

c. If we define a "good" split to mean choosing the pivot as $x = A'[i]$, where $n/3 \le i \le 2n/3$, by what amount have we increased the likelihood of getting a good split compared with the ordinary implementation? (*Hint:* Approximate the sum by an integral.)

d. Argue that in the $\Omega(n \lg n)$ running time of quicksort, the median-of-3 method affects only the constant factor.

7-6 Fuzzy sorting of intervals

Consider a sorting problem in which we do not know the numbers exactly. Instead, for each number, we know an interval on the real line to which it belongs. That is, we are given n closed intervals of the form $[a_i, b_i]$, where $a_i \le b_i$. We wish to ***fuzzy-sort*** these intervals, i.e., to produce a permutation $\langle i_1, i_2, \ldots, i_n \rangle$ of the intervals such that for $j = 1, 2, \ldots, n$, there exist $c_j \in [a_{i_j}, b_{i_j}]$ satisfying $c_1 \le c_2 \le \cdots \le c_n$.

a. Design a randomized algorithm for fuzzy-sorting n intervals. Your algorithm should have the general structure of an algorithm that quicksorts the left endpoints (the a_i values), but it should take advantage of overlapping intervals to improve the running time. (As the intervals overlap more and more, the problem of fuzzy-sorting the intervals becomes progressively easier. Your algorithm should take advantage of such overlapping, to the extent that it exists.)

b. Argue that your algorithm runs in expected time $\Theta(n \lg n)$ in general, but runs in expected time $\Theta(n)$ when all of the intervals overlap (i.e., when there exists a value x such that $x \in [a_i, b_i]$ for all i). Your algorithm should not be checking for this case explicitly; rather, its performance should naturally improve as the amount of overlap increases.

Chapter notes

The quicksort procedure was invented by Hoare [170]; Hoare's version appears in Problem 7-1. The PARTITION procedure given in Section 7.1 is due to N. Lomuto. The analysis in Section 7.4 is due to Avrim Blum. Sedgewick [305] and Bentley [43] provide a good reference on the details of implementation and how they matter.

McIlroy [248] showed how to engineer a "killer adversary" that produces an array on which virtually any implementation of quicksort takes $\Theta(n^2)$ time. If the implementation is randomized, the adversary produces the array after seeing the random choices of the quicksort algorithm.

8 Sorting in Linear Time

We have now introduced several algorithms that can sort n numbers in $O(n \lg n)$ time. Merge sort and heapsort achieve this upper bound in the worst case; quicksort achieves it on average. Moreover, for each of these algorithms, we can produce a sequence of n input numbers that causes the algorithm to run in $\Omega(n \lg n)$ time.

These algorithms share an interesting property: *the sorted order they determine is based only on comparisons between the input elements*. We call such sorting algorithms ***comparison sorts***. All the sorting algorithms introduced thus far are comparison sorts.

In Section 8.1, we shall prove that any comparison sort must make $\Omega(n \lg n)$ comparisons in the worst case to sort n elements. Thus, merge sort and heapsort are asymptotically optimal, and no comparison sort exists that is faster by more than a constant factor.

Sections 8.2, 8.3, and 8.4 examine three sorting algorithms—counting sort, radix sort, and bucket sort—that run in linear time. Of course, these algorithms use operations other than comparisons to determine the sorted order. Consequently, the $\Omega(n \lg n)$ lower bound does not apply to them.

8.1 Lower bounds for sorting

In a comparison sort, we use only comparisons between elements to gain order information about an input sequence $\langle a_1, a_2, \ldots, a_n \rangle$. That is, given two elements a_i and a_j, we perform one of the tests $a_i < a_j$, $a_i \leq a_j$, $a_i = a_j$, $a_i \geq a_j$, or $a_i > a_j$ to determine their relative order. We may not inspect the values of the elements or gain order information about them in any other way.

In this section, we assume without loss of generality that all the input elements are distinct. Given this assumption, comparisons of the form $a_i = a_j$ are useless, so we can assume that no comparisons of this form are made. We also note that the comparisons $a_i \leq a_j$, $a_i \geq a_j$, $a_i > a_j$, and $a_i < a_j$ are all equivalent in that

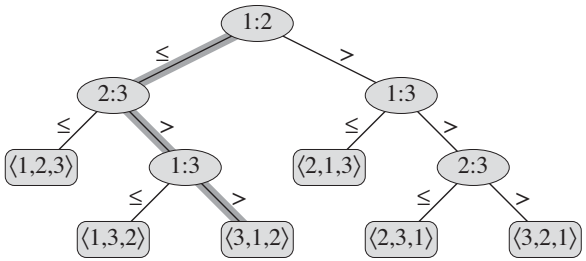


Figure 8.1 The decision tree for insertion sort operating on three elements. An internal node annotated by $i{:}j$ indicates a comparison between a_i and a_j. A leaf annotated by the permutation $\langle \pi(1), \pi(2), \ldots, \pi(n) \rangle$ indicates the ordering $a_{\pi(1)} \leq a_{\pi(2)} \leq \cdots \leq a_{\pi(n)}$. The shaded path indicates the decisions made when sorting the input sequence $\langle a_1 = 6, a_2 = 8, a_3 = 5 \rangle$; the permutation $\langle 3, 1, 2 \rangle$ at the leaf indicates that the sorted ordering is $a_3 = 5 \leq a_1 = 6 \leq a_2 = 8$. There are $3! = 6$ possible permutations of the input elements, and so the decision tree must have at least 6 leaves.

they yield identical information about the relative order of a_i and a_j. We therefore assume that all comparisons have the form $a_i \leq a_j$.

The decision-tree model

We can view comparison sorts abstractly in terms of decision trees. A ***decision tree*** is a full binary tree that represents the comparisons between elements that are performed by a particular sorting algorithm operating on an input of a given size. Control, data movement, and all other aspects of the algorithm are ignored. Figure 8.1 shows the decision tree corresponding to the insertion sort algorithm from Section 2.1 operating on an input sequence of three elements.

In a decision tree, we annotate each internal node by $i{:}j$ for some i and j in the range $1 \leq i, j \leq n$, where n is the number of elements in the input sequence. We also annotate each leaf by a permutation $\langle \pi(1), \pi(2), \ldots, \pi(n) \rangle$. (See Section C.1 for background on permutations.) The execution of the sorting algorithm corresponds to tracing a simple path from the root of the decision tree down to a leaf. Each internal node indicates a comparison $a_i \leq a_j$. The left subtree then dictates subsequent comparisons once we know that $a_i \leq a_j$, and the right subtree dictates subsequent comparisons knowing that $a_i > a_j$. When we come to a leaf, the sorting algorithm has established the ordering $a_{\pi(1)} \leq a_{\pi(2)} \leq \cdots \leq a_{\pi(n)}$. Because any correct sorting algorithm must be able to produce each permutation of its input, each of the $n!$ permutations on n elements must appear as one of the leaves of the decision tree for a comparison sort to be correct. Furthermore, each of these leaves must be reachable from the root by a downward path corresponding to an actual

execution of the comparison sort. (We shall refer to such leaves as "reachable.") Thus, we shall consider only decision trees in which each permutation appears as a reachable leaf.

A lower bound for the worst case

The length of the longest simple path from the root of a decision tree to any of its reachable leaves represents the worst-case number of comparisons that the corresponding sorting algorithm performs. Consequently, the worst-case number of comparisons for a given comparison sort algorithm equals the height of its decision tree. A lower bound on the heights of all decision trees in which each permutation appears as a reachable leaf is therefore a lower bound on the running time of any comparison sort algorithm. The following theorem establishes such a lower bound.

Theorem 8.1
Any comparison sort algorithm requires $\Omega(n \lg n)$ comparisons in the worst case.

Proof From the preceding discussion, it suffices to determine the height of a decision tree in which each permutation appears as a reachable leaf. Consider a decision tree of height h with l reachable leaves corresponding to a comparison sort on n elements. Because each of the $n!$ permutations of the input appears as some leaf, we have $n! \leq l$. Since a binary tree of height h has no more than 2^h leaves, we have

$$n! \leq l \leq 2^h ,$$

which, by taking logarithms, implies

$$\begin{aligned} h &\geq \lg(n!) && \text{(since the lg function is monotonically increasing)} \\ &= \Omega(n \lg n) && \text{(by equation (3.19))} . \end{aligned}$$

■

Corollary 8.2
Heapsort and merge sort are asymptotically optimal comparison sorts.

Proof The $O(n \lg n)$ upper bounds on the running times for heapsort and merge sort match the $\Omega(n \lg n)$ worst-case lower bound from Theorem 8.1. ■

Exercises

8.1-1
What is the smallest possible depth of a leaf in a decision tree for a comparison sort?

8.1-2
Obtain asymptotically tight bounds on $\lg(n!)$ without using Stirling's approximation. Instead, evaluate the summation $\sum_{k=1}^{n} \lg k$ using techniques from Section A.2.

8.1-3
Show that there is no comparison sort whose running time is linear for at least half of the $n!$ inputs of length n. What about a fraction of $1/n$ of the inputs of length n? What about a fraction $1/2^n$?

8.1-4
Suppose that you are given a sequence of n elements to sort. The input sequence consists of n/k subsequences, each containing k elements. The elements in a given subsequence are all smaller than the elements in the succeeding subsequence and larger than the elements in the preceding subsequence. Thus, all that is needed to sort the whole sequence of length n is to sort the k elements in each of the n/k subsequences. Show an $\Omega(n \lg k)$ lower bound on the number of comparisons needed to solve this variant of the sorting problem. (*Hint:* It is not rigorous to simply combine the lower bounds for the individual subsequences.)

8.2 Counting sort

Counting sort assumes that each of the n input elements is an integer in the range 0 to k, for some integer k. When $k = O(n)$, the sort runs in $\Theta(n)$ time.

Counting sort determines, for each input element x, the number of elements less than x. It uses this information to place element x directly into its position in the output array. For example, if 17 elements are less than x, then x belongs in output position 18. We must modify this scheme slightly to handle the situation in which several elements have the same value, since we do not want to put them all in the same position.

In the code for counting sort, we assume that the input is an array $A[1..n]$, and thus $A.length = n$. We require two other arrays: the array $B[1..n]$ holds the sorted output, and the array $C[0..k]$ provides temporary working storage.

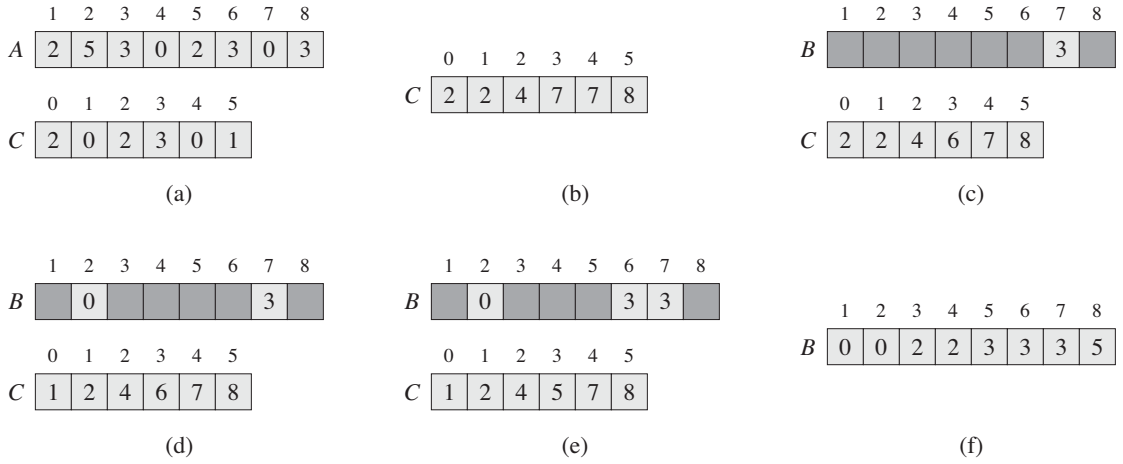


Figure 8.2 The operation of COUNTING-SORT on an input array $A[1..8]$, where each element of A is a nonnegative integer no larger than $k = 5$. **(a)** The array A and the auxiliary array C after line 5. **(b)** The array C after line 8. **(c)–(e)** The output array B and the auxiliary array C after one, two, and three iterations of the loop in lines 10–12, respectively. Only the lightly shaded elements of array B have been filled in. **(f)** The final sorted output array B.

```
COUNTING-SORT(A, B, k)
 1  let C[0..k] be a new array
 2  for i = 0 to k
 3      C[i] = 0
 4  for j = 1 to A.length
 5      C[A[j]] = C[A[j]] + 1
 6  // C[i] now contains the number of elements equal to i.
 7  for i = 1 to k
 8      C[i] = C[i] + C[i − 1]
 9  // C[i] now contains the number of elements less than or equal to i.
10  for j = A.length downto 1
11      B[C[A[j]]] = A[j]
12      C[A[j]] = C[A[j]] − 1
```

Figure 8.2 illustrates counting sort. After the **for** loop of lines 2–3 initializes the array C to all zeros, the **for** loop of lines 4–5 inspects each input element. If the value of an input element is i, we increment $C[i]$. Thus, after line 5, $C[i]$ holds the number of input elements equal to i for each integer $i = 0, 1, \ldots, k$. Lines 7–8 determine for each $i = 0, 1, \ldots, k$ how many input elements are less than or equal to i by keeping a running sum of the array C.

Finally, the **for** loop of lines 10–12 places each element $A[j]$ into its correct sorted position in the output array B. If all n elements are distinct, then when we first enter line 10, for each $A[j]$, the value $C[A[j]]$ is the correct final position of $A[j]$ in the output array, since there are $C[A[j]]$ elements less than or equal to $A[j]$. Because the elements might not be distinct, we decrement $C[A[j]]$ each time we place a value $A[j]$ into the B array. Decrementing $C[A[j]]$ causes the next input element with a value equal to $A[j]$, if one exists, to go to the position immediately before $A[j]$ in the output array.

How much time does counting sort require? The **for** loop of lines 2–3 takes time $\Theta(k)$, the **for** loop of lines 4–5 takes time $\Theta(n)$, the **for** loop of lines 7–8 takes time $\Theta(k)$, and the **for** loop of lines 10–12 takes time $\Theta(n)$. Thus, the overall time is $\Theta(k + n)$. In practice, we usually use counting sort when we have $k = O(n)$, in which case the running time is $\Theta(n)$.

Counting sort beats the lower bound of $\Omega(n \lg n)$ proved in Section 8.1 because it is not a comparison sort. In fact, no comparisons between input elements occur anywhere in the code. Instead, counting sort uses the actual values of the elements to index into an array. The $\Omega(n \lg n)$ lower bound for sorting does not apply when we depart from the comparison sort model.

An important property of counting sort is that it is ***stable***: numbers with the same value appear in the output array in the same order as they do in the input array. That is, it breaks ties between two numbers by the rule that whichever number appears first in the input array appears first in the output array. Normally, the property of stability is important only when satellite data are carried around with the element being sorted. Counting sort's stability is important for another reason: counting sort is often used as a subroutine in radix sort. As we shall see in the next section, in order for radix sort to work correctly, counting sort must be stable.

Exercises

8.2-1

Using Figure 8.2 as a model, illustrate the operation of COUNTING-SORT on the array $A = \langle 6, 0, 2, 0, 1, 3, 4, 6, 1, 3, 2 \rangle$.

8.2-2

Prove that COUNTING-SORT is stable.

8.2-3

Suppose that we were to rewrite the **for** loop header in line 10 of the COUNTING-SORT as

10 **for** $j = 1$ **to** $A.length$

Show that the algorithm still works properly. Is the modified algorithm stable?

8.2-4
Describe an algorithm that, given n integers in the range 0 to k, preprocesses its input and then answers any query about how many of the n integers fall into a range $[a\,..\,b]$ in $O(1)$ time. Your algorithm should use $\Theta(n + k)$ preprocessing time.

8.3 Radix sort

Radix sort is the algorithm used by the card-sorting machines you now find only in computer museums. The cards have 80 columns, and in each column a machine can punch a hole in one of 12 places. The sorter can be mechanically "programmed" to examine a given column of each card in a deck and distribute the card into one of 12 bins depending on which place has been punched. An operator can then gather the cards bin by bin, so that cards with the first place punched are on top of cards with the second place punched, and so on.

For decimal digits, each column uses only 10 places. (The other two places are reserved for encoding nonnumeric characters.) A d-digit number would then occupy a field of d columns. Since the card sorter can look at only one column at a time, the problem of sorting n cards on a d-digit number requires a sorting algorithm.

Intuitively, you might sort numbers on their *most significant* digit, sort each of the resulting bins recursively, and then combine the decks in order. Unfortunately, since the cards in 9 of the 10 bins must be put aside to sort each of the bins, this procedure generates many intermediate piles of cards that you would have to keep track of. (See Exercise 8.3-5.)

Radix sort solves the problem of card sorting—counterintuitively—by sorting on the *least significant* digit first. The algorithm then combines the cards into a single deck, with the cards in the 0 bin preceding the cards in the 1 bin preceding the cards in the 2 bin, and so on. Then it sorts the entire deck again on the second-least significant digit and recombines the deck in a like manner. The process continues until the cards have been sorted on all d digits. Remarkably, at that point the cards are fully sorted on the d-digit number. Thus, only d passes through the deck are required to sort. Figure 8.3 shows how radix sort operates on a "deck" of seven 3-digit numbers.

In order for radix sort to work correctly, the digit sorts must be stable. The sort performed by a card sorter is stable, but the operator has to be wary about not changing the order of the cards as they come out of a bin, even though all the cards in a bin have the same digit in the chosen column.

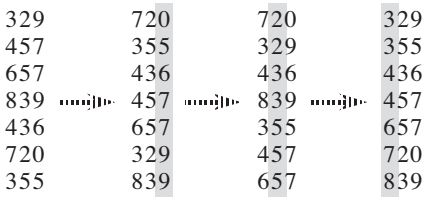


Figure 8.3 The operation of radix sort on a list of seven 3-digit numbers. The leftmost column is the input. The remaining columns show the list after successive sorts on increasingly significant digit positions. Shading indicates the digit position sorted on to produce each list from the previous one.

In a typical computer, which is a sequential random-access machine, we sometimes use radix sort to sort records of information that are keyed by multiple fields. For example, we might wish to sort dates by three keys: year, month, and day. We could run a sorting algorithm with a comparison function that, given two dates, compares years, and if there is a tie, compares months, and if another tie occurs, compares days. Alternatively, we could sort the information three times with a stable sort: first on day, next on month, and finally on year.

The code for radix sort is straightforward. The following procedure assumes that each element in the n-element array A has d digits, where digit 1 is the lowest-order digit and digit d is the highest-order digit.

RADIX-SORT(A, d)

1 **for** $i = 1$ **to** d
2 use a stable sort to sort array A on digit i

Lemma 8.3

Given n d-digit numbers in which each digit can take on up to k possible values, RADIX-SORT correctly sorts these numbers in $\Theta(d(n + k))$ time if the stable sort it uses takes $\Theta(n + k)$ time.

Proof The correctness of radix sort follows by induction on the column being sorted (see Exercise 8.3-3). The analysis of the running time depends on the stable sort used as the intermediate sorting algorithm. When each digit is in the range 0 to $k-1$ (so that it can take on k possible values), and k is not too large, counting sort is the obvious choice. Each pass over n d-digit numbers then takes time $\Theta(n+k)$. There are d passes, and so the total time for radix sort is $\Theta(d(n + k))$. ■

When d is constant and $k = O(n)$, we can make radix sort run in linear time. More generally, we have some flexibility in how to break each key into digits.

Lemma 8.4
Given n b-bit numbers and any positive integer $r \leq b$, RADIX-SORT correctly sorts these numbers in $\Theta((b/r)(n + 2^r))$ time if the stable sort it uses takes $\Theta(n + k)$ time for inputs in the range 0 to k.

Proof For a value $r \leq b$, we view each key as having $d = \lceil b/r \rceil$ digits of r bits each. Each digit is an integer in the range 0 to $2^r - 1$, so that we can use counting sort with $k = 2^r - 1$. (For example, we can view a 32-bit word as having four 8-bit digits, so that $b = 32$, $r = 8$, $k = 2^r - 1 = 255$, and $d = b/r = 4$.) Each pass of counting sort takes time $\Theta(n + k) = \Theta(n + 2^r)$ and there are d passes, for a total running time of $\Theta(d(n + 2^r)) = \Theta((b/r)(n + 2^r))$. ■

For given values of n and b, we wish to choose the value of r, with $r \leq b$, that minimizes the expression $(b/r)(n + 2^r)$. If $b < \lfloor \lg n \rfloor$, then for any value of $r \leq b$, we have that $(n + 2^r) = \Theta(n)$. Thus, choosing $r = b$ yields a running time of $(b/b)(n + 2^b) = \Theta(n)$, which is asymptotically optimal. If $b \geq \lfloor \lg n \rfloor$, then choosing $r = \lfloor \lg n \rfloor$ gives the best time to within a constant factor, which we can see as follows. Choosing $r = \lfloor \lg n \rfloor$ yields a running time of $\Theta(bn/\lg n)$. As we increase r above $\lfloor \lg n \rfloor$, the 2^r term in the numerator increases faster than the r term in the denominator, and so increasing r above $\lfloor \lg n \rfloor$ yields a running time of $\Omega(bn/\lg n)$. If instead we were to decrease r below $\lfloor \lg n \rfloor$, then the b/r term increases and the $n + 2^r$ term remains at $\Theta(n)$.

Is radix sort preferable to a comparison-based sorting algorithm, such as quicksort? If $b = O(\lg n)$, as is often the case, and we choose $r \approx \lg n$, then radix sort's running time is $\Theta(n)$, which appears to be better than quicksort's expected running time of $\Theta(n \lg n)$. The constant factors hidden in the Θ-notation differ, however. Although radix sort may make fewer passes than quicksort over the n keys, each pass of radix sort may take significantly longer. Which sorting algorithm we prefer depends on the characteristics of the implementations, of the underlying machine (e.g., quicksort often uses hardware caches more effectively than radix sort), and of the input data. Moreover, the version of radix sort that uses counting sort as the intermediate stable sort does not sort in place, which many of the $\Theta(n \lg n)$-time comparison sorts do. Thus, when primary memory storage is at a premium, we might prefer an in-place algorithm such as quicksort.

Exercises

8.3-1
Using Figure 8.3 as a model, illustrate the operation of RADIX-SORT on the following list of English words: COW, DOG, SEA, RUG, ROW, MOB, BOX, TAB, BAR, EAR, TAR, DIG, BIG, TEA, NOW, FOX.

8.3-2
Which of the following sorting algorithms are stable: insertion sort, merge sort, heapsort, and quicksort? Give a simple scheme that makes any sorting algorithm stable. How much additional time and space does your scheme entail?

8.3-3
Use induction to prove that radix sort works. Where does your proof need the assumption that the intermediate sort is stable?

8.3-4
Show how to sort n integers in the range 0 to $n^3 - 1$ in $O(n)$ time.

8.3-5 ⋆
In the first card-sorting algorithm in this section, exactly how many sorting passes are needed to sort d-digit decimal numbers in the worst case? How many piles of cards would an operator need to keep track of in the worst case?

8.4 Bucket sort

Bucket sort assumes that the input is drawn from a uniform distribution and has an average-case running time of $O(n)$. Like counting sort, bucket sort is fast because it assumes something about the input. Whereas counting sort assumes that the input consists of integers in a small range, bucket sort assumes that the input is generated by a random process that distributes elements uniformly and independently over the interval $[0, 1)$. (See Section C.2 for a definition of uniform distribution.)

Bucket sort divides the interval $[0, 1)$ into n equal-sized subintervals, or ***buckets***, and then distributes the n input numbers into the buckets. Since the inputs are uniformly and independently distributed over $[0, 1)$, we do not expect many numbers to fall into each bucket. To produce the output, we simply sort the numbers in each bucket and then go through the buckets in order, listing the elements in each.

Our code for bucket sort assumes that the input is an n-element array A and that each element $A[i]$ in the array satisfies $0 \leq A[i] < 1$. The code requires an auxiliary array $B[0..n-1]$ of linked lists (buckets) and assumes that there is a mechanism for maintaining such lists. (Section 10.2 describes how to implement basic operations on linked lists.)

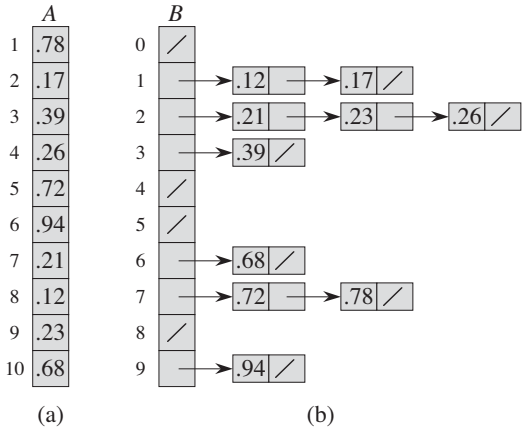


Figure 8.4 The operation of BUCKET-SORT for $n = 10$. **(a)** The input array $A[1..10]$. **(b)** The array $B[0..9]$ of sorted lists (buckets) after line 8 of the algorithm. Bucket i holds values in the half-open interval $[i/10, (i+1)/10)$. The sorted output consists of a concatenation in order of the lists $B[0], B[1], \ldots, B[9]$.

BUCKET-SORT(A)

```
1  let B[0..n − 1] be a new array
2  n = A.length
3  for i = 0 to n − 1
4      make B[i] an empty list
5  for i = 1 to n
6      insert A[i] into list B[⌊nA[i]⌋]
7  for i = 0 to n − 1
8      sort list B[i] with insertion sort
9  concatenate the lists B[0], B[1], ..., B[n − 1] together in order
```

Figure 8.4 shows the operation of bucket sort on an input array of 10 numbers.

To see that this algorithm works, consider two elements $A[i]$ and $A[j]$. Assume without loss of generality that $A[i] \le A[j]$. Since $\lfloor nA[i] \rfloor \le \lfloor nA[j] \rfloor$, either element $A[i]$ goes into the same bucket as $A[j]$ or it goes into a bucket with a lower index. If $A[i]$ and $A[j]$ go into the same bucket, then the **for** loop of lines 7–8 puts them into the proper order. If $A[i]$ and $A[j]$ go into different buckets, then line 9 puts them into the proper order. Therefore, bucket sort works correctly.

To analyze the running time, observe that all lines except line 8 take $O(n)$ time in the worst case. We need to analyze the total time taken by the n calls to insertion sort in line 8.

To analyze the cost of the calls to insertion sort, let n_i be the random variable denoting the number of elements placed in bucket $B[i]$. Since insertion sort runs in quadratic time (see Section 2.2), the running time of bucket sort is

$$T(n) = \Theta(n) + \sum_{i=0}^{n-1} O(n_i^2) \ .$$

We now analyze the average-case running time of bucket sort, by computing the expected value of the running time, where we take the expectation over the input distribution. Taking expectations of both sides and using linearity of expectation, we have

$$\begin{aligned} \mathrm{E}[T(n)] &= \mathrm{E}\left[\Theta(n) + \sum_{i=0}^{n-1} O(n_i^2)\right] \\ &= \Theta(n) + \sum_{i=0}^{n-1} \mathrm{E}\left[O(n_i^2)\right] \quad \text{(by linearity of expectation)} \\ &= \Theta(n) + \sum_{i=0}^{n-1} O\left(\mathrm{E}\left[n_i^2\right]\right) \quad \text{(by equation (C.22))} \ . \end{aligned} \tag{8.1}$$

We claim that

$$\mathrm{E}\left[n_i^2\right] = 2 - 1/n \tag{8.2}$$

for $i = 0, 1, \ldots, n-1$. It is no surprise that each bucket i has the same value of $\mathrm{E}[n_i^2]$, since each value in the input array A is equally likely to fall in any bucket. To prove equation (8.2), we define indicator random variables

$$X_{ij} = \mathrm{I}\{A[j] \text{ falls in bucket } i\}$$

for $i = 0, 1, \ldots, n-1$ and $j = 1, 2, \ldots, n$. Thus,

$$n_i = \sum_{j=1}^{n} X_{ij} \ .$$

To compute $\mathrm{E}[n_i^2]$, we expand the square and regroup terms:

$$\begin{aligned}
\mathrm{E}\left[n_i^2\right] &= \mathrm{E}\left[\left(\sum_{j=1}^{n} X_{ij}\right)^2\right] \\
&= \mathrm{E}\left[\sum_{j=1}^{n}\sum_{k=1}^{n} X_{ij}X_{ik}\right] \\
&= \mathrm{E}\left[\sum_{j=1}^{n} X_{ij}^2 + \sum_{1\le j\le n}\ \sum_{\substack{1\le k\le n\\ k\ne j}} X_{ij}X_{ik}\right] \\
&= \sum_{j=1}^{n}\mathrm{E}\left[X_{ij}^2\right] + \sum_{1\le j\le n}\ \sum_{\substack{1\le k\le n\\ k\ne j}} \mathrm{E}\left[X_{ij}X_{ik}\right] , \qquad (8.3)
\end{aligned}$$

where the last line follows by linearity of expectation. We evaluate the two summations separately. Indicator random variable X_{ij} is 1 with probability $1/n$ and 0 otherwise, and therefore

$$\begin{aligned}
\mathrm{E}\left[X_{ij}^2\right] &= 1^2 \cdot \frac{1}{n} + 0^2 \cdot \left(1 - \frac{1}{n}\right) \\
&= \frac{1}{n} .
\end{aligned}$$

When $k \ne j$, the variables X_{ij} and X_{ik} are independent, and hence

$$\begin{aligned}
\mathrm{E}\left[X_{ij}X_{ik}\right] &= \mathrm{E}\left[X_{ij}\right]\mathrm{E}\left[X_{ik}\right] \\
&= \frac{1}{n}\cdot\frac{1}{n} \\
&= \frac{1}{n^2} .
\end{aligned}$$

Substituting these two expected values in equation (8.3), we obtain

$$\begin{aligned}
\mathrm{E}\left[n_i^2\right] &= \sum_{j=1}^{n}\frac{1}{n} + \sum_{1\le j\le n}\ \sum_{\substack{1\le k\le n\\ k\ne j}} \frac{1}{n^2} \\
&= n\cdot\frac{1}{n} + n(n-1)\cdot\frac{1}{n^2} \\
&= 1 + \frac{n-1}{n} \\
&= 2 - \frac{1}{n} ,
\end{aligned}$$

which proves equation (8.2).

Using this expected value in equation (8.1), we conclude that the average-case running time for bucket sort is $\Theta(n) + n \cdot O(2 - 1/n) = \Theta(n)$.

Even if the input is not drawn from a uniform distribution, bucket sort may still run in linear time. As long as the input has the property that the sum of the squares of the bucket sizes is linear in the total number of elements, equation (8.1) tells us that bucket sort will run in linear time.

Exercises

8.4-1

Using Figure 8.4 as a model, illustrate the operation of BUCKET-SORT on the array $A = \langle .79, .13, .16, .64, .39, .20, .89, .53, .71, .42 \rangle$.

8.4-2

Explain why the worst-case running time for bucket sort is $\Theta(n^2)$. What simple change to the algorithm preserves its linear average-case running time and makes its worst-case running time $O(n \lg n)$?

8.4-3

Let X be a random variable that is equal to the number of heads in two flips of a fair coin. What is $\mathrm{E}[X^2]$? What is $\mathrm{E}^2[X]$?

8.4-4 ⋆

We are given n points in the unit circle, $p_i = (x_i, y_i)$, such that $0 < x_i^2 + y_i^2 \leq 1$ for $i = 1, 2, \ldots, n$. Suppose that the points are uniformly distributed; that is, the probability of finding a point in any region of the circle is proportional to the area of that region. Design an algorithm with an average-case running time of $\Theta(n)$ to sort the n points by their distances $d_i = \sqrt{x_i^2 + y_i^2}$ from the origin. (*Hint:* Design the bucket sizes in BUCKET-SORT to reflect the uniform distribution of the points in the unit circle.)

8.4-5 ⋆

A ***probability distribution function*** $P(x)$ for a random variable X is defined by $P(x) = \Pr\{X \leq x\}$. Suppose that we draw a list of n random variables $X_1, X_2, \ldots, X_n$ from a continuous probability distribution function P that is computable in $O(1)$ time. Give an algorithm that sorts these numbers in linear average-case time.

Problems

8-1 Probabilistic lower bounds on comparison sorting

In this problem, we prove a probabilistic $\Omega(n \lg n)$ lower bound on the running time of any deterministic or randomized comparison sort on n distinct input elements. We begin by examining a deterministic comparison sort A with decision tree T_A. We assume that every permutation of A's inputs is equally likely.

a. Suppose that each leaf of T_A is labeled with the probability that it is reached given a random input. Prove that exactly $n!$ leaves are labeled $1/n!$ and that the rest are labeled 0.

b. Let $D(T)$ denote the external path length of a decision tree T; that is, $D(T)$ is the sum of the depths of all the leaves of T. Let T be a decision tree with $k > 1$ leaves, and let LT and RT be the left and right subtrees of T. Show that $D(T) = D(LT) + D(RT) + k$.

c. Let $d(k)$ be the minimum value of $D(T)$ over all decision trees T with $k > 1$ leaves. Show that $d(k) = \min_{1 \le i \le k-1} \{d(i) + d(k-i) + k\}$. (*Hint:* Consider a decision tree T with k leaves that achieves the minimum. Let i_0 be the number of leaves in LT and $k - i_0$ the number of leaves in RT.)

d. Prove that for a given value of $k > 1$ and i in the range $1 \le i \le k-1$, the function $i \lg i + (k-i) \lg(k-i)$ is minimized at $i = k/2$. Conclude that $d(k) = \Omega(k \lg k)$.

e. Prove that $D(T_A) = \Omega(n! \lg(n!))$, and conclude that the average-case time to sort n elements is $\Omega(n \lg n)$.

Now, consider a *randomized* comparison sort B. We can extend the decision-tree model to handle randomization by incorporating two kinds of nodes: ordinary comparison nodes and "randomization" nodes. A randomization node models a random choice of the form $\text{RANDOM}(1, r)$ made by algorithm B; the node has r children, each of which is equally likely to be chosen during an execution of the algorithm.

f. Show that for any randomized comparison sort B, there exists a deterministic comparison sort A whose expected number of comparisons is no more than those made by B.

8-2 Sorting in place in linear time

Suppose that we have an array of n data records to sort and that the key of each record has the value 0 or 1. An algorithm for sorting such a set of records might possess some subset of the following three desirable characteristics:

1. The algorithm runs in $O(n)$ time.
2. The algorithm is stable.
3. The algorithm sorts in place, using no more than a constant amount of storage space in addition to the original array.

a. Give an algorithm that satisfies criteria 1 and 2 above.

b. Give an algorithm that satisfies criteria 1 and 3 above.

c. Give an algorithm that satisfies criteria 2 and 3 above.

d. Can you use any of your sorting algorithms from parts (a)–(c) as the sorting method used in line 2 of RADIX-SORT, so that RADIX-SORT sorts n records with b-bit keys in $O(bn)$ time? Explain how or why not.

e. Suppose that the n records have keys in the range from 1 to k. Show how to modify counting sort so that it sorts the records in place in $O(n + k)$ time. You may use $O(k)$ storage outside the input array. Is your algorithm stable? (*Hint:* How would you do it for $k = 3$?)

8-3 Sorting variable-length items

a. You are given an array of integers, where different integers may have different numbers of digits, but the total number of digits over *all* the integers in the array is n. Show how to sort the array in $O(n)$ time.

b. You are given an array of strings, where different strings may have different numbers of characters, but the total number of characters over all the strings is n. Show how to sort the strings in $O(n)$ time.

(Note that the desired order here is the standard alphabetical order; for example, `a` < `ab` < `b`.)

8-4 Water jugs

Suppose that you are given n red and n blue water jugs, all of different shapes and sizes. All red jugs hold different amounts of water, as do the blue ones. Moreover, for every red jug, there is a blue jug that holds the same amount of water, and vice versa.

Your task is to find a grouping of the jugs into pairs of red and blue jugs that hold the same amount of water. To do so, you may perform the following operation: pick a pair of jugs in which one is red and one is blue, fill the red jug with water, and then pour the water into the blue jug. This operation will tell you whether the red or the blue jug can hold more water, or that they have the same volume. Assume that such a comparison takes one time unit. Your goal is to find an algorithm that makes a minimum number of comparisons to determine the grouping. Remember that you may not directly compare two red jugs or two blue jugs.

a. Describe a deterministic algorithm that uses $\Theta(n^2)$ comparisons to group the jugs into pairs.

b. Prove a lower bound of $\Omega(n \lg n)$ for the number of comparisons that an algorithm solving this problem must make.

c. Give a randomized algorithm whose expected number of comparisons is $O(n \lg n)$, and prove that this bound is correct. What is the worst-case number of comparisons for your algorithm?

8-5 Average sorting

Suppose that, instead of sorting an array, we just require that the elements increase on average. More precisely, we call an n-element array A ***k-sorted*** if, for all $i = 1, 2, \ldots, n-k$, the following holds:

$$\frac{\sum_{j=i}^{i+k-1} A[j]}{k} \leq \frac{\sum_{j=i+1}^{i+k} A[j]}{k} .$$

a. What does it mean for an array to be 1-sorted?

b. Give a permutation of the numbers $1, 2, \ldots, 10$ that is 2-sorted, but not sorted.

c. Prove that an n-element array is k-sorted if and only if $A[i] \leq A[i+k]$ for all $i = 1, 2, \ldots, n-k$.

d. Give an algorithm that k-sorts an n-element array in $O(n \lg(n/k))$ time.

We can also show a lower bound on the time to produce a k-sorted array, when k is a constant.

e. Show that we can sort a k-sorted array of length n in $O(n \lg k)$ time. (*Hint:* Use the solution to Exercise 6.5-9.)

f. Show that when k is a constant, k-sorting an n-element array requires $\Omega(n \lg n)$ time. (*Hint:* Use the solution to the previous part along with the lower bound on comparison sorts.)

8-6 Lower bound on merging sorted lists

The problem of merging two sorted lists arises frequently. We have seen a procedure for it as the subroutine MERGE in Section 2.3.1. In this problem, we will prove a lower bound of $2n - 1$ on the worst-case number of comparisons required to merge two sorted lists, each containing n items.

First we will show a lower bound of $2n - o(n)$ comparisons by using a decision tree.

a. Given $2n$ numbers, compute the number of possible ways to divide them into two sorted lists, each with n numbers.

b. Using a decision tree and your answer to part (a), show that any algorithm that correctly merges two sorted lists must perform at least $2n - o(n)$ comparisons.

Now we will show a slightly tighter $2n - 1$ bound.

c. Show that if two elements are consecutive in the sorted order and from different lists, then they must be compared.

d. Use your answer to the previous part to show a lower bound of $2n - 1$ comparisons for merging two sorted lists.

8-7 The 0-1 sorting lemma and columnsort

A ***compare-exchange*** operation on two array elements $A[i]$ and $A[j]$, where $i < j$, has the form

```
COMPARE-EXCHANGE(A, i, j)
1  if A[i] > A[j]
2      exchange A[i] with A[j]
```

After the compare-exchange operation, we know that $A[i] \leq A[j]$.

An ***oblivious compare-exchange algorithm*** operates solely by a sequence of prespecified compare-exchange operations. The indices of the positions compared in the sequence must be determined in advance, and although they can depend on the number of elements being sorted, they cannot depend on the values being sorted, nor can they depend on the result of any prior compare-exchange operation. For example, here is insertion sort expressed as an oblivious compare-exchange algorithm:

```
INSERTION-SORT(A)
1  for j = 2 to A.length
2      for i = j − 1 downto 1
3          COMPARE-EXCHANGE(A, i, i + 1)
```

The ***0-1 sorting lemma*** provides a powerful way to prove that an oblivious compare-exchange algorithm produces a sorted result. It states that if an oblivious compare-exchange algorithm correctly sorts all input sequences consisting of only 0s and 1s, then it correctly sorts all inputs containing arbitrary values.

You will prove the 0-1 sorting lemma by proving its contrapositive: if an oblivious compare-exchange algorithm fails to sort an input containing arbitrary values, then it fails to sort some 0-1 input. Assume that an oblivious compare-exchange algorithm X fails to correctly sort the array $A[1\,..\,n]$. Let $A[p]$ be the smallest value in A that algorithm X puts into the wrong location, and let $A[q]$ be the value that algorithm X moves to the location into which $A[p]$ should have gone. Define an array $B[1\,..\,n]$ of 0s and 1s as follows:

$$B[i] = \begin{cases} 0 & \text{if } A[i] \le A[p]\,, \\ 1 & \text{if } A[i] > A[p]\,. \end{cases}$$

a. Argue that $A[q] > A[p]$, so that $B[p] = 0$ and $B[q] = 1$.

b. To complete the proof of the 0-1 sorting lemma, prove that algorithm X fails to sort array B correctly.

Now you will use the 0-1 sorting lemma to prove that a particular sorting algorithm works correctly. The algorithm, ***columnsort***, works on a rectangular array of n elements. The array has r rows and s columns (so that $n = rs$), subject to three restrictions:

- r must be even,
- s must be a divisor of r, and
- $r \ge 2s^2$.

When columnsort completes, the array is sorted in ***column-major order***: reading down the columns, from left to right, the elements monotonically increase.

Columnsort operates in eight steps, regardless of the value of n. The odd steps are all the same: sort each column individually. Each even step is a fixed permutation. Here are the steps:

1. Sort each column.
2. Transpose the array, but reshape it back to r rows and s columns. In other words, turn the leftmost column into the top r/s rows, in order; turn the next column into the next r/s rows, in order; and so on.
3. Sort each column.
4. Perform the inverse of the permutation performed in step 2.

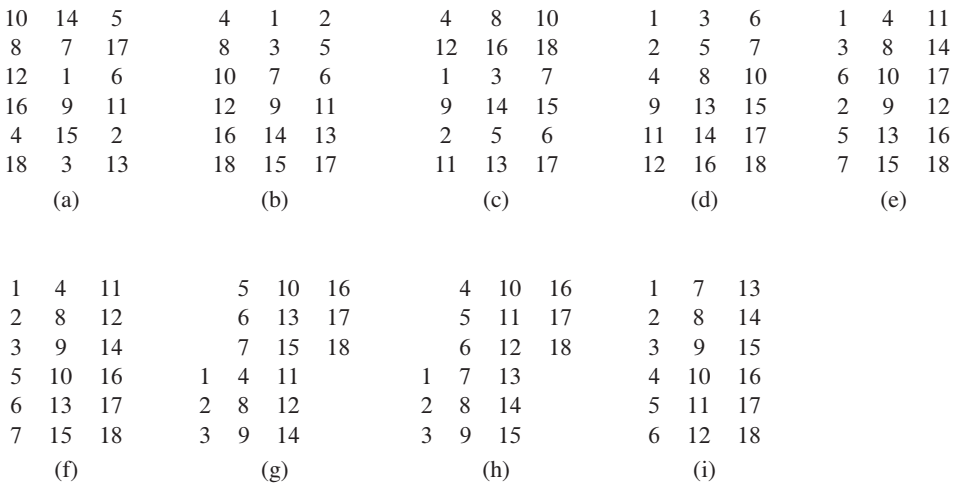


Figure 8.5 The steps of columnsort. **(a)** The input array with 6 rows and 3 columns. **(b)** After sorting each column in step 1. **(c)** After transposing and reshaping in step 2. **(d)** After sorting each column in step 3. **(e)** After performing step 4, which inverts the permutation from step 2. **(f)** After sorting each column in step 5. **(g)** After shifting by half a column in step 6. **(h)** After sorting each column in step 7. **(i)** After performing step 8, which inverts the permutation from step 6. The array is now sorted in column-major order.

5. Sort each column.
6. Shift the top half of each column into the bottom half of the same column, and shift the bottom half of each column into the top half of the next column to the right. Leave the top half of the leftmost column empty. Shift the bottom half of the last column into the top half of a new rightmost column, and leave the bottom half of this new column empty.
7. Sort each column.
8. Perform the inverse of the permutation performed in step 6.

Figure 8.5 shows an example of the steps of columnsort with $r = 6$ and $s = 3$. (Even though this example violates the requirement that $r \geq 2s^2$, it happens to work.)

c. Argue that we can treat columnsort as an oblivious compare-exchange algorithm, even if we do not know what sorting method the odd steps use.

Although it might seem hard to believe that columnsort actually sorts, you will use the 0-1 sorting lemma to prove that it does. The 0-1 sorting lemma applies because we can treat columnsort as an oblivious compare-exchange algorithm. A

couple of definitions will help you apply the 0-1 sorting lemma. We say that an area of an array is ***clean*** if we know that it contains either all 0s or all 1s. Otherwise, the area might contain mixed 0s and 1s, and it is ***dirty***. From here on, assume that the input array contains only 0s and 1s, and that we can treat it as an array with r rows and s columns.

d. Prove that after steps 1–3, the array consists of some clean rows of 0s at the top, some clean rows of 1s at the bottom, and at most s dirty rows between them.

e. Prove that after step 4, the array, read in column-major order, starts with a clean area of 0s, ends with a clean area of 1s, and has a dirty area of at most s^2 elements in the middle.

f. Prove that steps 5–8 produce a fully sorted 0-1 output. Conclude that columnsort correctly sorts all inputs containing arbitrary values.

g. Now suppose that s does not divide r. Prove that after steps 1–3, the array consists of some clean rows of 0s at the top, some clean rows of 1s at the bottom, and at most $2s - 1$ dirty rows between them. How large must r be, compared with s, for columnsort to correctly sort when s does not divide r?

h. Suggest a simple change to step 1 that allows us to maintain the requirement that $r \geq 2s^2$ even when s does not divide r, and prove that with your change, columnsort correctly sorts.

Chapter notes

The decision-tree model for studying comparison sorts was introduced by Ford and Johnson [110]. Knuth's comprehensive treatise on sorting [211] covers many variations on the sorting problem, including the information-theoretic lower bound on the complexity of sorting given here. Ben-Or [39] studied lower bounds for sorting using generalizations of the decision-tree model.

Knuth credits H. H. Seward with inventing counting sort in 1954, as well as with the idea of combining counting sort with radix sort. Radix sorting starting with the least significant digit appears to be a folk algorithm widely used by operators of mechanical card-sorting machines. According to Knuth, the first published reference to the method is a 1929 document by L. J. Comrie describing punched-card equipment. Bucket sorting has been in use since 1956, when the basic idea was proposed by E. J. Isaac and R. C. Singleton [188].

Munro and Raman [263] give a stable sorting algorithm that performs $O(n^{1+\epsilon})$ comparisons in the worst case, where $0 < \epsilon \leq 1$ is any fixed constant. Although

any of the $O(n \lg n)$-time algorithms make fewer comparisons, the algorithm by Munro and Raman moves data only $O(n)$ times and operates in place.

The case of sorting n b-bit integers in $o(n \lg n)$ time has been considered by many researchers. Several positive results have been obtained, each under slightly different assumptions about the model of computation and the restrictions placed on the algorithm. All the results assume that the computer memory is divided into addressable b-bit words. Fredman and Willard [115] introduced the fusion tree data structure and used it to sort n integers in $O(n \lg n / \lg \lg n)$ time. This bound was later improved to $O(n \sqrt{\lg n})$ time by Andersson [16]. These algorithms require the use of multiplication and several precomputed constants. Andersson, Hagerup, Nilsson, and Raman [17] have shown how to sort n integers in $O(n \lg \lg n)$ time without using multiplication, but their method requires storage that can be unbounded in terms of n. Using multiplicative hashing, we can reduce the storage needed to $O(n)$, but then the $O(n \lg \lg n)$ worst-case bound on the running time becomes an expected-time bound. Generalizing the exponential search trees of Andersson [16], Thorup [335] gave an $O(n(\lg \lg n)^2)$-time sorting algorithm that does not use multiplication or randomization, and it uses linear space. Combining these techniques with some new ideas, Han [158] improved the bound for sorting to $O(n \lg \lg n \lg \lg \lg n)$ time. Although these algorithms are important theoretical breakthroughs, they are all fairly complicated and at the present time seem unlikely to compete with existing sorting algorithms in practice.

The columnsort algorithm in Problem 8-7 is by Leighton [227].

9 Medians and Order Statistics

The ith ***order statistic*** of a set of n elements is the ith smallest element. For example, the ***minimum*** of a set of elements is the first order statistic ($i = 1$), and the ***maximum*** is the nth order statistic ($i = n$). A ***median***, informally, is the "halfway point" of the set. When n is odd, the median is unique, occurring at $i = (n + 1)/2$. When n is even, there are two medians, occurring at $i = n/2$ and $i = n/2+1$. Thus, regardless of the parity of n, medians occur at $i = \lfloor (n + 1)/2 \rfloor$ (the ***lower median***) and $i = \lceil (n + 1)/2 \rceil$ (the ***upper median***). For simplicity in this text, however, we consistently use the phrase "the median" to refer to the lower median.

This chapter addresses the problem of selecting the ith order statistic from a set of n distinct numbers. We assume for convenience that the set contains distinct numbers, although virtually everything that we do extends to the situation in which a set contains repeated values. We formally specify the ***selection problem*** as follows:

Input: A set A of n (distinct) numbers and an integer i, with $1 \le i \le n$.

Output: The element $x \in A$ that is larger than exactly $i - 1$ other elements of A.

We can solve the selection problem in $O(n \lg n)$ time, since we can sort the numbers using heapsort or merge sort and then simply index the ith element in the output array. This chapter presents faster algorithms.

In Section 9.1, we examine the problem of selecting the minimum and maximum of a set of elements. More interesting is the general selection problem, which we investigate in the subsequent two sections. Section 9.2 analyzes a practical randomized algorithm that achieves an $O(n)$ expected running time, assuming distinct elements. Section 9.3 contains an algorithm of more theoretical interest that achieves the $O(n)$ running time in the worst case.

9.1 Minimum and maximum

How many comparisons are necessary to determine the minimum of a set of n elements? We can easily obtain an upper bound of $n - 1$ comparisons: examine each element of the set in turn and keep track of the smallest element seen so far. In the following procedure, we assume that the set resides in array A, where $A.length = n$.

```
MINIMUM(A)
1  min = A[1]
2  for i = 2 to A.length
3      if min > A[i]
4          min = A[i]
5  return min
```

We can, of course, find the maximum with $n - 1$ comparisons as well.

Is this the best we can do? Yes, since we can obtain a lower bound of $n - 1$ comparisons for the problem of determining the minimum. Think of any algorithm that determines the minimum as a tournament among the elements. Each comparison is a match in the tournament in which the smaller of the two elements wins. Observing that every element except the winner must lose at least one match, we conclude that $n - 1$ comparisons are necessary to determine the minimum. Hence, the algorithm MINIMUM is optimal with respect to the number of comparisons performed.

Simultaneous minimum and maximum

In some applications, we must find both the minimum and the maximum of a set of n elements. For example, a graphics program may need to scale a set of (x, y) data to fit onto a rectangular display screen or other graphical output device. To do so, the program must first determine the minimum and maximum value of each coordinate.

At this point, it should be obvious how to determine both the minimum and the maximum of n elements using $\Theta(n)$ comparisons, which is asymptotically optimal: simply find the minimum and maximum independently, using $n - 1$ comparisons for each, for a total of $2n - 2$ comparisons.

In fact, we can find both the minimum and the maximum using at most $3\lfloor n/2 \rfloor$ comparisons. We do so by maintaining both the minimum and maximum elements seen thus far. Rather than processing each element of the input by comparing it against the current minimum and maximum, at a cost of 2 comparisons per element,

we process elements in pairs. We compare pairs of elements from the input first *with each other*, and then we compare the smaller with the current minimum and the larger to the current maximum, at a cost of 3 comparisons for every 2 elements.

How we set up initial values for the current minimum and maximum depends on whether n is odd or even. If n is odd, we set both the minimum and maximum to the value of the first element, and then we process the rest of the elements in pairs. If n is even, we perform 1 comparison on the first 2 elements to determine the initial values of the minimum and maximum, and then process the rest of the elements in pairs as in the case for odd n.

Let us analyze the total number of comparisons. If n is odd, then we perform $3\lfloor n/2 \rfloor$ comparisons. If n is even, we perform 1 initial comparison followed by $3(n-2)/2$ comparisons, for a total of $3n/2 - 2$. Thus, in either case, the total number of comparisons is at most $3\lfloor n/2 \rfloor$.

Exercises

9.1-1

Show that the second smallest of n elements can be found with $n + \lceil \lg n \rceil - 2$ comparisons in the worst case. (*Hint:* Also find the smallest element.)

9.1-2 ⋆

Prove the lower bound of $\lceil 3n/2 \rceil - 2$ comparisons in the worst case to find both the maximum and minimum of n numbers. (*Hint:* Consider how many numbers are potentially either the maximum or minimum, and investigate how a comparison affects these counts.)

9.2 Selection in expected linear time

The general selection problem appears more difficult than the simple problem of finding a minimum. Yet, surprisingly, the asymptotic running time for both problems is the same: $\Theta(n)$. In this section, we present a divide-and-conquer algorithm for the selection problem. The algorithm RANDOMIZED-SELECT is modeled after the quicksort algorithm of Chapter 7. As in quicksort, we partition the input array recursively. But unlike quicksort, which recursively processes both sides of the partition, RANDOMIZED-SELECT works on only one side of the partition. This difference shows up in the analysis: whereas quicksort has an expected running time of $\Theta(n \lg n)$, the expected running time of RANDOMIZED-SELECT is $\Theta(n)$, assuming that the elements are distinct.

RANDOMIZED-SELECT uses the procedure RANDOMIZED-PARTITION introduced in Section 7.3. Thus, like RANDOMIZED-QUICKSORT, it is a randomized algorithm, since its behavior is determined in part by the output of a random-number generator. The following code for RANDOMIZED-SELECT returns the ith smallest element of the array $A[p..r]$.

```
RANDOMIZED-SELECT(A, p, r, i)
1  if p == r
2      return A[p]
3  q = RANDOMIZED-PARTITION(A, p, r)
4  k = q - p + 1
5  if i == k            // the pivot value is the answer
6      return A[q]
7  elseif i < k
8      return RANDOMIZED-SELECT(A, p, q - 1, i)
9  else return RANDOMIZED-SELECT(A, q + 1, r, i - k)
```

The RANDOMIZED-SELECT procedure works as follows. Line 1 checks for the base case of the recursion, in which the subarray $A[p..r]$ consists of just one element. In this case, i must equal 1, and we simply return $A[p]$ in line 2 as the ith smallest element. Otherwise, the call to RANDOMIZED-PARTITION in line 3 partitions the array $A[p..r]$ into two (possibly empty) subarrays $A[p..q-1]$ and $A[q+1..r]$ such that each element of $A[p..q-1]$ is less than or equal to $A[q]$, which in turn is less than each element of $A[q+1..r]$. As in quicksort, we will refer to $A[q]$ as the ***pivot*** element. Line 4 computes the number k of elements in the subarray $A[p..q]$, that is, the number of elements in the low side of the partition, plus one for the pivot element. Line 5 then checks whether $A[q]$ is the ith smallest element. If it is, then line 6 returns $A[q]$. Otherwise, the algorithm determines in which of the two subarrays $A[p..q-1]$ and $A[q+1..r]$ the ith smallest element lies. If $i < k$, then the desired element lies on the low side of the partition, and line 8 recursively selects it from the subarray. If $i > k$, however, then the desired element lies on the high side of the partition. Since we already know k values that are smaller than the ith smallest element of $A[p..r]$—namely, the elements of $A[p..q]$—the desired element is the $(i-k)$th smallest element of $A[q+1..r]$, which line 9 finds recursively. The code appears to allow recursive calls to subarrays with 0 elements, but Exercise 9.2-1 asks you to show that this situation cannot happen.

The worst-case running time for RANDOMIZED-SELECT is $\Theta(n^2)$, even to find the minimum, because we could be extremely unlucky and always partition around the largest remaining element, and partitioning takes $\Theta(n)$ time. We will see that

the algorithm has a linear expected running time, though, and because it is randomized, no particular input elicits the worst-case behavior.

To analyze the expected running time of RANDOMIZED-SELECT, we let the running time on an input array $A[p..r]$ of n elements be a random variable that we denote by $T(n)$, and we obtain an upper bound on $\mathrm{E}[T(n)]$ as follows. The procedure RANDOMIZED-PARTITION is equally likely to return any element as the pivot. Therefore, for each k such that $1 \le k \le n$, the subarray $A[p..q]$ has k elements (all less than or equal to the pivot) with probability $1/n$. For $k = 1, 2, \ldots, n$, we define indicator random variables X_k where

$$X_k = \mathrm{I}\{\text{the subarray } A[p..q] \text{ has exactly } k \text{ elements}\} ,$$

and so, assuming that the elements are distinct, we have

$$\mathrm{E}[X_k] = 1/n . \tag{9.1}$$

When we call RANDOMIZED-SELECT and choose $A[q]$ as the pivot element, we do not know, a priori, if we will terminate immediately with the correct answer, recurse on the subarray $A[p..q-1]$, or recurse on the subarray $A[q+1..r]$. This decision depends on where the ith smallest element falls relative to $A[q]$. Assuming that $T(n)$ is monotonically increasing, we can upper-bound the time needed for the recursive call by the time needed for the recursive call on the largest possible input. In other words, to obtain an upper bound, we assume that the ith element is always on the side of the partition with the greater number of elements. For a given call of RANDOMIZED-SELECT, the indicator random variable X_k has the value 1 for exactly one value of k, and it is 0 for all other k. When $X_k = 1$, the two subarrays on which we might recurse have sizes $k-1$ and $n-k$. Hence, we have the recurrence

$$\begin{aligned} T(n) &\le \sum_{k=1}^{n} X_k \cdot (T(\max(k-1, n-k)) + O(n)) \\ &= \sum_{k=1}^{n} X_k \cdot T(\max(k-1, n-k)) + O(n) . \end{aligned}$$

Taking expected values, we have

$$\begin{aligned}
&\mathrm{E}[T(n)] \\
&\le \mathrm{E}\left[\sum_{k=1}^{n} X_k \cdot T(\max(k-1, n-k)) + O(n)\right] \\
&= \sum_{k=1}^{n} \mathrm{E}[X_k \cdot T(\max(k-1, n-k))] + O(n) && \text{(by linearity of expectation)} \\
&= \sum_{k=1}^{n} \mathrm{E}[X_k] \cdot \mathrm{E}[T(\max(k-1, n-k))] + O(n) && \text{(by equation (C.24))} \\
&= \sum_{k=1}^{n} \frac{1}{n} \cdot \mathrm{E}[T(\max(k-1, n-k))] + O(n) && \text{(by equation (9.1))} \ .
\end{aligned}$$

In order to apply equation (C.24), we rely on X_k and $T(\max(k-1, n-k))$ being independent random variables. Exercise 9.2-2 asks you to justify this assertion.

Let us consider the expression $\max(k-1, n-k)$. We have

$$\max(k-1, n-k) = \begin{cases} k-1 & \text{if } k > \lceil n/2 \rceil \ , \\ n-k & \text{if } k \le \lceil n/2 \rceil \ . \end{cases}$$

If n is even, each term from $T(\lceil n/2 \rceil)$ up to $T(n-1)$ appears exactly twice in the summation, and if n is odd, all these terms appear twice and $T(\lfloor n/2 \rfloor)$ appears once. Thus, we have

$$\mathrm{E}[T(n)] \le \frac{2}{n} \sum_{k=\lfloor n/2 \rfloor}^{n-1} \mathrm{E}[T(k)] + O(n) \ .$$

We show that $\mathrm{E}[T(n)] = O(n)$ by substitution. Assume that $\mathrm{E}[T(n)] \le cn$ for some constant c that satisfies the initial conditions of the recurrence. We assume that $T(n) = O(1)$ for n less than some constant; we shall pick this constant later. We also pick a constant a such that the function described by the $O(n)$ term above (which describes the non-recursive component of the running time of the algorithm) is bounded from above by an for all $n > 0$. Using this inductive hypothesis, we have

$$\begin{aligned}
\mathrm{E}[T(n)] &\le \frac{2}{n} \sum_{k=\lfloor n/2 \rfloor}^{n-1} ck + an \\
&= \frac{2c}{n} \left(\sum_{k=1}^{n-1} k - \sum_{k=1}^{\lfloor n/2 \rfloor - 1} k \right) + an
\end{aligned}$$

$$
\begin{aligned}
&= \frac{2c}{n}\left(\frac{(n-1)n}{2} - \frac{(\lfloor n/2\rfloor - 1)\,\lfloor n/2\rfloor}{2}\right) + an \\
&\le \frac{2c}{n}\left(\frac{(n-1)n}{2} - \frac{(n/2-2)(n/2-1)}{2}\right) + an \\
&= \frac{2c}{n}\left(\frac{n^2-n}{2} - \frac{n^2/4 - 3n/2 + 2}{2}\right) + an \\
&= \frac{c}{n}\left(\frac{3n^2}{4} + \frac{n}{2} - 2\right) + an \\
&= c\left(\frac{3n}{4} + \frac{1}{2} - \frac{2}{n}\right) + an \\
&\le \frac{3cn}{4} + \frac{c}{2} + an \\
&= cn - \left(\frac{cn}{4} - \frac{c}{2} - an\right) .
\end{aligned}
$$

In order to complete the proof, we need to show that for sufficiently large n, this last expression is at most cn or, equivalently, that $cn/4 - c/2 - an \ge 0$. If we add $c/2$ to both sides and factor out n, we get $n(c/4 - a) \ge c/2$. As long as we choose the constant c so that $c/4 - a > 0$, i.e., $c > 4a$, we can divide both sides by $c/4 - a$, giving

$$n \ge \frac{c/2}{c/4 - a} = \frac{2c}{c - 4a} .$$

Thus, if we assume that $T(n) = O(1)$ for $n < 2c/(c-4a)$, then $\mathrm{E}[T(n)] = O(n)$. We conclude that we can find any order statistic, and in particular the median, in expected linear time, assuming that the elements are distinct.

Exercises

9.2-1

Show that RANDOMIZED-SELECT never makes a recursive call to a 0-length array.

9.2-2

Argue that the indicator random variable X_k and the value $T(\max(k-1, n-k))$ are independent.

9.2-3

Write an iterative version of RANDOMIZED-SELECT.

9.2-4

Suppose we use RANDOMIZED-SELECT to select the minimum element of the array $A = \langle 3, 2, 9, 0, 7, 5, 4, 8, 6, 1 \rangle$. Describe a sequence of partitions that results in a worst-case performance of RANDOMIZED-SELECT.

9.3 Selection in worst-case linear time

We now examine a selection algorithm whose running time is $O(n)$ in the worst case. Like RANDOMIZED-SELECT, the algorithm SELECT finds the desired element by recursively partitioning the input array. Here, however, we *guarantee* a good split upon partitioning the array. SELECT uses the deterministic partitioning algorithm PARTITION from quicksort (see Section 7.1), but modified to take the element to partition around as an input parameter.

The SELECT algorithm determines the ith smallest of an input array of $n > 1$ distinct elements by executing the following steps. (If $n = 1$, then SELECT merely returns its only input value as the ith smallest.)

1. Divide the n elements of the input array into $\lfloor n/5 \rfloor$ groups of 5 elements each and at most one group made up of the remaining n mod 5 elements.
2. Find the median of each of the $\lceil n/5 \rceil$ groups by first insertion-sorting the elements of each group (of which there are at most 5) and then picking the median from the sorted list of group elements.
3. Use SELECT recursively to find the median x of the $\lceil n/5 \rceil$ medians found in step 2. (If there are an even number of medians, then by our convention, x is the lower median.)
4. Partition the input array around the median-of-medians x using the modified version of PARTITION. Let k be one more than the number of elements on the low side of the partition, so that x is the kth smallest element and there are $n-k$ elements on the high side of the partition.
5. If $i = k$, then return x. Otherwise, use SELECT recursively to find the ith smallest element on the low side if $i < k$, or the $(i-k)$th smallest element on the high side if $i > k$.

To analyze the running time of SELECT, we first determine a lower bound on the number of elements that are greater than the partitioning element x. Figure 9.1 helps us to visualize this bookkeeping. At least half of the medians found in

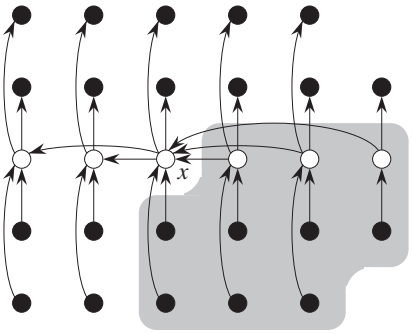


Figure 9.1 Analysis of the algorithm SELECT. The n elements are represented by small circles, and each group of 5 elements occupies a column. The medians of the groups are whitened, and the median-of-medians x is labeled. (When finding the median of an even number of elements, we use the lower median.) Arrows go from larger elements to smaller, from which we can see that 3 out of every full group of 5 elements to the right of x are greater than x, and 3 out of every group of 5 elements to the left of x are less than x. The elements known to be greater than x appear on a shaded background.

step 2 are greater than or equal to the median-of-medians x.[1] Thus, at least half of the $\lceil n/5 \rceil$ groups contribute at least 3 elements that are greater than x, except for the one group that has fewer than 5 elements if 5 does not divide n exactly, and the one group containing x itself. Discounting these two groups, it follows that the number of elements greater than x is at least

$$3\left(\left\lceil \frac{1}{2}\left\lceil \frac{n}{5}\right\rceil \right\rceil - 2\right) \;\geq\; \frac{3n}{10} - 6\,.$$

Similarly, at least $3n/10 - 6$ elements are less than x. Thus, in the worst case, step 5 calls SELECT recursively on at most $7n/10 + 6$ elements.

We can now develop a recurrence for the worst-case running time $T(n)$ of the algorithm SELECT. Steps 1, 2, and 4 take $O(n)$ time. (Step 2 consists of $O(n)$ calls of insertion sort on sets of size $O(1)$.) Step 3 takes time $T(\lceil n/5 \rceil)$, and step 5 takes time at most $T(7n/10 + 6)$, assuming that T is monotonically increasing. We make the assumption, which seems unmotivated at first, that any input of fewer than 140 elements requires $O(1)$ time; the origin of the magic constant 140 will be clear shortly. We can therefore obtain the recurrence

[1] Because of our assumption that the numbers are distinct, all medians except x are either greater than or less than x.

$$T(n) \le \begin{cases} O(1) & \text{if } n < 140 , \\ T(\lceil n/5 \rceil) + T(7n/10 + 6) + O(n) & \text{if } n \ge 140 . \end{cases}$$

We show that the running time is linear by substitution. More specifically, we will show that $T(n) \le cn$ for some suitably large constant c and all $n > 0$. We begin by assuming that $T(n) \le cn$ for some suitably large constant c and all $n < 140$; this assumption holds if c is large enough. We also pick a constant a such that the function described by the $O(n)$ term above (which describes the non-recursive component of the running time of the algorithm) is bounded above by an for all $n > 0$. Substituting this inductive hypothesis into the right-hand side of the recurrence yields

$$\begin{aligned} T(n) &\le c\lceil n/5 \rceil + c(7n/10 + 6) + an \\ &\le cn/5 + c + 7cn/10 + 6c + an \\ &= 9cn/10 + 7c + an \\ &= cn + (-cn/10 + 7c + an) , \end{aligned}$$

which is at most cn if

$$-cn/10 + 7c + an \le 0 . \tag{9.2}$$

Inequality (9.2) is equivalent to the inequality $c \ge 10a(n/(n-70))$ when $n > 70$. Because we assume that $n \ge 140$, we have $n/(n-70) \le 2$, and so choosing $c \ge 20a$ will satisfy inequality (9.2). (Note that there is nothing special about the constant 140; we could replace it by any integer strictly greater than 70 and then choose c accordingly.) The worst-case running time of SELECT is therefore linear.

As in a comparison sort (see Section 8.1), SELECT and RANDOMIZED-SELECT determine information about the relative order of elements only by comparing elements. Recall from Chapter 8 that sorting requires $\Omega(n \lg n)$ time in the comparison model, even on average (see Problem 8-1). The linear-time sorting algorithms in Chapter 8 make assumptions about the input. In contrast, the linear-time selection algorithms in this chapter do not require any assumptions about the input. They are not subject to the $\Omega(n \lg n)$ lower bound because they manage to solve the selection problem without sorting. Thus, solving the selection problem by sorting and indexing, as presented in the introduction to this chapter, is asymptotically inefficient.

Exercises

9.3-1
In the algorithm SELECT, the input elements are divided into groups of 5. Will the algorithm work in linear time if they are divided into groups of 7? Argue that SELECT does not run in linear time if groups of 3 are used.

9.3-2
Analyze SELECT to show that if $n \geq 140$, then at least $\lceil n/4 \rceil$ elements are greater than the median-of-medians x and at least $\lceil n/4 \rceil$ elements are less than x.

9.3-3
Show how quicksort can be made to run in $O(n \lg n)$ time in the worst case, assuming that all elements are distinct.

9.3-4 ⋆
Suppose that an algorithm uses only comparisons to find the ith smallest element in a set of n elements. Show that it can also find the $i - 1$ smaller elements and the $n - i$ larger elements without performing any additional comparisons.

9.3-5
Suppose that you have a "black-box" worst-case linear-time median subroutine. Give a simple, linear-time algorithm that solves the selection problem for an arbitrary order statistic.

9.3-6
The kth ***quantiles*** of an n-element set are the $k - 1$ order statistics that divide the sorted set into k equal-sized sets (to within 1). Give an $O(n \lg k)$-time algorithm to list the kth quantiles of a set.

9.3-7
Describe an $O(n)$-time algorithm that, given a set S of n distinct numbers and a positive integer $k \leq n$, determines the k numbers in S that are closest to the median of S.

9.3-8
Let $X[1..n]$ and $Y[1..n]$ be two arrays, each containing n numbers already in sorted order. Give an $O(\lg n)$-time algorithm to find the median of all $2n$ elements in arrays X and Y.

9.3-9
Professor Olay is consulting for an oil company, which is planning a large pipeline running east to west through an oil field of n wells. The company wants to connect

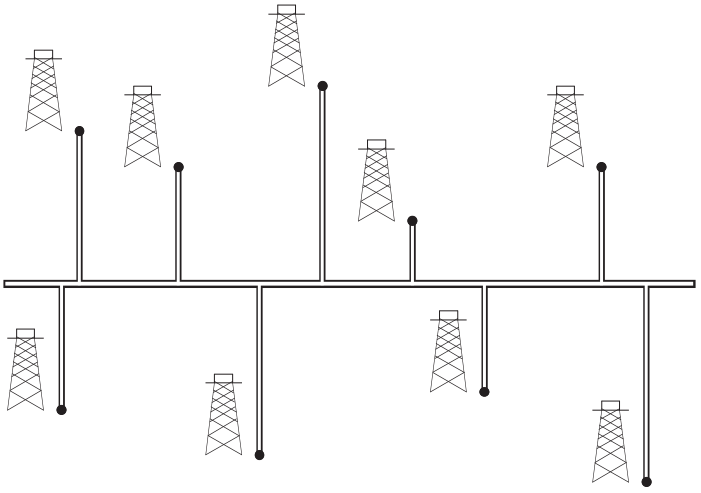


Figure 9.2 Professor Olay needs to determine the position of the east-west oil pipeline that minimizes the total length of the north-south spurs.

a spur pipeline from each well directly to the main pipeline along a shortest route (either north or south), as shown in Figure 9.2. Given the x- and y-coordinates of the wells, how should the professor pick the optimal location of the main pipeline, which would be the one that minimizes the total length of the spurs? Show how to determine the optimal location in linear time.

Problems

9-1 Largest i numbers in sorted order

Given a set of n numbers, we wish to find the i largest in sorted order using a comparison-based algorithm. Find the algorithm that implements each of the following methods with the best asymptotic worst-case running time, and analyze the running times of the algorithms in terms of n and i.

a. Sort the numbers, and list the i largest.

b. Build a max-priority queue from the numbers, and call EXTRACT-MAX i times.

c. Use an order-statistic algorithm to find the ith largest number, partition around that number, and sort the i largest numbers.

9-2 Weighted median

For n distinct elements $x_1, x_2, \ldots, x_n$ with positive weights $w_1, w_2, \ldots, w_n$ such that $\sum_{i=1}^{n} w_i = 1$, the ***weighted (lower) median*** is the element x_k satisfying

$$\sum_{x_i < x_k} w_i < \frac{1}{2}$$

and

$$\sum_{x_i > x_k} w_i \le \frac{1}{2} .$$

For example, if the elements are $0.1, 0.35, 0.05, 0.1, 0.15, 0.05, 0.2$ and each element equals its weight (that is, $w_i = x_i$ for $i = 1, 2, \ldots, 7$), then the median is 0.1, but the weighted median is 0.2.

a. Argue that the median of $x_1, x_2, \ldots, x_n$ is the weighted median of the x_i with weights $w_i = 1/n$ for $i = 1, 2, \ldots, n$.

b. Show how to compute the weighted median of n elements in $O(n \lg n)$ worst-case time using sorting.

c. Show how to compute the weighted median in $\Theta(n)$ worst-case time using a linear-time median algorithm such as SELECT from Section 9.3.

The ***post-office location problem*** is defined as follows. We are given n points $p_1, p_2, \ldots, p_n$ with associated weights $w_1, w_2, \ldots, w_n$. We wish to find a point p (not necessarily one of the input points) that minimizes the sum $\sum_{i=1}^{n} w_i \, d(p, p_i)$, where $d(a, b)$ is the distance between points a and b.

d. Argue that the weighted median is a best solution for the 1-dimensional post-office location problem, in which points are simply real numbers and the distance between points a and b is $d(a, b) = |a - b|$.

e. Find the best solution for the 2-dimensional post-office location problem, in which the points are (x, y) coordinate pairs and the distance between points $a = (x_1, y_1)$ and $b = (x_2, y_2)$ is the ***Manhattan distance*** given by $d(a, b) = |x_1 - x_2| + |y_1 - y_2|$.

9-3 Small order statistics

We showed that the worst-case number $T(n)$ of comparisons used by SELECT to select the ith order statistic from n numbers satisfies $T(n) = \Theta(n)$, but the constant hidden by the Θ-notation is rather large. When i is small relative to n, we can implement a different procedure that uses SELECT as a subroutine but makes fewer comparisons in the worst case.

a. Describe an algorithm that uses $U_i(n)$ comparisons to find the ith smallest of n elements, where

$$U_i(n) = \begin{cases} T(n) & \text{if } i \geq n/2\,, \\ \lfloor n/2 \rfloor + U_i(\lceil n/2 \rceil) + T(2i) & \text{otherwise}\,. \end{cases}$$

(*Hint:* Begin with $\lfloor n/2 \rfloor$ disjoint pairwise comparisons, and recurse on the set containing the smaller element from each pair.)

b. Show that, if $i < n/2$, then $U_i(n) = n + O(T(2i)\lg(n/i))$.

c. Show that if i is a constant less than $n/2$, then $U_i(n) = n + O(\lg n)$.

d. Show that if $i = n/k$ for $k \geq 2$, then $U_i(n) = n + O(T(2n/k)\lg k)$.

9-4 Alternative analysis of randomized selection

In this problem, we use indicator random variables to analyze the RANDOMIZED-SELECT procedure in a manner akin to our analysis of RANDOMIZED-QUICKSORT in Section 7.4.2.

As in the quicksort analysis, we assume that all elements are distinct, and we rename the elements of the input array A as $z_1, z_2, \ldots, z_n$, where z_i is the ith smallest element. Thus, the call RANDOMIZED-SELECT$(A, 1, n, k)$ returns z_k.

For $1 \leq i < j \leq n$, let

$$X_{ijk} = \mathrm{I}\{z_i \text{ is compared with } z_j \text{ sometime during the execution of the algorithm to find } z_k\}\,.$$

a. Give an exact expression for $\mathrm{E}[X_{ijk}]$. (*Hint:* Your expression may have different values, depending on the values of i, j, and k.)

b. Let X_k denote the total number of comparisons between elements of array A when finding z_k. Show that

$$\mathrm{E}[X_k] \leq 2\left(\sum_{i=1}^{k}\sum_{j=k}^{n}\frac{1}{j-i+1} + \sum_{j=k+1}^{n}\frac{j-k-1}{j-k+1} + \sum_{i=1}^{k-2}\frac{k-i-1}{k-i+1}\right)\,.$$

c. Show that $\mathrm{E}[X_k] \leq 4n$.

d. Conclude that, assuming all elements of array A are distinct, RANDOMIZED-SELECT runs in expected time $O(n)$.

Chapter notes

The worst-case linear-time median-finding algorithm was devised by Blum, Floyd, Pratt, Rivest, and Tarjan [50]. The fast randomized version is due to Hoare [169]. Floyd and Rivest [108] have developed an improved randomized version that partitions around an element recursively selected from a small sample of the elements.

It is still unknown exactly how many comparisons are needed to determine the median. Bent and John [41] gave a lower bound of $2n$ comparisons for median finding, and Schönhage, Paterson, and Pippenger [302] gave an upper bound of $3n$. Dor and Zwick have improved on both of these bounds. Their upper bound [93] is slightly less than $2.95n$, and their lower bound [94] is $(2 + \epsilon)n$, for a small positive constant ϵ, thereby improving slightly on related work by Dor et al. [92]. Paterson [272] describes some of these results along with other related work.

III Data Structures

28 Matrix Operations

Because operations on matrices lie at the heart of scientific computing, efficient algorithms for working with matrices have many practical applications. This chapter focuses on how to multiply matrices and solve sets of simultaneous linear equations. Appendix D reviews the basics of matrices.

Section 28.1 shows how to solve a set of linear equations using LUP decompositions. Then, Section 28.2 explores the close relationship between multiplying and inverting matrices. Finally, Section 28.3 discusses the important class of symmetric positive-definite matrices and shows how we can use them to find a least-squares solution to an overdetermined set of linear equations.

One important issue that arises in practice is ***numerical stability***. Due to the limited precision of floating-point representations in actual computers, round-off errors in numerical computations may become amplified over the course of a computation, leading to incorrect results; we call such computations ***numerically unstable***. Although we shall briefly consider numerical stability on occasion, we do not focus on it in this chapter. We refer you to the excellent book by Golub and Van Loan [144] for a thorough discussion of stability issues.

28.1 Solving systems of linear equations

Numerous applications need to solve sets of simultaneous linear equations. We can formulate a linear system as a matrix equation in which each matrix or vector element belongs to a field, typically the real numbers $\mathbb{R}$. This section discusses how to solve a system of linear equations using a method called LUP decomposition.

We start with a set of linear equations in n unknowns $x_1, x_2, \ldots, x_n$:

$$\begin{aligned} a_{11}x_1 + a_{12}x_2 + \cdots + a_{1n}x_n &= b_1 , \\ a_{21}x_1 + a_{22}x_2 + \cdots + a_{2n}x_n &= b_2 , \\ &\vdots \\ a_{n1}x_1 + a_{n2}x_2 + \cdots + a_{nn}x_n &= b_n . \end{aligned} \tag{28.1}$$

A ***solution*** to the equations (28.1) is a set of values for $x_1, x_2, \ldots, x_n$ that satisfy all of the equations simultaneously. In this section, we treat only the case in which there are exactly n equations in n unknowns.

We can conveniently rewrite equations (28.1) as the matrix-vector equation

$$\begin{pmatrix} a_{11} & a_{12} & \cdots & a_{1n} \\ a_{21} & a_{22} & \cdots & a_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n1} & a_{n2} & \cdots & a_{nn} \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \\ \vdots \\ x_n \end{pmatrix} = \begin{pmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{pmatrix}$$

or, equivalently, letting $A = (a_{ij})$, $x = (x_i)$, and $b = (b_i)$, as

$$Ax = b . \tag{28.2}$$

If A is nonsingular, it possesses an inverse A^{-1}, and

$$x = A^{-1}b \tag{28.3}$$

is the solution vector. We can prove that x is the unique solution to equation (28.2) as follows. If there are two solutions, x and x', then $Ax = Ax' = b$ and, letting I denote an identity matrix,

$$\begin{aligned} x &= Ix \\ &= (A^{-1}A)x \\ &= A^{-1}(Ax) \\ &= A^{-1}(Ax') \\ &= (A^{-1}A)x' \\ &= x' . \end{aligned}$$

In this section, we shall be concerned predominantly with the case in which A is nonsingular or, equivalently (by Theorem D.1), the rank of A is equal to the number n of unknowns. There are other possibilities, however, which merit a brief discussion. If the number of equations is less than the number n of unknowns—or, more generally, if the rank of A is less than n—then the system is ***underdetermined***. An underdetermined system typically has infinitely many solutions, although it may have no solutions at all if the equations are inconsistent. If the number of equations exceeds the number n of unknowns, the system is ***overdetermined***, and there may not exist any solutions. Section 28.3 addresses the important

problem of finding good approximate solutions to overdetermined systems of linear equations.

Let us return to our problem of solving the system $Ax = b$ of n equations in n unknowns. We could compute A^{-1} and then, using equation (28.3), multiply b by A^{-1}, yielding $x = A^{-1}b$. This approach suffers in practice from numerical instability. Fortunately, another approach—LUP decomposition—is numerically stable and has the further advantage of being faster in practice.

Overview of LUP decomposition

The idea behind LUP decomposition is to find three $n \times n$ matrices L, U, and P such that

$$PA = LU \ , \tag{28.4}$$

where

- L is a unit lower-triangular matrix,
- U is an upper-triangular matrix, and
- P is a permutation matrix.

We call matrices L, U, and P satisfying equation (28.4) an ***LUP decomposition*** of the matrix A. We shall show that every nonsingular matrix A possesses such a decomposition.

Computing an LUP decomposition for the matrix A has the advantage that we can more easily solve linear systems when they are triangular, as is the case for both matrices L and U. Once we have found an LUP decomposition for A, we can solve equation (28.2), $Ax = b$, by solving only triangular linear systems, as follows. Multiplying both sides of $Ax = b$ by P yields the equivalent equation $PAx = Pb$, which, by Exercise D.1-4, amounts to permuting the equations (28.1). Using our decomposition (28.4), we obtain

$$LUx = Pb \ .$$

We can now solve this equation by solving two triangular linear systems. Let us define $y = Ux$, where x is the desired solution vector. First, we solve the lower-triangular system

$$Ly = Pb \tag{28.5}$$

for the unknown vector y by a method called "forward substitution." Having solved for y, we then solve the upper-triangular system

$$Ux = y \tag{28.6}$$

for the unknown x by a method called "back substitution." Because the permutation matrix P is invertible (Exercise D.2-3), multiplying both sides of equation (28.4) by P^{-1} gives $P^{-1}PA = P^{-1}LU$, so that

$$A = P^{-1}LU \; . \tag{28.7}$$

Hence, the vector x is our solution to $Ax = b$:

$$\begin{aligned} Ax &= P^{-1}LUx && \text{(by equation (28.7))} \\ &= P^{-1}Ly && \text{(by equation (28.6))} \\ &= P^{-1}Pb && \text{(by equation (28.5))} \\ &= b \; . \end{aligned}$$

Our next step is to show how forward and back substitution work and then attack the problem of computing the LUP decomposition itself.

Forward and back substitution

Forward substitution can solve the lower-triangular system (28.5) in $\Theta(n^2)$ time, given L, P, and b. For convenience, we represent the permutation P compactly by an array $\pi[1..n]$. For $i = 1, 2, \ldots, n$, the entry $\pi[i]$ indicates that $P_{i,\pi[i]} = 1$ and $P_{ij} = 0$ for $j \neq \pi[i]$. Thus, PA has $a_{\pi[i],j}$ in row i and column j, and Pb has $b_{\pi[i]}$ as its ith element. Since L is unit lower-triangular, we can rewrite equation (28.5) as

$$\begin{aligned} y_1 &= b_{\pi[1]} \; , \\ l_{21}y_1 + y_2 &= b_{\pi[2]} \; , \\ l_{31}y_1 + l_{32}y_2 + y_3 &= b_{\pi[3]} \; , \\ &\vdots \\ l_{n1}y_1 + l_{n2}y_2 + l_{n3}y_3 + \cdots + y_n &= b_{\pi[n]} \; . \end{aligned}$$

The first equation tells us that $y_1 = b_{\pi[1]}$. Knowing the value of y_1, we can substitute it into the second equation, yielding

$$y_2 = b_{\pi[2]} - l_{21}y_1 \; .$$

Now, we can substitute both y_1 and y_2 into the third equation, obtaining

$$y_3 = b_{\pi[3]} - (l_{31}y_1 + l_{32}y_2) \; .$$

In general, we substitute $y_1, y_2, \ldots, y_{i-1}$ "forward" into the ith equation to solve for y_i:

$$y_i = b_{\pi[i]} - \sum_{j=1}^{i-1} l_{ij} y_j \ .$$

Having solved for y, we solve for x in equation (28.6) using ***back substitution***, which is similar to forward substitution. Here, we solve the nth equation first and work backward to the first equation. Like forward substitution, this process runs in $\Theta(n^2)$ time. Since U is upper-triangular, we can rewrite the system (28.6) as

$$\begin{aligned}
u_{11}x_1 + u_{12}x_2 + \cdots + u_{1,n-2}x_{n-2} + u_{1,n-1}x_{n-1} + u_{1n}x_n &= y_1 \ , \\
u_{22}x_2 + \cdots + u_{2,n-2}x_{n-2} + u_{2,n-1}x_{n-1} + u_{2n}x_n &= y_2 \ , \\
&\vdots \\
u_{n-2,n-2}x_{n-2} + u_{n-2,n-1}x_{n-1} + u_{n-2,n}x_n &= y_{n-2} \ , \\
u_{n-1,n-1}x_{n-1} + u_{n-1,n}x_n &= y_{n-1} \ , \\
u_{n,n}x_n &= y_n \ .
\end{aligned}$$

Thus, we can solve for $x_n, x_{n-1}, \ldots, x_1$ successively as follows:

$$\begin{aligned}
x_n &= y_n/u_{n,n} \ , \\
x_{n-1} &= (y_{n-1} - u_{n-1,n}x_n)/u_{n-1,n-1} \ , \\
x_{n-2} &= (y_{n-2} - (u_{n-2,n-1}x_{n-1} + u_{n-2,n}x_n))/u_{n-2,n-2} \ , \\
&\vdots
\end{aligned}$$

or, in general,

$$x_i = \left(y_i - \sum_{j=i+1}^{n} u_{ij} x_j \right) / u_{ii} \ .$$

Given P, L, U, and b, the procedure LUP-SOLVE solves for x by combining forward and back substitution. The pseudocode assumes that the dimension n appears in the attribute $L.rows$ and that the permutation matrix P is represented by the array π.

```
LUP-SOLVE(L, U, π, b)
1  n = L.rows
2  let x be a new vector of length n
3  for i = 1 to n
4       y_i = b_{π[i]} − Σ_{j=1}^{i−1} l_ij y_j
5  for i = n downto 1
6       x_i = (y_i − Σ_{j=i+1}^{n} u_ij x_j) / u_ii
7  return x
```

Procedure LUP-SOLVE solves for y using forward substitution in lines 3–4, and then it solves for x using backward substitution in lines 5–6. Since the summation within each of the **for** loops includes an implicit loop, the running time is $\Theta(n^2)$.

As an example of these methods, consider the system of linear equations defined by

$$\begin{pmatrix} 1 & 2 & 0 \\ 3 & 4 & 4 \\ 5 & 6 & 3 \end{pmatrix} x = \begin{pmatrix} 3 \\ 7 \\ 8 \end{pmatrix},$$

where

$$A = \begin{pmatrix} 1 & 2 & 0 \\ 3 & 4 & 4 \\ 5 & 6 & 3 \end{pmatrix},$$

$$b = \begin{pmatrix} 3 \\ 7 \\ 8 \end{pmatrix},$$

and we wish to solve for the unknown x. The LUP decomposition is

$$L = \begin{pmatrix} 1 & 0 & 0 \\ 0.2 & 1 & 0 \\ 0.6 & 0.5 & 1 \end{pmatrix},$$

$$U = \begin{pmatrix} 5 & 6 & 3 \\ 0 & 0.8 & -0.6 \\ 0 & 0 & 2.5 \end{pmatrix},$$

$$P = \begin{pmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix}.$$

(You might want to verify that $PA = LU$.) Using forward substitution, we solve $Ly = Pb$ for y:

$$\begin{pmatrix} 1 & 0 & 0 \\ 0.2 & 1 & 0 \\ 0.6 & 0.5 & 1 \end{pmatrix} \begin{pmatrix} y_1 \\ y_2 \\ y_3 \end{pmatrix} = \begin{pmatrix} 8 \\ 3 \\ 7 \end{pmatrix},$$

obtaining

$$y = \begin{pmatrix} 8 \\ 1.4 \\ 1.5 \end{pmatrix}$$

by computing first y_1, then y_2, and finally y_3. Using back substitution, we solve $Ux = y$ for x:

$$\begin{pmatrix} 5 & 6 & 3 \\ 0 & 0.8 & -0.6 \\ 0 & 0 & 2.5 \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \\ x_3 \end{pmatrix} = \begin{pmatrix} 8 \\ 1.4 \\ 1.5 \end{pmatrix},$$

thereby obtaining the desired answer

$$x = \begin{pmatrix} -1.4 \\ 2.2 \\ 0.6 \end{pmatrix}$$

by computing first x_3, then x_2, and finally x_1.

Computing an LU decomposition

We have now shown that if we can create an LUP decomposition for a nonsingular matrix A, then forward and back substitution can solve the system $Ax = b$ of linear equations. Now we show how to efficiently compute an LUP decomposition for A. We start with the case in which A is an $n \times n$ nonsingular matrix and P is absent (or, equivalently, $P = I_n$). In this case, we factor $A = LU$. We call the two matrices L and U an ***LU decomposition*** of A.

We use a process known as ***Gaussian elimination*** to create an LU decomposition. We start by subtracting multiples of the first equation from the other equations in order to remove the first variable from those equations. Then, we subtract multiples of the second equation from the third and subsequent equations so that now the first and second variables are removed from them. We continue this process until the system that remains has an upper-triangular form—in fact, it is the matrix U. The matrix L is made up of the row multipliers that cause variables to be eliminated.

Our algorithm to implement this strategy is recursive. We wish to construct an LU decomposition for an $n \times n$ nonsingular matrix A. If $n = 1$, then we are done, since we can choose $L = I_1$ and $U = A$. For $n > 1$, we break A into four parts:

$$\begin{aligned} A &= \left(\begin{array}{c|ccc} a_{11} & a_{12} & \cdots & a_{1n} \\ \hline a_{21} & a_{22} & \cdots & a_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n1} & a_{n2} & \cdots & a_{nn} \end{array}\right) \\ &= \begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ v & A' \end{pmatrix}, \end{aligned}$$

where v is a column $(n-1)$-vector, w^{T} is a row $(n-1)$-vector, and A' is an $(n-1) \times (n-1)$ matrix. Then, using matrix algebra (verify the equations by

simply multiplying through), we can factor A as

$$\begin{aligned} A &= \begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ v & A' \end{pmatrix} \\ &= \begin{pmatrix} 1 & 0 \\ v/a_{11} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ 0 & A' - vw^{\mathrm{T}}/a_{11} \end{pmatrix} . \end{aligned} \tag{28.8}$$

The 0s in the first and second matrices of equation (28.8) are row and column $(n-1)$-vectors, respectively. The term vw^{T}/a_{11}, formed by taking the outer product of v and w and dividing each element of the result by a_{11}, is an $(n-1) \times (n-1)$ matrix, which conforms in size to the matrix A' from which it is subtracted. The resulting $(n-1) \times (n-1)$ matrix

$$A' - vw^{\mathrm{T}}/a_{11} \tag{28.9}$$

is called the ***Schur complement*** of A with respect to a_{11}.

We claim that if A is nonsingular, then the Schur complement is nonsingular, too. Why? Suppose that the Schur complement, which is $(n-1) \times (n-1)$, is singular. Then by Theorem D.1, it has row rank strictly less than $n-1$. Because the bottom $n-1$ entries in the first column of the matrix

$$\begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ 0 & A' - vw^{\mathrm{T}}/a_{11} \end{pmatrix}$$

are all 0, the bottom $n-1$ rows of this matrix must have row rank strictly less than $n-1$. The row rank of the entire matrix, therefore, is strictly less than n. Applying Exercise D.2-8 to equation (28.8), A has rank strictly less than n, and from Theorem D.1 we derive the contradiction that A is singular.

Because the Schur complement is nonsingular, we can now recursively find an LU decomposition for it. Let us say that

$$A' - vw^{\mathrm{T}}/a_{11} = L'U' ,$$

where L' is unit lower-triangular and U' is upper-triangular. Then, using matrix algebra, we have

$$\begin{aligned} A &= \begin{pmatrix} 1 & 0 \\ v/a_{11} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ 0 & A' - vw^{\mathrm{T}}/a_{11} \end{pmatrix} \\ &= \begin{pmatrix} 1 & 0 \\ v/a_{11} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ 0 & L'U' \end{pmatrix} \\ &= \begin{pmatrix} 1 & 0 \\ v/a_{11} & L' \end{pmatrix} \begin{pmatrix} a_{11} & w^{\mathrm{T}} \\ 0 & U' \end{pmatrix} \\ &= LU , \end{aligned}$$

thereby providing our LU decomposition. (Note that because L' is unit lower-triangular, so is L, and because U' is upper-triangular, so is U.)

Of course, if $a_{11} = 0$, this method doesn't work, because it divides by 0. It also doesn't work if the upper leftmost entry of the Schur complement $A' - vw^{\mathrm{T}}/a_{11}$ is 0, since we divide by it in the next step of the recursion. The elements by which we divide during LU decomposition are called ***pivots***, and they occupy the diagonal elements of the matrix U. The reason we include a permutation matrix P during LUP decomposition is that it allows us to avoid dividing by 0. When we use permutations to avoid division by 0 (or by small numbers, which would contribute to numerical instability), we are ***pivoting***.

An important class of matrices for which LU decomposition always works correctly is the class of symmetric positive-definite matrices. Such matrices require no pivoting, and thus we can employ the recursive strategy outlined above without fear of dividing by 0. We shall prove this result, as well as several others, in Section 28.3.

Our code for LU decomposition of a matrix A follows the recursive strategy, except that an iteration loop replaces the recursion. (This transformation is a standard optimization for a "tail-recursive" procedure—one whose last operation is a recursive call to itself. See Problem 7-4.) It assumes that the attribute $A.rows$ gives the dimension of A. We initialize the matrix U with 0s below the diagonal and matrix L with 1s on its diagonal and 0s above the diagonal.

LU-DECOMPOSITION(A)

```
 1  n = A.rows
 2  let L and U be new n × n matrices
 3  initialize U with 0s below the diagonal
 4  initialize L with 1s on the diagonal and 0s above the diagonal
 5  for k = 1 to n
 6      u_kk = a_kk
 7      for i = k + 1 to n
 8          l_ik = a_ik/u_kk          // l_ik holds v_i
 9          u_ki = a_ki               // u_ki holds w_i^T
10      for i = k + 1 to n
11          for j = k + 1 to n
12              a_ij = a_ij − l_ik u_kj
13  return L and U
```

The outer **for** loop beginning in line 5 iterates once for each recursive step. Within this loop, line 6 determines the pivot to be $u_{kk} = a_{kk}$. The **for** loop in lines 7–9 (which does not execute when $k = n$), uses the v and w^{T} vectors to update L and U. Line 8 determines the elements of the v vector, storing v_i in l_{ik}, and line 9 computes the elements of the w^{T} vector, storing w_i^{T} in u_{ki}. Finally, lines 10–12 compute the elements of the Schur complement and store them back into the ma-

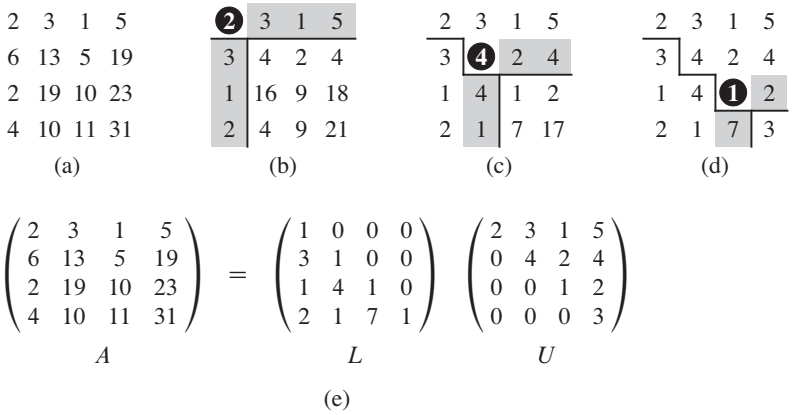


Figure 28.1 The operation of LU-DECOMPOSITION. **(a)** The matrix A. **(b)** The element $a_{11} = 2$ in the black circle is the pivot, the shaded column is v/a_{11}, and the shaded row is w^{T}. The elements of U computed thus far are above the horizontal line, and the elements of L are to the left of the vertical line. The Schur complement matrix $A' - vw^{\mathrm{T}}/a_{11}$ occupies the lower right. **(c)** We now operate on the Schur complement matrix produced from part (b). The element $a_{22} = 4$ in the black circle is the pivot, and the shaded column and row are v/a_{22} and w^{T} (in the partitioning of the Schur complement), respectively. Lines divide the matrix into the elements of U computed so far (above), the elements of L computed so far (left), and the new Schur complement (lower right). **(d)** After the next step, the matrix A is factored. (The element 3 in the new Schur complement becomes part of U when the recursion terminates.) **(e)** The factorization $A = LU$.

trix A. (We don't need to divide by a_{kk} in line 12 because we already did so when we computed l_{ik} in line 8.) Because line 12 is triply nested, LU-DECOMPOSITION runs in time $\Theta(n^3)$.

Figure 28.1 illustrates the operation of LU-DECOMPOSITION. It shows a standard optimization of the procedure in which we store the significant elements of L and U in place in the matrix A. That is, we can set up a correspondence between each element a_{ij} and either l_{ij} (if $i > j$) or u_{ij} (if $i \leq j$) and update the matrix A so that it holds both L and U when the procedure terminates. To obtain the pseudocode for this optimization from the above pseudocode, just replace each reference to l or u by a; you can easily verify that this transformation preserves correctness.

Computing an LUP decomposition

Generally, in solving a system of linear equations $Ax = b$, we must pivot on off-diagonal elements of A to avoid dividing by 0. Dividing by 0 would, of course, be disastrous. But we also want to avoid dividing by a small value—even if A is

nonsingular—because numerical instabilities can result. We therefore try to pivot on a large value.

The mathematics behind LUP decomposition is similar to that of LU decomposition. Recall that we are given an $n \times n$ nonsingular matrix A, and we wish to find a permutation matrix P, a unit lower-triangular matrix L, and an upper-triangular matrix U such that $PA = LU$. Before we partition the matrix A, as we did for LU decomposition, we move a nonzero element, say a_{k1}, from somewhere in the first column to the $(1,1)$ position of the matrix. For numerical stability, we choose a_{k1} as the element in the first column with the greatest absolute value. (The first column cannot contain only 0s, for then A would be singular, because its determinant would be 0, by Theorems D.4 and D.5.) In order to preserve the set of equations, we exchange row 1 with row k, which is equivalent to multiplying A by a permutation matrix Q on the left (Exercise D.1-4). Thus, we can write QA as

$$QA = \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ v & A' \end{pmatrix},$$

where $v = (a_{21}, a_{31}, \ldots, a_{n1})^{\mathrm{T}}$, except that a_{11} replaces a_{k1}; $w^{\mathrm{T}} = (a_{k2}, a_{k3}, \ldots, a_{kn})$; and A' is an $(n-1) \times (n-1)$ matrix. Since $a_{k1} \neq 0$, we can now perform much the same linear algebra as for LU decomposition, but now guaranteeing that we do not divide by 0:

$$\begin{aligned} QA &= \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ v & A' \end{pmatrix} \\ &= \begin{pmatrix} 1 & 0 \\ v/a_{k1} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ 0 & A' - vw^{\mathrm{T}}/a_{k1} \end{pmatrix}. \end{aligned}$$

As we saw for LU decomposition, if A is nonsingular, then the Schur complement $A' - vw^{\mathrm{T}}/a_{k1}$ is nonsingular, too. Therefore, we can recursively find an LUP decomposition for it, with unit lower-triangular matrix L', upper-triangular matrix U', and permutation matrix P', such that

$$P'(A' - vw^{\mathrm{T}}/a_{k1}) = L'U' .$$

Define

$$P = \begin{pmatrix} 1 & 0 \\ 0 & P' \end{pmatrix} Q ,$$

which is a permutation matrix, since it is the product of two permutation matrices (Exercise D.1-4). We now have

$$
\begin{aligned}
PA &= \begin{pmatrix} 1 & 0 \\ 0 & P' \end{pmatrix} QA \\
&= \begin{pmatrix} 1 & 0 \\ 0 & P' \end{pmatrix} \begin{pmatrix} 1 & 0 \\ v/a_{k1} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ 0 & A' - vw^{\mathrm{T}}/a_{k1} \end{pmatrix} \\
&= \begin{pmatrix} 1 & 0 \\ P'v/a_{k1} & P' \end{pmatrix} \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ 0 & A' - vw^{\mathrm{T}}/a_{k1} \end{pmatrix} \\
&= \begin{pmatrix} 1 & 0 \\ P'v/a_{k1} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ 0 & P'(A' - vw^{\mathrm{T}}/a_{k1}) \end{pmatrix} \\
&= \begin{pmatrix} 1 & 0 \\ P'v/a_{k1} & I_{n-1} \end{pmatrix} \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ 0 & L'U' \end{pmatrix} \\
&= \begin{pmatrix} 1 & 0 \\ P'v/a_{k1} & L' \end{pmatrix} \begin{pmatrix} a_{k1} & w^{\mathrm{T}} \\ 0 & U' \end{pmatrix} \\
&= LU \ ,
\end{aligned}
$$

yielding the LUP decomposition. Because L' is unit lower-triangular, so is L, and because U' is upper-triangular, so is U.

Notice that in this derivation, unlike the one for LU decomposition, we must multiply both the column vector v/a_{k1} and the Schur complement $A' - vw^{\mathrm{T}}/a_{k1}$ by the permutation matrix P'. Here is the pseudocode for LUP decomposition:

```
LUP-DECOMPOSITION(A)
 1  n = A.rows
 2  let π[1..n] be a new array
 3  for i = 1 to n
 4      π[i] = i
 5  for k = 1 to n
 6      p = 0
 7      for i = k to n
 8          if |a_ik| > p
 9              p = |a_ik|
10              k' = i
11      if p == 0
12          error "singular matrix"
13      exchange π[k] with π[k']
14      for i = 1 to n
15          exchange a_ki with a_k'i
16      for i = k + 1 to n
17          a_ik = a_ik/a_kk
18          for j = k + 1 to n
19              a_ij = a_ij − a_ik a_kj
```

Like LU-DECOMPOSITION, our LUP-DECOMPOSITION procedure replaces the recursion with an iteration loop. As an improvement over a direct implementation of the recursion, we dynamically maintain the permutation matrix P as an array π, where $\pi[i] = j$ means that the ith row of P contains a 1 in column j. We also implement the code to compute L and U "in place" in the matrix A. Thus, when the procedure terminates,

$$a_{ij} = \begin{cases} l_{ij} & \text{if } i > j \ , \\ u_{ij} & \text{if } i \le j \ . \end{cases}$$

Figure 28.2 illustrates how LUP-DECOMPOSITION factors a matrix. Lines 3–4 initialize the array π to represent the identity permutation. The outer **for** loop beginning in line 5 implements the recursion. Each time through the outer loop, lines 6–10 determine the element $a_{k'k}$ with largest absolute value of those in the current first column (column k) of the $(n - k + 1) \times (n - k + 1)$ matrix whose LUP decomposition we are finding. If all elements in the current first column are zero, lines 11–12 report that the matrix is singular. To pivot, we exchange $\pi[k']$ with $\pi[k]$ in line 13 and exchange the kth and k'th rows of A in lines 14–15, thereby making the pivot element a_{kk}. (The entire rows are swapped because in the derivation of the method above, not only is $A' - vw^{\mathrm{T}}/a_{k1}$ multiplied by P', but so is v/a_{k1}.) Finally, the Schur complement is computed by lines 16–19 in much the same way as it is computed by lines 7–12 of LU-DECOMPOSITION, except that here the operation is written to work in place.

Because of its triply nested loop structure, LUP-DECOMPOSITION has a running time of $\Theta(n^3)$, which is the same as that of LU-DECOMPOSITION. Thus, pivoting costs us at most a constant factor in time.

Exercises

28.1-1

Solve the equation

$$\begin{pmatrix} 1 & 0 & 0 \\ 4 & 1 & 0 \\ -6 & 5 & 1 \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \\ x_3 \end{pmatrix} = \begin{pmatrix} 3 \\ 14 \\ -7 \end{pmatrix}$$

by using forward substitution.

28.1-2

Find an LU decomposition of the matrix

$$\begin{pmatrix} 4 & -5 & 6 \\ 8 & -6 & 7 \\ 12 & -7 & 12 \end{pmatrix} .$$

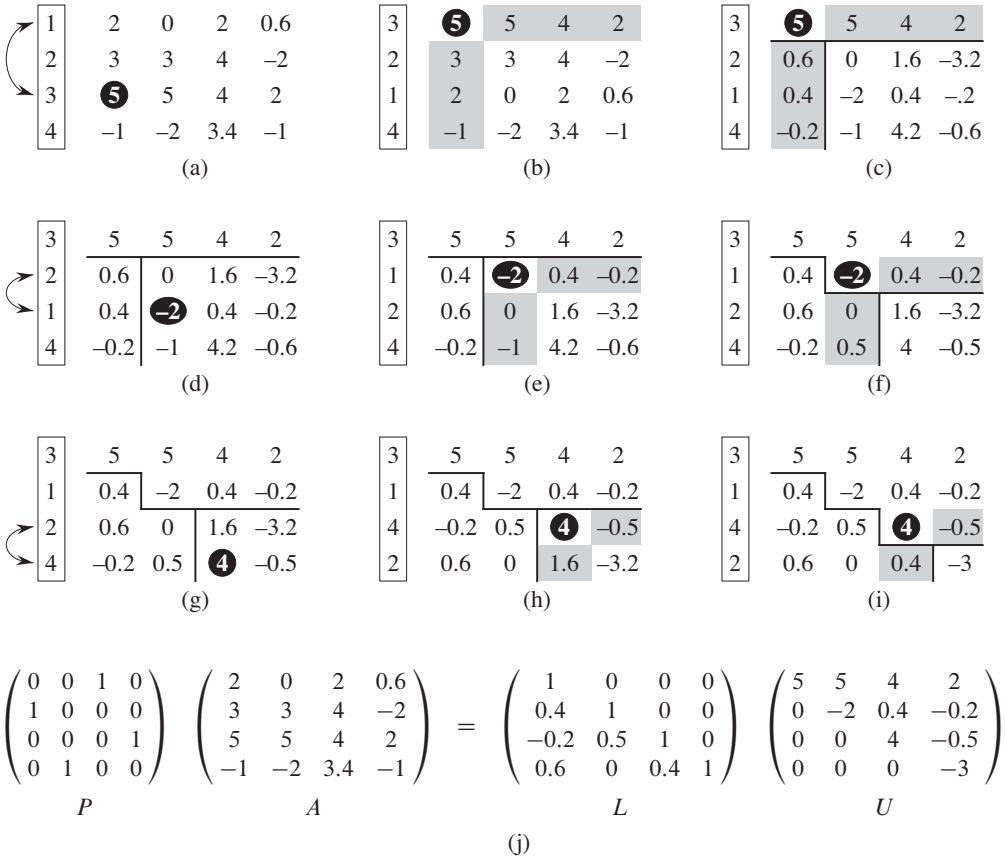


Figure 28.2 The operation of LUP-DECOMPOSITION. **(a)** The input matrix A with the identity permutation of the rows on the left. The first step of the algorithm determines that the element 5 in the black circle in the third row is the pivot for the first column. **(b)** Rows 1 and 3 are swapped and the permutation is updated. The shaded column and row represent v and w^T. **(c)** The vector v is replaced by $v/5$, and the lower right of the matrix is updated with the Schur complement. Lines divide the matrix into three regions: elements of U (above), elements of L (left), and elements of the Schur complement (lower right). **(d)–(f)** The second step. **(g)–(i)** The third step. No further changes occur on the fourth (final) step. **(j)** The LUP decomposition $PA = LU$.

28.1-3
Solve the equation

$$\begin{pmatrix} 1 & 5 & 4 \\ 2 & 0 & 3 \\ 5 & 8 & 2 \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \\ x_3 \end{pmatrix} = \begin{pmatrix} 12 \\ 9 \\ 5 \end{pmatrix}$$

by using an LUP decomposition.

28.1-4
Describe the LUP decomposition of a diagonal matrix.

28.1-5
Describe the LUP decomposition of a permutation matrix A, and prove that it is unique.

28.1-6
Show that for all $n \geq 1$, there exists a singular $n \times n$ matrix that has an LU decomposition.

28.1-7
In LU-DECOMPOSITION, is it necessary to perform the outermost **for** loop iteration when $k = n$? How about in LUP-DECOMPOSITION?

28.2 Inverting matrices

Although in practice we do not generally use matrix inverses to solve systems of linear equations, preferring instead to use more numerically stable techniques such as LUP decomposition, sometimes we need to compute a matrix inverse. In this section, we show how to use LUP decomposition to compute a matrix inverse. We also prove that matrix multiplication and computing the inverse of a matrix are equivalently hard problems, in that (subject to technical conditions) we can use an algorithm for one to solve the other in the same asymptotic running time. Thus, we can use Strassen's algorithm (see Section 4.2) for matrix multiplication to invert a matrix. Indeed, Strassen's original paper was motivated by the problem of showing that a set of a linear equations could be solved more quickly than by the usual method.

Computing a matrix inverse from an LUP decomposition

Suppose that we have an LUP decomposition of a matrix A in the form of three matrices L, U, and P such that $PA = LU$. Using LUP-SOLVE, we can solve an equation of the form $Ax = b$ in time $\Theta(n^2)$. Since the LUP decomposition depends on A but not b, we can run LUP-SOLVE on a second set of equations of the form $Ax = b'$ in additional time $\Theta(n^2)$. In general, once we have the LUP decomposition of A, we can solve, in time $\Theta(kn^2)$, k versions of the equation $Ax = b$ that differ only in b.

We can think of the equation

$$AX = I_n \,, \tag{28.10}$$

which defines the matrix X, the inverse of A, as a set of n distinct equations of the form $Ax = b$. To be precise, let X_i denote the ith column of X, and recall that the unit vector e_i is the ith column of I_n. We can then solve equation (28.10) for X by using the LUP decomposition for A to solve each equation

$$AX_i = e_i$$

separately for X_i. Once we have the LUP decomposition, we can compute each of the n columns X_i in time $\Theta(n^2)$, and so we can compute X from the LUP decomposition of A in time $\Theta(n^3)$. Since we can determine the LUP decomposition of A in time $\Theta(n^3)$, we can compute the inverse A^{-1} of a matrix A in time $\Theta(n^3)$.

Matrix multiplication and matrix inversion

We now show that the theoretical speedups obtained for matrix multiplication translate to speedups for matrix inversion. In fact, we prove something stronger: matrix inversion is equivalent to matrix multiplication, in the following sense. If $M(n)$ denotes the time to multiply two $n \times n$ matrices, then we can invert a nonsingular $n \times n$ matrix in time $O(M(n))$. Moreover, if $I(n)$ denotes the time to invert a nonsingular $n \times n$ matrix, then we can multiply two $n \times n$ matrices in time $O(I(n))$. We prove these results as two separate theorems.

Theorem 28.1 (Multiplication is no harder than inversion)
If we can invert an $n \times n$ matrix in time $I(n)$, where $I(n) = \Omega(n^2)$ and $I(n)$ satisfies the regularity condition $I(3n) = O(I(n))$, then we can multiply two $n \times n$ matrices in time $O(I(n))$.

Proof Let A and B be $n \times n$ matrices whose matrix product C we wish to compute. We define the $3n \times 3n$ matrix D by

$$D = \begin{pmatrix} I_n & A & 0 \\ 0 & I_n & B \\ 0 & 0 & I_n \end{pmatrix}.$$

The inverse of D is

$$D^{-1} = \begin{pmatrix} I_n & -A & AB \\ 0 & I_n & -B \\ 0 & 0 & I_n \end{pmatrix},$$

and thus we can compute the product AB by taking the upper right $n \times n$ submatrix of D^{-1}.

We can construct matrix D in $\Theta(n^2)$ time, which is $O(I(n))$ because we assume that $I(n) = \Omega(n^2)$, and we can invert D in $O(I(3n)) = O(I(n))$ time, by the regularity condition on $I(n)$. We thus have $M(n) = O(I(n))$. ■

Note that $I(n)$ satisfies the regularity condition whenever $I(n) = \Theta(n^c \lg^d n)$ for any constants $c > 0$ and $d \geq 0$.

The proof that matrix inversion is no harder than matrix multiplication relies on some properties of symmetric positive-definite matrices that we will prove in Section 28.3.

Theorem 28.2 (Inversion is no harder than multiplication)
Suppose we can multiply two $n \times n$ real matrices in time $M(n)$, where $M(n) = \Omega(n^2)$ and $M(n)$ satisfies the two regularity conditions $M(n+k) = O(M(n))$ for any k in the range $0 \leq k \leq n$ and $M(n/2) \leq cM(n)$ for some constant $c < 1/2$. Then we can compute the inverse of any real nonsingular $n \times n$ matrix in time $O(M(n))$.

Proof We prove the theorem here for real matrices. Exercise 28.2-6 asks you to generalize the proof for matrices whose entries are complex numbers.

We can assume that n is an exact power of 2, since we have

$$\begin{pmatrix} A & 0 \\ 0 & I_k \end{pmatrix}^{-1} = \begin{pmatrix} A^{-1} & 0 \\ 0 & I_k \end{pmatrix}$$

for any $k > 0$. Thus, by choosing k such that $n + k$ is a power of 2, we enlarge the matrix to a size that is the next power of 2 and obtain the desired answer A^{-1} from the answer to the enlarged problem. The first regularity condition on $M(n)$ ensures that this enlargement does not cause the running time to increase by more than a constant factor.

For the moment, let us assume that the $n \times n$ matrix A is symmetric and positive-definite. We partition each of A and its inverse A^{-1} into four $n/2 \times n/2$ submatrices:

$$A = \begin{pmatrix} B & C^{\mathrm{T}} \\ C & D \end{pmatrix} \quad \text{and} \quad A^{-1} = \begin{pmatrix} R & T \\ U & V \end{pmatrix}. \tag{28.11}$$

Then, if we let

$$S = D - CB^{-1}C^{\mathrm{T}} \tag{28.12}$$

be the Schur complement of A with respect to B (we shall see more about this form of Schur complement in Section 28.3), we have

$$A^{-1} = \begin{pmatrix} R & T \\ U & V \end{pmatrix} = \begin{pmatrix} B^{-1} + B^{-1}C^{\mathrm{T}}S^{-1}CB^{-1} & -B^{-1}C^{\mathrm{T}}S^{-1} \\ -S^{-1}CB^{-1} & S^{-1} \end{pmatrix}, \tag{28.13}$$

since $AA^{-1} = I_n$, as you can verify by performing the matrix multiplication. Because A is symmetric and positive-definite, Lemmas 28.4 and 28.5 in Section 28.3 imply that B and S are both symmetric and positive-definite. By Lemma 28.3 in Section 28.3, therefore, the inverses B^{-1} and S^{-1} exist, and by Exercise D.2-6, B^{-1} and S^{-1} are symmetric, so that $(B^{-1})^{\mathrm{T}} = B^{-1}$ and $(S^{-1})^{\mathrm{T}} = S^{-1}$. Therefore, we can compute the submatrices R, T, U, and V of A^{-1} as follows, where all matrices mentioned are $n/2 \times n/2$:

1. Form the submatrices B, C, C^{T}, and D of A.
2. Recursively compute the inverse B^{-1} of B.
3. Compute the matrix product $W = CB^{-1}$, and then compute its transpose W^{T}, which equals $B^{-1}C^{\mathrm{T}}$ (by Exercise D.1-2 and $(B^{-1})^{\mathrm{T}} = B^{-1}$).
4. Compute the matrix product $X = WC^{\mathrm{T}}$, which equals $CB^{-1}C^{\mathrm{T}}$, and then compute the matrix $S = D - X = D - CB^{-1}C^{\mathrm{T}}$.
5. Recursively compute the inverse S^{-1} of S, and set V to S^{-1}.
6. Compute the matrix product $Y = S^{-1}W$, which equals $S^{-1}CB^{-1}$, and then compute its transpose Y^{T}, which equals $B^{-1}C^{\mathrm{T}}S^{-1}$ (by Exercise D.1-2, $(B^{-1})^{\mathrm{T}} = B^{-1}$, and $(S^{-1})^{\mathrm{T}} = S^{-1}$). Set T to $-Y^{\mathrm{T}}$ and U to $-Y$.
7. Compute the matrix product $Z = W^{\mathrm{T}}Y$, which equals $B^{-1}C^{\mathrm{T}}S^{-1}CB^{-1}$, and set R to $B^{-1} + Z$.

Thus, we can invert an $n \times n$ symmetric positive-definite matrix by inverting two $n/2 \times n/2$ matrices in steps 2 and 5; performing four multiplications of $n/2 \times n/2$ matrices in steps 3, 4, 6, and 7; plus an additional cost of $O(n^2)$ for extracting submatrices from A, inserting submatrices into A^{-1}, and performing a constant number of additions, subtractions, and transposes on $n/2 \times n/2$ matrices. We get the recurrence

$$\begin{aligned} I(n) &\le 2I(n/2) + 4M(n/2) + O(n^2) \\ &= 2I(n/2) + \Theta(M(n)) \\ &= O(M(n)) \,. \end{aligned}$$

The second line holds because the second regularity condition in the statement of the theorem implies that $4M(n/2) < 2M(n)$ and because we assume that $M(n) = \Omega(n^2)$. The third line follows because the second regularity condition allows us to apply case 3 of the master theorem (Theorem 4.1).

It remains to prove that we can obtain the same asymptotic running time for matrix multiplication as for matrix inversion when A is invertible but not symmetric and positive-definite. The basic idea is that for any nonsingular matrix A, the matrix $A^{\mathrm{T}}A$ is symmetric (by Exercise D.1-2) and positive-definite (by Theorem D.6). The trick, then, is to reduce the problem of inverting A to the problem of inverting $A^{\mathrm{T}}A$.

The reduction is based on the observation that when A is an $n \times n$ nonsingular matrix, we have

$$A^{-1} = (A^{\mathrm{T}}A)^{-1}A^{\mathrm{T}} ,$$

since $((A^{\mathrm{T}}A)^{-1}A^{\mathrm{T}})A = (A^{\mathrm{T}}A)^{-1}(A^{\mathrm{T}}A) = I_n$ and a matrix inverse is unique. Therefore, we can compute A^{-1} by first multiplying A^{T} by A to obtain $A^{\mathrm{T}}A$, then inverting the symmetric positive-definite matrix $A^{\mathrm{T}}A$ using the above divide-and-conquer algorithm, and finally multiplying the result by A^{T}. Each of these three steps takes $O(M(n))$ time, and thus we can invert any nonsingular matrix with real entries in $O(M(n))$ time. ■

The proof of Theorem 28.2 suggests a means of solving the equation $Ax = b$ by using LU decomposition without pivoting, so long as A is nonsingular. We multiply both sides of the equation by A^{T}, yielding $(A^{\mathrm{T}}A)x = A^{\mathrm{T}}b$. This transformation doesn't affect the solution x, since A^{T} is invertible, and so we can factor the symmetric positive-definite matrix $A^{\mathrm{T}}A$ by computing an LU decomposition. We then use forward and back substitution to solve for x with the right-hand side $A^{\mathrm{T}}b$. Although this method is theoretically correct, in practice the procedure LUP-DECOMPOSITION works much better. LUP decomposition requires fewer arithmetic operations by a constant factor, and it has somewhat better numerical properties.

Exercises

28.2-1

Let $M(n)$ be the time to multiply two $n \times n$ matrices, and let $S(n)$ denote the time required to square an $n \times n$ matrix. Show that multiplying and squaring matrices have essentially the same difficulty: an $M(n)$-time matrix-multiplication algorithm implies an $O(M(n))$-time squaring algorithm, and an $S(n)$-time squaring algorithm implies an $O(S(n))$-time matrix-multiplication algorithm.

28.2-2
Let $M(n)$ be the time to multiply two $n \times n$ matrices, and let $L(n)$ be the time to compute the LUP decomposition of an $n \times n$ matrix. Show that multiplying matrices and computing LUP decompositions of matrices have essentially the same difficulty: an $M(n)$-time matrix-multiplication algorithm implies an $O(M(n))$-time LUP-decomposition algorithm, and an $L(n)$-time LUP-decomposition algorithm implies an $O(L(n))$-time matrix-multiplication algorithm.

28.2-3
Let $M(n)$ be the time to multiply two $n \times n$ matrices, and let $D(n)$ denote the time required to find the determinant of an $n \times n$ matrix. Show that multiplying matrices and computing the determinant have essentially the same difficulty: an $M(n)$-time matrix-multiplication algorithm implies an $O(M(n))$-time determinant algorithm, and a $D(n)$-time determinant algorithm implies an $O(D(n))$-time matrix-multiplication algorithm.

28.2-4
Let $M(n)$ be the time to multiply two $n \times n$ boolean matrices, and let $T(n)$ be the time to find the transitive closure of an $n \times n$ boolean matrix. (See Section 25.2.) Show that an $M(n)$-time boolean matrix-multiplication algorithm implies an $O(M(n) \lg n)$-time transitive-closure algorithm, and a $T(n)$-time transitive-closure algorithm implies an $O(T(n))$-time boolean matrix-multiplication algorithm.

28.2-5
Does the matrix-inversion algorithm based on Theorem 28.2 work when matrix elements are drawn from the field of integers modulo 2? Explain.

28.2-6 ⋆
Generalize the matrix-inversion algorithm of Theorem 28.2 to handle matrices of complex numbers, and prove that your generalization works correctly. (*Hint:* Instead of the transpose of A, use the ***conjugate transpose*** A^*, which you obtain from the transpose of A by replacing every entry with its complex conjugate. Instead of symmetric matrices, consider ***Hermitian*** matrices, which are matrices A such that $A = A^*$.)

28.3 Symmetric positive-definite matrices and least-squares approximation

Symmetric positive-definite matrices have many interesting and desirable properties. For example, they are nonsingular, and we can perform LU decomposition on them without having to worry about dividing by 0. In this section, we shall

prove several other important properties of symmetric positive-definite matrices and show an interesting application to curve fitting by a least-squares approximation.

The first property we prove is perhaps the most basic.

Lemma 28.3
Any positive-definite matrix is nonsingular.

Proof Suppose that a matrix A is singular. Then by Corollary D.3, there exists a nonzero vector x such that $Ax = 0$. Hence, $x^{\mathrm{T}}Ax = 0$, and A cannot be positive-definite. ■

The proof that we can perform LU decomposition on a symmetric positive-definite matrix A without dividing by 0 is more involved. We begin by proving properties about certain submatrices of A. Define the kth ***leading submatrix*** of A to be the matrix A_k consisting of the intersection of the first k rows and first k columns of A.

Lemma 28.4
If A is a symmetric positive-definite matrix, then every leading submatrix of A is symmetric and positive-definite.

Proof That each leading submatrix A_k is symmetric is obvious. To prove that A_k is positive-definite, we assume that it is not and derive a contradiction. If A_k is not positive-definite, then there exists a k-vector $x_k \neq 0$ such that $x_k^{\mathrm{T}} A_k x_k \leq 0$. Let A be $n \times n$, and

$$A = \begin{pmatrix} A_k & B^{\mathrm{T}} \\ B & C \end{pmatrix} \tag{28.14}$$

for submatrices B (which is $(n-k)\times k$) and C (which is $(n-k)\times(n-k)$). Define the n-vector $x = (\, x_k^{\mathrm{T}} \quad 0\,)^{\mathrm{T}}$, where $n-k$ 0s follow x_k. Then we have

$$\begin{aligned} x^{\mathrm{T}}Ax &= (\, x_k^{\mathrm{T}} \quad 0\,)\begin{pmatrix} A_k & B^{\mathrm{T}} \\ B & C \end{pmatrix}\begin{pmatrix} x_k \\ 0 \end{pmatrix} \\ &= (\, x_k^{\mathrm{T}} \quad 0\,)\begin{pmatrix} A_k x_k \\ B x_k \end{pmatrix} \\ &= x_k^{\mathrm{T}} A_k x_k \\ &\leq 0\,, \end{aligned}$$

which contradicts A being positive-definite. ■

We now turn to some essential properties of the Schur complement. Let A be a symmetric positive-definite matrix, and let A_k be a leading $k \times k$ submatrix of A. Partition A once again according to equation (28.14). We generalize equation (28.9) to define the ***Schur complement*** S of A with respect to A_k as

$$S = C - BA_k^{-1}B^{\mathrm{T}} . \tag{28.15}$$

(By Lemma 28.4, A_k is symmetric and positive-definite; therefore, A_k^{-1} exists by Lemma 28.3, and S is well defined.) Note that our earlier definition (28.9) of the Schur complement is consistent with equation (28.15), by letting $k = 1$.

The next lemma shows that the Schur-complement matrices of symmetric positive-definite matrices are themselves symmetric and positive-definite. We used this result in Theorem 28.2, and we need its corollary to prove the correctness of LU decomposition for symmetric positive-definite matrices.

Lemma 28.5 (Schur complement lemma)
If A is a symmetric positive-definite matrix and A_k is a leading $k \times k$ submatrix of A, then the Schur complement S of A with respect to A_k is symmetric and positive-definite.

Proof Because A is symmetric, so is the submatrix C. By Exercise D.2-6, the product $BA_k^{-1}B^{\mathrm{T}}$ is symmetric, and by Exercise D.1-1, S is symmetric.

It remains to show that S is positive-definite. Consider the partition of A given in equation (28.14). For any nonzero vector x, we have $x^{\mathrm{T}}Ax > 0$ by the assumption that A is positive-definite. Let us break x into two subvectors y and z compatible with A_k and C, respectively. Because A_k^{-1} exists, we have

$$\begin{aligned}
x^{\mathrm{T}}Ax &= \begin{pmatrix} y^{\mathrm{T}} & z^{\mathrm{T}} \end{pmatrix} \begin{pmatrix} A_k & B^{\mathrm{T}} \\ B & C \end{pmatrix} \begin{pmatrix} y \\ z \end{pmatrix} \\
&= \begin{pmatrix} y^{\mathrm{T}} & z^{\mathrm{T}} \end{pmatrix} \begin{pmatrix} A_k y + B^{\mathrm{T}} z \\ By + Cz \end{pmatrix} \\
&= y^{\mathrm{T}} A_k y + y^{\mathrm{T}} B^{\mathrm{T}} z + z^{\mathrm{T}} By + z^{\mathrm{T}} Cz \\
&= (y + A_k^{-1}B^{\mathrm{T}}z)^{\mathrm{T}} A_k (y + A_k^{-1}B^{\mathrm{T}}z) + z^{\mathrm{T}}(C - BA_k^{-1}B^{\mathrm{T}})z , \qquad (28.16)
\end{aligned}$$

by matrix magic. (Verify by multiplying through.) This last equation amounts to "completing the square" of the quadratic form. (See Exercise 28.3-2.)

Since $x^{\mathrm{T}}Ax > 0$ holds for any nonzero x, let us pick any nonzero z and then choose $y = -A_k^{-1}B^{\mathrm{T}}z$, which causes the first term in equation (28.16) to vanish, leaving

$$z^{\mathrm{T}}(C - BA_k^{-1}B^{\mathrm{T}})z = z^{\mathrm{T}}Sz$$

as the value of the expression. For any $z \neq 0$, we therefore have $z^{\mathrm{T}}Sz = x^{\mathrm{T}}Ax > 0$, and thus S is positive-definite. ∎

Corollary 28.6
LU decomposition of a symmetric positive-definite matrix never causes a division by 0.

Proof Let A be a symmetric positive-definite matrix. We shall prove something stronger than the statement of the corollary: every pivot is strictly positive. The first pivot is a_{11}. Let e_1 be the first unit vector, from which we obtain $a_{11} = e_1^{\mathrm{T}} A e_1 > 0$. Since the first step of LU decomposition produces the Schur complement of A with respect to $A_1 = (a_{11})$, Lemma 28.5 implies by induction that all pivots are positive. ■

Least-squares approximation

One important application of symmetric positive-definite matrices arises in fitting curves to given sets of data points. Suppose that we are given a set of m data points

$$(x_1, y_1), (x_2, y_2), \ldots, (x_m, y_m) ,$$

where we know that the y_i are subject to measurement errors. We would like to determine a function $F(x)$ such that the approximation errors

$$\eta_i = F(x_i) - y_i \tag{28.17}$$

are small for $i = 1, 2, \ldots, m$. The form of the function F depends on the problem at hand. Here, we assume that it has the form of a linearly weighted sum,

$$F(x) = \sum_{j=1}^{n} c_j f_j(x) ,$$

where the number of summands n and the specific ***basis functions*** f_j are chosen based on knowledge of the problem at hand. A common choice is $f_j(x) = x^{j-1}$, which means that

$$F(x) = c_1 + c_2 x + c_3 x^2 + \cdots + c_n x^{n-1}$$

is a polynomial of degree $n - 1$ in x. Thus, given m data points $(x_1, y_1), (x_2, y_2), \ldots, (x_m, y_m)$, we wish to calculate n coefficients $c_1, c_2, \ldots, c_n$ that minimize the approximation errors $\eta_1, \eta_2, \ldots, \eta_m$.

By choosing $n = m$, we can calculate each y_i *exactly* in equation (28.17). Such a high-degree F "fits the noise" as well as the data, however, and generally gives poor results when used to predict y for previously unseen values of x. It is usually better to choose n significantly smaller than m and hope that by choosing the coefficients c_j well, we can obtain a function F that finds the significant patterns in the data points without paying undue attention to the noise. Some theoretical

principles exist for choosing n, but they are beyond the scope of this text. In any case, once we choose a value of n that is less than m, we end up with an overdetermined set of equations whose solution we wish to approximate. We now show how to do so.

Let

$$A = \begin{pmatrix} f_1(x_1) & f_2(x_1) & \dots & f_n(x_1) \\ f_1(x_2) & f_2(x_2) & \dots & f_n(x_2) \\ \vdots & \vdots & \ddots & \vdots \\ f_1(x_m) & f_2(x_m) & \dots & f_n(x_m) \end{pmatrix}$$

denote the matrix of values of the basis functions at the given points; that is, $a_{ij} = f_j(x_i)$. Let $c = (c_k)$ denote the desired n-vector of coefficients. Then,

$$\begin{aligned} Ac &= \begin{pmatrix} f_1(x_1) & f_2(x_1) & \dots & f_n(x_1) \\ f_1(x_2) & f_2(x_2) & \dots & f_n(x_2) \\ \vdots & \vdots & \ddots & \vdots \\ f_1(x_m) & f_2(x_m) & \dots & f_n(x_m) \end{pmatrix} \begin{pmatrix} c_1 \\ c_2 \\ \vdots \\ c_n \end{pmatrix} \\ &= \begin{pmatrix} F(x_1) \\ F(x_2) \\ \vdots \\ F(x_m) \end{pmatrix} \end{aligned}$$

is the m-vector of "predicted values" for y. Thus,

$$\eta = Ac - y$$

is the m-vector of ***approximation errors***.

To minimize approximation errors, we choose to minimize the norm of the error vector η, which gives us a ***least-squares solution***, since

$$\|\eta\| = \left(\sum_{i=1}^{m} \eta_i^2 \right)^{1/2} .$$

Because

$$\|\eta\|^2 = \|Ac - y\|^2 = \sum_{i=1}^{m} \left(\sum_{j=1}^{n} a_{ij} c_j - y_i \right)^2 ,$$

we can minimize $\|\eta\|$ by differentiating $\|\eta\|^2$ with respect to each c_k and then setting the result to 0:

$$\frac{d\,\|\eta\|^2}{dc_k} = \sum_{i=1}^{m} 2\left(\sum_{j=1}^{n} a_{ij}c_j - y_i\right) a_{ik} = 0\,. \tag{28.18}$$

The n equations (28.18) for $k = 1, 2, \ldots, n$ are equivalent to the single matrix equation

$$(Ac - y)^{\mathrm{T}} A = 0$$

or, equivalently (using Exercise D.1-2), to

$$A^{\mathrm{T}}(Ac - y) = 0\,,$$

which implies

$$A^{\mathrm{T}}Ac = A^{\mathrm{T}}y\,. \tag{28.19}$$

In statistics, this is called the ***normal equation***. The matrix $A^{\mathrm{T}}A$ is symmetric by Exercise D.1-2, and if A has full column rank, then by Theorem D.6, $A^{\mathrm{T}}A$ is positive-definite as well. Hence, $(A^{\mathrm{T}}A)^{-1}$ exists, and the solution to equation (28.19) is

$$\begin{aligned} c &= \left((A^{\mathrm{T}}A)^{-1}A^{\mathrm{T}}\right) y \\ &= A^{+}y\,, \end{aligned} \tag{28.20}$$

where the matrix $A^{+} = ((A^{\mathrm{T}}A)^{-1}A^{\mathrm{T}})$ is the ***pseudoinverse*** of the matrix A. The pseudoinverse naturally generalizes the notion of a matrix inverse to the case in which A is not square. (Compare equation (28.20) as the approximate solution to $Ac = y$ with the solution $A^{-1}b$ as the exact solution to $Ax = b$.)

As an example of producing a least-squares fit, suppose that we have five data points

$$\begin{aligned} (x_1, y_1) &= (-1, 2)\,, \\ (x_2, y_2) &= (1, 1)\,, \\ (x_3, y_3) &= (2, 1)\,, \\ (x_4, y_4) &= (3, 0)\,, \\ (x_5, y_5) &= (5, 3)\,, \end{aligned}$$

shown as black dots in Figure 28.3. We wish to fit these points with a quadratic polynomial

$$F(x) = c_1 + c_2 x + c_3 x^2\,.$$

We start with the matrix of basis-function values

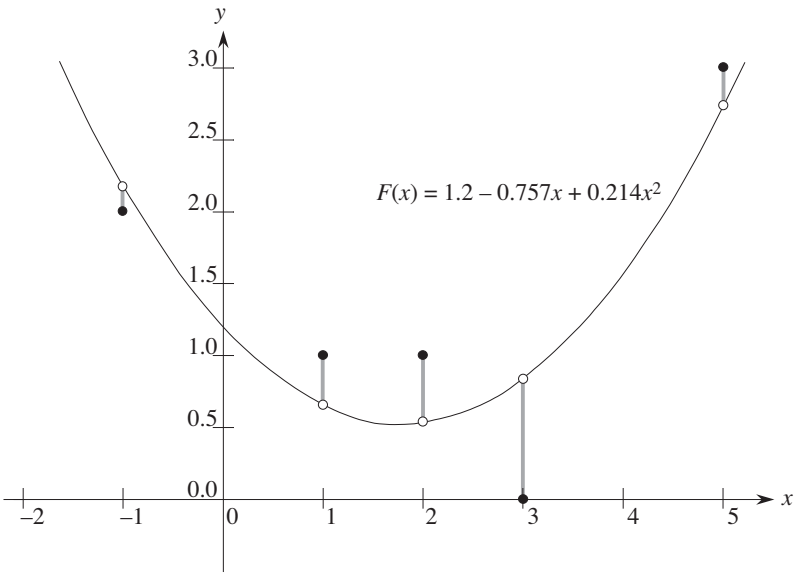


Figure 28.3 The least-squares fit of a quadratic polynomial to the set of five data points $\{(-1, 2), (1, 1), (2, 1), (3, 0), (5, 3)\}$. The black dots are the data points, and the white dots are their estimated values predicted by the polynomial $F(x) = 1.2 - 0.757x + 0.214x^2$, the quadratic polynomial that minimizes the sum of the squared errors. Each shaded line shows the error for one data point.

$$A = \begin{pmatrix} 1 & x_1 & x_1^2 \\ 1 & x_2 & x_2^2 \\ 1 & x_3 & x_3^2 \\ 1 & x_4 & x_4^2 \\ 1 & x_5 & x_5^2 \end{pmatrix} = \begin{pmatrix} 1 & -1 & 1 \\ 1 & 1 & 1 \\ 1 & 2 & 4 \\ 1 & 3 & 9 \\ 1 & 5 & 25 \end{pmatrix},$$

whose pseudoinverse is

$$A^+ = \begin{pmatrix} 0.500 & 0.300 & 0.200 & 0.100 & -0.100 \\ -0.388 & 0.093 & 0.190 & 0.193 & -0.088 \\ 0.060 & -0.036 & -0.048 & -0.036 & 0.060 \end{pmatrix}.$$

Multiplying y by A^+, we obtain the coefficient vector

$$c = \begin{pmatrix} 1.200 \\ -0.757 \\ 0.214 \end{pmatrix},$$

which corresponds to the quadratic polynomial

$$F(x) = 1.200 - 0.757x + 0.214x^2$$

as the closest-fitting quadratic to the given data, in a least-squares sense.

As a practical matter, we solve the normal equation (28.19) by multiplying y by A^{T} and then finding an LU decomposition of $A^{\mathrm{T}}A$. If A has full rank, the matrix $A^{\mathrm{T}}A$ is guaranteed to be nonsingular, because it is symmetric and positive-definite. (See Exercise D.1-2 and Theorem D.6.)

Exercises

28.3-1
Prove that every diagonal element of a symmetric positive-definite matrix is positive.

28.3-2
Let $A = \begin{pmatrix} a & b \\ b & c \end{pmatrix}$ be a 2×2 symmetric positive-definite matrix. Prove that its determinant $ac - b^2$ is positive by "completing the square" in a manner similar to that used in the proof of Lemma 28.5.

28.3-3
Prove that the maximum element in a symmetric positive-definite matrix lies on the diagonal.

28.3-4
Prove that the determinant of each leading submatrix of a symmetric positive-definite matrix is positive.

28.3-5
Let A_k denote the kth leading submatrix of a symmetric positive-definite matrix A. Prove that $\det(A_k)/\det(A_{k-1})$ is the kth pivot during LU decomposition, where, by convention, $\det(A_0) = 1$.

28.3-6
Find the function of the form

$$F(x) = c_1 + c_2 x \lg x + c_3 e^x$$

that is the best least-squares fit to the data points

$$(1, 1), (2, 1), (3, 3), (4, 8) .$$

28.3-7
Show that the pseudoinverse A^+ satisfies the following four equations:

$$\begin{aligned} AA^+A &= A\,, \\ A^+AA^+ &= A^+\,, \\ (AA^+)^{\mathrm{T}} &= AA^+\,, \\ (A^+A)^{\mathrm{T}} &= A^+A\,. \end{aligned}$$

Problems

28-1 Tridiagonal systems of linear equations
Consider the tridiagonal matrix

$$A = \begin{pmatrix} 1 & -1 & 0 & 0 & 0 \\ -1 & 2 & -1 & 0 & 0 \\ 0 & -1 & 2 & -1 & 0 \\ 0 & 0 & -1 & 2 & -1 \\ 0 & 0 & 0 & -1 & 2 \end{pmatrix}.$$

a. Find an LU decomposition of A.

b. Solve the equation $Ax = \begin{pmatrix} 1 & 1 & 1 & 1 & 1 \end{pmatrix}^{\mathrm{T}}$ by using forward and back substitution.

c. Find the inverse of A.

d. Show how, for any $n \times n$ symmetric positive-definite, tridiagonal matrix A and any n-vector b, to solve the equation $Ax = b$ in $O(n)$ time by performing an LU decomposition. Argue that any method based on forming A^{-1} is asymptotically more expensive in the worst case.

e. Show how, for any $n \times n$ nonsingular, tridiagonal matrix A and any n-vector b, to solve the equation $Ax = b$ in $O(n)$ time by performing an LUP decomposition.

28-2 Splines
A practical method for interpolating a set of points with a curve is to use ***cubic splines***. We are given a set $\{(x_i, y_i) : i = 0, 1, \ldots, n\}$ of $n + 1$ point-value pairs, where $x_0 < x_1 < \cdots < x_n$. We wish to fit a piecewise-cubic curve (spline) $f(x)$ to the points. That is, the curve $f(x)$ is made up of n cubic polynomials $f_i(x) = a_i + b_i x + c_i x^2 + d_i x^3$ for $i = 0, 1, \ldots, n - 1$, where if x falls in

the range $x_i \le x \le x_{i+1}$, then the value of the curve is given by $f(x) = f_i(x - x_i)$. The points x_i at which the cubic polynomials are "pasted" together are called ***knots***. For simplicity, we shall assume that $x_i = i$ for $i = 0, 1, \ldots, n$.

To ensure continuity of $f(x)$, we require that

$$\begin{aligned} f(x_i) &= f_i(0) = y_i \,, \\ f(x_{i+1}) &= f_i(1) = y_{i+1} \end{aligned}$$

for $i = 0, 1, \ldots, n-1$. To ensure that $f(x)$ is sufficiently smooth, we also insist that the first derivative be continuous at each knot:

$$f'(x_{i+1}) = f_i'(1) = f_{i+1}'(0)$$

for $i = 0, 1, \ldots, n-2$.

a. Suppose that for $i = 0, 1, \ldots, n$, we are given not only the point-value pairs $\{(x_i, y_i)\}$ but also the first derivatives $D_i = f'(x_i)$ at each knot. Express each coefficient a_i, b_i, c_i, and d_i in terms of the values y_i, y_{i+1}, D_i, and D_{i+1}. (Remember that $x_i = i$.) How quickly can we compute the $4n$ coefficients from the point-value pairs and first derivatives?

The question remains of how to choose the first derivatives of $f(x)$ at the knots. One method is to require the second derivatives to be continuous at the knots:

$$f''(x_{i+1}) = f_i''(1) = f_{i+1}''(0)$$

for $i = 0, 1, \ldots, n-2$. At the first and last knots, we assume that $f''(x_0) = f_0''(0) = 0$ and $f''(x_n) = f_{n-1}''(1) = 0$; these assumptions make $f(x)$ a ***natural*** cubic spline.

b. Use the continuity constraints on the second derivative to show that for $i = 1, 2, \ldots, n-1$,

$$D_{i-1} + 4D_i + D_{i+1} = 3(y_{i+1} - y_{i-1}) \,. \tag{28.21}$$

c. Show that

$$2D_0 + D_1 = 3(y_1 - y_0) \,, \tag{28.22}$$

$$D_{n-1} + 2D_n = 3(y_n - y_{n-1}) \,. \tag{28.23}$$

d. Rewrite equations (28.21)–(28.23) as a matrix equation involving the vector $D = \langle D_0, D_1, \ldots, D_n \rangle$ of unknowns. What attributes does the matrix in your equation have?

e. Argue that a natural cubic spline can interpolate a set of $n + 1$ point-value pairs in $O(n)$ time (see Problem 28-1).

f. Show how to determine a natural cubic spline that interpolates a set of $n + 1$ points (x_i, y_i) satisfying $x_0 < x_1 < \cdots < x_n$, even when x_i is not necessarily equal to i. What matrix equation must your method solve, and how quickly does your algorithm run?

Chapter notes

Many excellent texts describe numerical and scientific computation in much greater detail than we have room for here. The following are especially readable: George and Liu [132], Golub and Van Loan [144], Press, Teukolsky, Vetterling, and Flannery [283, 284], and Strang [323, 324].

Golub and Van Loan [144] discuss numerical stability. They show why $\det(A)$ is not necessarily a good indicator of the stability of a matrix A, proposing instead to use $\|A\|_\infty \|A^{-1}\|_\infty$, where $\|A\|_\infty = \max_{1 \le i \le n} \sum_{j=1}^{n} |a_{ij}|$. They also address the question of how to compute this value without actually computing A^{-1}.

Gaussian elimination, upon which the LU and LUP decompositions are based, was the first systematic method for solving linear systems of equations. It was also one of the earliest numerical algorithms. Although it was known earlier, its discovery is commonly attributed to C. F. Gauss (1777–1855). In his famous paper [325], Strassen showed that an $n \times n$ matrix can be inverted in $O(n^{\lg 7})$ time. Winograd [358] originally proved that matrix multiplication is no harder than matrix inversion, and the converse is due to Aho, Hopcroft, and Ullman [5].

Another important matrix decomposition is the ***singular value decomposition***, or ***SVD***. The SVD factors an $m \times n$ matrix A into $A = Q_1 \Sigma Q_2^{\mathrm{T}}$, where Σ is an $m \times n$ matrix with nonzero values only on the diagonal, Q_1 is $m \times m$ with mutually orthonormal columns, and Q_2 is $n \times n$, also with mutually orthonormal columns. Two vectors are ***orthonormal*** if their inner product is 0 and each vector has a norm of 1. The books by Strang [323, 324] and Golub and Van Loan [144] contain good treatments of the SVD.

Strang [324] has an excellent presentation of symmetric positive-definite matrices and of linear algebra in general.

30 Polynomials and the FFT

The straightforward method of adding two polynomials of degree n takes $\Theta(n)$ time, but the straightforward method of multiplying them takes $\Theta(n^2)$ time. In this chapter, we shall show how the fast Fourier transform, or FFT, can reduce the time to multiply polynomials to $\Theta(n \lg n)$.

The most common use for Fourier transforms, and hence the FFT, is in signal processing. A signal is given in the ***time domain***: as a function mapping time to amplitude. Fourier analysis allows us to express the signal as a weighted sum of phase-shifted sinusoids of varying frequencies. The weights and phases associated with the frequencies characterize the signal in the ***frequency domain***. Among the many everyday applications of FFT's are compression techniques used to encode digital video and audio information, including MP3 files. Several fine books delve into the rich area of signal processing; the chapter notes reference a few of them.

Polynomials

A ***polynomial*** in the variable x over an algebraic field F represents a function $A(x)$ as a formal sum:

$$A(x) = \sum_{j=0}^{n-1} a_j x^j \ .$$

We call the values $a_0, a_1, \ldots, a_{n-1}$ the ***coefficients*** of the polynomial. The coefficients are drawn from a field F, typically the set $\mathbb{C}$ of complex numbers. A polynomial $A(x)$ has ***degree*** k if its highest nonzero coefficient is a_k; we write that degree$(A) = k$. Any integer strictly greater than the degree of a polynomial is a ***degree-bound*** of that polynomial. Therefore, the degree of a polynomial of degree-bound n may be any integer between 0 and $n - 1$, inclusive.

We can define a variety of operations on polynomials. For ***polynomial addition***, if $A(x)$ and $B(x)$ are polynomials of degree-bound n, their ***sum*** is a polyno-

mial $C(x)$, also of degree-bound n, such that $C(x) = A(x) + B(x)$ for all x in the underlying field. That is, if

$$A(x) = \sum_{j=0}^{n-1} a_j x^j$$

and

$$B(x) = \sum_{j=0}^{n-1} b_j x^j ,$$

then

$$C(x) = \sum_{j=0}^{n-1} c_j x^j ,$$

where $c_j = a_j + b_j$ for $j = 0, 1, \ldots, n-1$. For example, if we have the polynomials $A(x) = 6x^3 + 7x^2 - 10x + 9$ and $B(x) = -2x^3 + 4x - 5$, then $C(x) = 4x^3 + 7x^2 - 6x + 4$.

For ***polynomial multiplication***, if $A(x)$ and $B(x)$ are polynomials of degree-bound n, their ***product*** $C(x)$ is a polynomial of degree-bound $2n-1$ such that $C(x) = A(x)B(x)$ for all x in the underlying field. You probably have multiplied polynomials before, by multiplying each term in $A(x)$ by each term in $B(x)$ and then combining terms with equal powers. For example, we can multiply $A(x) = 6x^3 + 7x^2 - 10x + 9$ and $B(x) = -2x^3 + 4x - 5$ as follows:

$$\begin{array}{rrrrrrrrr}
 & & & & 6x^3 & + & 7x^2 & - 10x & + & 9 \\
 & & & - & 2x^3 & & & + 4x & - & 5 \\
\hline
 & & & - & 30x^3 & - & 35x^2 & + 50x & - & 45 \\
 & & 24x^4 & + & 28x^3 & - & 40x^2 & + 36x & & \\
- 12x^6 & - & 14x^5 & + & 20x^4 & - & 18x^3 & & & \\
\hline
- 12x^6 & - & 14x^5 & + & 44x^4 & - & 20x^3 & - 75x^2 & + 86x & - 45
\end{array}$$

Another way to express the product $C(x)$ is

$$C(x) = \sum_{j=0}^{2n-2} c_j x^j , \tag{30.1}$$

where

$$c_j = \sum_{k=0}^{j} a_k b_{j-k} . \tag{30.2}$$

Note that degree(C) = degree(A) + degree(B), implying that if A is a polynomial of degree-bound n_a and B is a polynomial of degree-bound n_b, then C is a polynomial of degree-bound $n_a + n_b - 1$. Since a polynomial of degree-bound k is also a polynomial of degree-bound $k + 1$, we will normally say that the product polynomial C is a polynomial of degree-bound $n_a + n_b$.

Chapter outline

Section 30.1 presents two ways to represent polynomials: the coefficient representation and the point-value representation. The straightforward methods for multiplying polynomials—equations (30.1) and (30.2)—take $\Theta(n^2)$ time when we represent polynomials in coefficient form, but only $\Theta(n)$ time when we represent them in point-value form. We can, however, multiply polynomials using the coefficient representation in only $\Theta(n \lg n)$ time by converting between the two representations. To see why this approach works, we must first study complex roots of unity, which we do in Section 30.2. Then, we use the FFT and its inverse, also described in Section 30.2, to perform the conversions. Section 30.3 shows how to implement the FFT quickly in both serial and parallel models.

This chapter uses complex numbers extensively, and within this chapter we use the symbol i exclusively to denote $\sqrt{-1}$.

30.1 Representing polynomials

The coefficient and point-value representations of polynomials are in a sense equivalent; that is, a polynomial in point-value form has a unique counterpart in coefficient form. In this section, we introduce the two representations and show how to combine them so that we can multiply two degree-bound n polynomials in $\Theta(n \lg n)$ time.

Coefficient representation

A ***coefficient representation*** of a polynomial $A(x) = \sum_{j=0}^{n-1} a_j x^j$ of degree-bound n is a vector of coefficients $a = (a_0, a_1, \ldots, a_{n-1})$. In matrix equations in this chapter, we shall generally treat vectors as column vectors.

The coefficient representation is convenient for certain operations on polynomials. For example, the operation of ***evaluating*** the polynomial $A(x)$ at a given point x_0 consists of computing the value of $A(x_0)$. We can evaluate a polynomial in $\Theta(n)$ time using ***Horner's rule***:

$$A(x_0) = a_0 + x_0(a_1 + x_0(a_2 + \cdots + x_0(a_{n-2} + x_0(a_{n-1}))\cdots)) \, .$$

Similarly, adding two polynomials represented by the coefficient vectors $a = (a_0, a_1, \ldots, a_{n-1})$ and $b = (b_0, b_1, \ldots, b_{n-1})$ takes $\Theta(n)$ time: we just produce the coefficient vector $c = (c_0, c_1, \ldots, c_{n-1})$, where $c_j = a_j + b_j$ for $j = 0, 1, \ldots, n-1$.

Now, consider multiplying two degree-bound n polynomials $A(x)$ and $B(x)$ represented in coefficient form. If we use the method described by equations (30.1) and (30.2), multiplying polynomials takes time $\Theta(n^2)$, since we must multiply each coefficient in the vector a by each coefficient in the vector b. The operation of multiplying polynomials in coefficient form seems to be considerably more difficult than that of evaluating a polynomial or adding two polynomials. The resulting coefficient vector c, given by equation (30.2), is also called the ***convolution*** of the input vectors a and b, denoted $c = a \otimes b$. Since multiplying polynomials and computing convolutions are fundamental computational problems of considerable practical importance, this chapter concentrates on efficient algorithms for them.

Point-value representation

A ***point-value representation*** of a polynomial $A(x)$ of degree-bound n is a set of n ***point-value pairs***

$$\{(x_0, y_0), (x_1, y_1), \ldots, (x_{n-1}, y_{n-1})\}$$

such that all of the x_k are distinct and

$$y_k = A(x_k) \tag{30.3}$$

for $k = 0, 1, \ldots, n-1$. A polynomial has many different point-value representations, since we can use any set of n distinct points $x_0, x_1, \ldots, x_{n-1}$ as a basis for the representation.

Computing a point-value representation for a polynomial given in coefficient form is in principle straightforward, since all we have to do is select n distinct points $x_0, x_1, \ldots, x_{n-1}$ and then evaluate $A(x_k)$ for $k = 0, 1, \ldots, n-1$. With Horner's method, evaluating a polynomial at n points takes time $\Theta(n^2)$. We shall see later that if we choose the points x_k cleverly, we can accelerate this computation to run in time $\Theta(n \lg n)$.

The inverse of evaluation—determining the coefficient form of a polynomial from a point-value representation—is ***interpolation***. The following theorem shows that interpolation is well defined when the desired interpolating polynomial must have a degree-bound equal to the given number of point-value pairs.

Theorem 30.1 (Uniqueness of an interpolating polynomial)
For any set $\{(x_0, y_0), (x_1, y_1), \ldots, (x_{n-1}, y_{n-1})\}$ of n point-value pairs such that all the x_k values are distinct, there is a unique polynomial $A(x)$ of degree-bound n such that $y_k = A(x_k)$ for $k = 0, 1, \ldots, n-1$.

Proof The proof relies on the existence of the inverse of a certain matrix. Equation (30.3) is equivalent to the matrix equation

$$\begin{pmatrix} 1 & x_0 & x_0^2 & \cdots & x_0^{n-1} \\ 1 & x_1 & x_1^2 & \cdots & x_1^{n-1} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_{n-1} & x_{n-1}^2 & \cdots & x_{n-1}^{n-1} \end{pmatrix} \begin{pmatrix} a_0 \\ a_1 \\ \vdots \\ a_{n-1} \end{pmatrix} = \begin{pmatrix} y_0 \\ y_1 \\ \vdots \\ y_{n-1} \end{pmatrix} . \tag{30.4}$$

The matrix on the left is denoted $V(x_0, x_1, \ldots, x_{n-1})$ and is known as a Vandermonde matrix. By Problem D-1, this matrix has determinant

$$\prod_{0 \le j < k \le n-1} (x_k - x_j) ,$$

and therefore, by Theorem D.5, it is invertible (that is, nonsingular) if the x_k are distinct. Thus, we can solve for the coefficients a_j uniquely given the point-value representation:

$$a = V(x_0, x_1, \ldots, x_{n-1})^{-1} y . \qquad \blacksquare$$

The proof of Theorem 30.1 describes an algorithm for interpolation based on solving the set (30.4) of linear equations. Using the LU decomposition algorithms of Chapter 28, we can solve these equations in time $O(n^3)$.

A faster algorithm for n-point interpolation is based on ***Lagrange's formula***:

$$A(x) = \sum_{k=0}^{n-1} y_k \frac{\prod_{j \ne k} (x - x_j)}{\prod_{j \ne k} (x_k - x_j)} . \tag{30.5}$$

You may wish to verify that the right-hand side of equation (30.5) is a polynomial of degree-bound n that satisfies $A(x_k) = y_k$ for all k. Exercise 30.1-5 asks you how to compute the coefficients of A using Lagrange's formula in time $\Theta(n^2)$.

Thus, n-point evaluation and interpolation are well-defined inverse operations that transform between the coefficient representation of a polynomial and a point-value representation.[1] The algorithms described above for these problems take time $\Theta(n^2)$.

The point-value representation is quite convenient for many operations on polynomials. For addition, if $C(x) = A(x) + B(x)$, then $C(x_k) = A(x_k) + B(x_k)$ for any point x_k. More precisely, if we have a point-value representation for A,

[1] Interpolation is a notoriously tricky problem from the point of view of numerical stability. Although the approaches described here are mathematically correct, small differences in the inputs or round-off errors during computation can cause large differences in the result.

$$\{(x_0, y_0), (x_1, y_1), \ldots, (x_{n-1}, y_{n-1})\} ,$$

and for B,

$$\{(x_0, y'_0), (x_1, y'_1), \ldots, (x_{n-1}, y'_{n-1})\}$$

(note that A and B are evaluated at the *same* n points), then a point-value representation for C is

$$\{(x_0, y_0 + y'_0), (x_1, y_1 + y'_1), \ldots, (x_{n-1}, y_{n-1} + y'_{n-1})\} .$$

Thus, the time to add two polynomials of degree-bound n in point-value form is $\Theta(n)$.

Similarly, the point-value representation is convenient for multiplying polynomials. If $C(x) = A(x)B(x)$, then $C(x_k) = A(x_k)B(x_k)$ for any point x_k, and we can pointwise multiply a point-value representation for A by a point-value representation for B to obtain a point-value representation for C. We must face the problem, however, that degree(C) = degree(A) + degree(B); if A and B are of degree-bound n, then C is of degree-bound $2n$. A standard point-value representation for A and B consists of n point-value pairs for each polynomial. When we multiply these together, we get n point-value pairs, but we need $2n$ pairs to interpolate a unique polynomial C of degree-bound $2n$. (See Exercise 30.1-4.) We must therefore begin with "extended" point-value representations for A and for B consisting of $2n$ point-value pairs each. Given an extended point-value representation for A,

$$\{(x_0, y_0), (x_1, y_1), \ldots, (x_{2n-1}, y_{2n-1})\} ,$$

and a corresponding extended point-value representation for B,

$$\{(x_0, y'_0), (x_1, y'_1), \ldots, (x_{2n-1}, y'_{2n-1})\} ,$$

then a point-value representation for C is

$$\{(x_0, y_0 y'_0), (x_1, y_1 y'_1), \ldots, (x_{2n-1}, y_{2n-1} y'_{2n-1})\} .$$

Given two input polynomials in extended point-value form, we see that the time to multiply them to obtain the point-value form of the result is $\Theta(n)$, much less than the time required to multiply polynomials in coefficient form.

Finally, we consider how to evaluate a polynomial given in point-value form at a new point. For this problem, we know of no simpler approach than converting the polynomial to coefficient form first, and then evaluating it at the new point.

Fast multiplication of polynomials in coefficient form

Can we use the linear-time multiplication method for polynomials in point-value form to expedite polynomial multiplication in coefficient form? The answer hinges

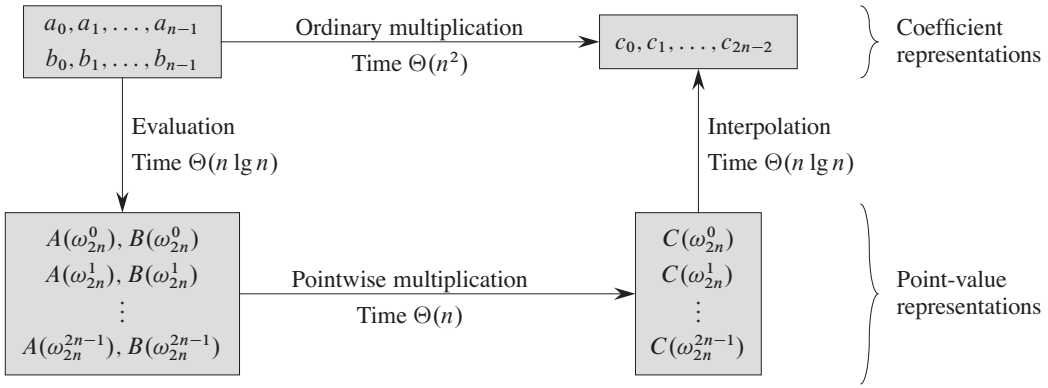


Figure 30.1 A graphical outline of an efficient polynomial-multiplication process. Representations on the top are in coefficient form, while those on the bottom are in point-value form. The arrows from left to right correspond to the multiplication operation. The ω_{2n} terms are complex $(2n)$th roots of unity.

on whether we can convert a polynomial quickly from coefficient form to point-value form (evaluate) and vice versa (interpolate).

We can use any points we want as evaluation points, but by choosing the evaluation points carefully, we can convert between representations in only $\Theta(n \lg n)$ time. As we shall see in Section 30.2, if we choose "complex roots of unity" as the evaluation points, we can produce a point-value representation by taking the discrete Fourier transform (or DFT) of a coefficient vector. We can perform the inverse operation, interpolation, by taking the "inverse DFT" of point-value pairs, yielding a coefficient vector. Section 30.2 will show how the FFT accomplishes the DFT and inverse DFT operations in $\Theta(n \lg n)$ time.

Figure 30.1 shows this strategy graphically. One minor detail concerns degree-bounds. The product of two polynomials of degree-bound n is a polynomial of degree-bound $2n$. Before evaluating the input polynomials A and B, therefore, we first double their degree-bounds to $2n$ by adding n high-order coefficients of 0. Because the vectors have $2n$ elements, we use "complex $(2n)$th roots of unity," which are denoted by the ω_{2n} terms in Figure 30.1.

Given the FFT, we have the following $\Theta(n \lg n)$-time procedure for multiplying two polynomials $A(x)$ and $B(x)$ of degree-bound n, where the input and output representations are in coefficient form. We assume that n is a power of 2; we can always meet this requirement by adding high-order zero coefficients.

1. *Double degree-bound:* Create coefficient representations of $A(x)$ and $B(x)$ as degree-bound $2n$ polynomials by adding n high-order zero coefficients to each.

2. *Evaluate:* Compute point-value representations of $A(x)$ and $B(x)$ of length $2n$ by applying the FFT of order $2n$ on each polynomial. These representations contain the values of the two polynomials at the $(2n)$th roots of unity.
3. *Pointwise multiply:* Compute a point-value representation for the polynomial $C(x) = A(x)B(x)$ by multiplying these values together pointwise. This representation contains the value of $C(x)$ at each $(2n)$th root of unity.
4. *Interpolate:* Create the coefficient representation of the polynomial $C(x)$ by applying the FFT on $2n$ point-value pairs to compute the inverse DFT.

Steps (1) and (3) take time $\Theta(n)$, and steps (2) and (4) take time $\Theta(n \lg n)$. Thus, once we show how to use the FFT, we will have proven the following.

Theorem 30.2
We can multiply two polynomials of degree-bound n in time $\Theta(n \lg n)$, with both the input and output representations in coefficient form. ■

Exercises

30.1-1
Multiply the polynomials $A(x) = 7x^3 - x^2 + x - 10$ and $B(x) = 8x^3 - 6x + 3$ using equations (30.1) and (30.2).

30.1-2
Another way to evaluate a polynomial $A(x)$ of degree-bound n at a given point x_0 is to divide $A(x)$ by the polynomial $(x - x_0)$, obtaining a quotient polynomial $q(x)$ of degree-bound $n - 1$ and a remainder r, such that

$$A(x) = q(x)(x - x_0) + r \ .$$

Clearly, $A(x_0) = r$. Show how to compute the remainder r and the coefficients of $q(x)$ in time $\Theta(n)$ from x_0 and the coefficients of A.

30.1-3
Derive a point-value representation for $A^{\mathrm{rev}}(x) = \sum_{j=0}^{n-1} a_{n-1-j} x^j$ from a point-value representation for $A(x) = \sum_{j=0}^{n-1} a_j x^j$, assuming that none of the points is 0.

30.1-4
Prove that n distinct point-value pairs are necessary to uniquely specify a polynomial of degree-bound n, that is, if fewer than n distinct point-value pairs are given, they fail to specify a unique polynomial of degree-bound n. (*Hint:* Using Theorem 30.1, what can you say about a set of $n - 1$ point-value pairs to which you add one more arbitrarily chosen point-value pair?)

30.1-5
Show how to use equation (30.5) to interpolate in time $\Theta(n^2)$. (*Hint:* First compute the coefficient representation of the polynomial $\prod_j (x - x_j)$ and then divide by $(x - x_k)$ as necessary for the numerator of each term; see Exercise 30.1-2. You can compute each of the n denominators in time $O(n)$.)

30.1-6
Explain what is wrong with the "obvious" approach to polynomial division using a point-value representation, i.e., dividing the corresponding y values. Discuss separately the case in which the division comes out exactly and the case in which it doesn't.

30.1-7
Consider two sets A and B, each having n integers in the range from 0 to $10n$. We wish to compute the ***Cartesian sum*** of A and B, defined by

$$C = \{x + y : x \in A \text{ and } y \in B\} .$$

Note that the integers in C are in the range from 0 to $20n$. We want to find the elements of C and the number of times each element of C is realized as a sum of elements in A and B. Show how to solve the problem in $O(n \lg n)$ time. (*Hint:* Represent A and B as polynomials of degree at most $10n$.)

30.2 The DFT and FFT

In Section 30.1, we claimed that if we use complex roots of unity, we can evaluate and interpolate polynomials in $\Theta(n \lg n)$ time. In this section, we define complex roots of unity and study their properties, define the DFT, and then show how the FFT computes the DFT and its inverse in $\Theta(n \lg n)$ time.

Complex roots of unity

A ***complex nth root of unity*** is a complex number ω such that

$$\omega^n = 1 .$$

There are exactly n complex nth roots of unity: $e^{2\pi i k/n}$ for $k = 0, 1, \ldots, n-1$. To interpret this formula, we use the definition of the exponential of a complex number:

$$e^{iu} = \cos(u) + i \sin(u) .$$

Figure 30.2 shows that the n complex roots of unity are equally spaced around the circle of unit radius centered at the origin of the complex plane. The value

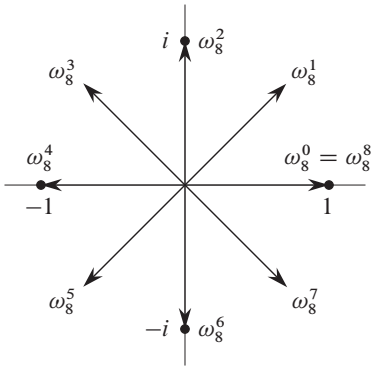


Figure 30.2 The values of $\omega_8^0, \omega_8^1, \ldots, \omega_8^7$ in the complex plane, where $\omega_8 = e^{2\pi i/8}$ is the principal 8th root of unity.

$$\omega_n = e^{2\pi i/n} \tag{30.6}$$

is the ***principal nth root of unity***;[2] all other complex nth roots of unity are powers of ω_n.

The n complex nth roots of unity,

$$\omega_n^0, \omega_n^1, \ldots, \omega_n^{n-1} ,$$

form a group under multiplication (see Section 31.3). This group has the same structure as the additive group $(\mathbb{Z}_n, +)$ modulo n, since $\omega_n^n = \omega_n^0 = 1$ implies that $\omega_n^j \omega_n^k = \omega_n^{j+k} = \omega_n^{(j+k) \bmod n}$. Similarly, $\omega_n^{-1} = \omega_n^{n-1}$. The following lemmas furnish some essential properties of the complex nth roots of unity.

Lemma 30.3 (Cancellation lemma)
For any integers $n \geq 0$, $k \geq 0$, and $d > 0$,

$$\omega_{dn}^{dk} = \omega_n^k . \tag{30.7}$$

Proof The lemma follows directly from equation (30.6), since

$$\begin{aligned} \omega_{dn}^{dk} &= \left(e^{2\pi i/dn}\right)^{dk} \\ &= \left(e^{2\pi i/n}\right)^{k} \\ &= \omega_n^k . \end{aligned}$$

■

[2]Many other authors define ω_n differently: $\omega_n = e^{-2\pi i/n}$. This alternative definition tends to be used for signal-processing applications. The underlying mathematics is substantially the same with either definition of ω_n.

Corollary 30.4
For any even integer $n > 0$,

$$\omega_n^{n/2} = \omega_2 = -1 .$$

Proof The proof is left as Exercise 30.2-1. ■

Lemma 30.5 (Halving lemma)
If $n > 0$ is even, then the squares of the n complex nth roots of unity are the $n/2$ complex $(n/2)$th roots of unity.

Proof By the cancellation lemma, we have $(\omega_n^k)^2 = \omega_{n/2}^k$, for any nonnegative integer k. Note that if we square all of the complex nth roots of unity, then we obtain each $(n/2)$th root of unity exactly twice, since

$$\begin{aligned}(\omega_n^{k+n/2})^2 &= \omega_n^{2k+n} \\ &= \omega_n^{2k}\omega_n^n \\ &= \omega_n^{2k} \\ &= (\omega_n^k)^2 .\end{aligned}$$

Thus, ω_n^k and $\omega_n^{k+n/2}$ have the same square. We could also have used Corollary 30.4 to prove this property, since $\omega_n^{n/2} = -1$ implies $\omega_n^{k+n/2} = -\omega_n^k$, and thus $(\omega_n^{k+n/2})^2 = (\omega_n^k)^2$. ■

As we shall see, the halving lemma is essential to our divide-and-conquer approach for converting between coefficient and point-value representations of polynomials, since it guarantees that the recursive subproblems are only half as large.

Lemma 30.6 (Summation lemma)
For any integer $n \geq 1$ and nonzero integer k not divisible by n,

$$\sum_{j=0}^{n-1} \left(\omega_n^k\right)^j = 0 .$$

Proof Equation (A.5) applies to complex values as well as to reals, and so we have

$$\begin{aligned}\sum_{j=0}^{n-1}\left(\omega_n^k\right)^j &= \frac{(\omega_n^k)^n - 1}{\omega_n^k - 1} \\ &= \frac{(\omega_n^n)^k - 1}{\omega_n^k - 1} \\ &= \frac{(1)^k - 1}{\omega_n^k - 1} \\ &= 0\,.\end{aligned}$$

Because we require that k is not divisible by n, and because $\omega_n^k = 1$ only when k is divisible by n, we ensure that the denominator is not 0. ■

The DFT

Recall that we wish to evaluate a polynomial

$$A(x) = \sum_{j=0}^{n-1} a_j x^j$$

of degree-bound n at $\omega_n^0, \omega_n^1, \omega_n^2, \ldots, \omega_n^{n-1}$ (that is, at the n complex nth roots of unity).[3] We assume that A is given in coefficient form: $a = (a_0, a_1, \ldots, a_{n-1})$. Let us define the results y_k, for $k = 0, 1, \ldots, n-1$, by

$$\begin{aligned}y_k &= A(\omega_n^k) \\ &= \sum_{j=0}^{n-1} a_j \omega_n^{kj}\,. \end{aligned} \tag{30.8}$$

The vector $y = (y_0, y_1, \ldots, y_{n-1})$ is the ***discrete Fourier transform (DFT)*** of the coefficient vector $a = (a_0, a_1, \ldots, a_{n-1})$. We also write $y = \mathrm{DFT}_n(a)$.

The FFT

By using a method known as the ***fast Fourier transform (FFT)***, which takes advantage of the special properties of the complex roots of unity, we can compute $\mathrm{DFT}_n(a)$ in time $\Theta(n \lg n)$, as opposed to the $\Theta(n^2)$ time of the straightforward method. We assume throughout that n is an exact power of 2. Although strategies

[3] The length n is actually what we referred to as $2n$ in Section 30.1, since we double the degree-bound of the given polynomials prior to evaluation. In the context of polynomial multiplication, therefore, we are actually working with complex $(2n)$th roots of unity.

for dealing with non-power-of-2 sizes are known, they are beyond the scope of this book.

The FFT method employs a divide-and-conquer strategy, using the even-indexed and odd-indexed coefficients of $A(x)$ separately to define the two new polynomials $A^{[0]}(x)$ and $A^{[1]}(x)$ of degree-bound $n/2$:

$$\begin{aligned} A^{[0]}(x) &= a_0 + a_2 x + a_4 x^2 + \cdots + a_{n-2} x^{n/2-1} , \\ A^{[1]}(x) &= a_1 + a_3 x + a_5 x^2 + \cdots + a_{n-1} x^{n/2-1} . \end{aligned}$$

Note that $A^{[0]}$ contains all the even-indexed coefficients of A (the binary representation of the index ends in 0) and $A^{[1]}$ contains all the odd-indexed coefficients (the binary representation of the index ends in 1). It follows that

$$A(x) = A^{[0]}(x^2) + x A^{[1]}(x^2) , \tag{30.9}$$

so that the problem of evaluating $A(x)$ at $\omega_n^0, \omega_n^1, \ldots, \omega_n^{n-1}$ reduces to

1. evaluating the degree-bound $n/2$ polynomials $A^{[0]}(x)$ and $A^{[1]}(x)$ at the points

   $$(\omega_n^0)^2, (\omega_n^1)^2, \ldots, (\omega_n^{n-1})^2 , \tag{30.10}$$

   and then
2. combining the results according to equation (30.9).

By the halving lemma, the list of values (30.10) consists not of n distinct values but only of the $n/2$ complex $(n/2)$th roots of unity, with each root occurring exactly twice. Therefore, we recursively evaluate the polynomials $A^{[0]}$ and $A^{[1]}$ of degree-bound $n/2$ at the $n/2$ complex $(n/2)$th roots of unity. These subproblems have exactly the same form as the original problem, but are half the size. We have now successfully divided an n-element DFT_n computation into two $n/2$-element $\mathrm{DFT}_{n/2}$ computations. This decomposition is the basis for the following recursive FFT algorithm, which computes the DFT of an n-element vector $a = (a_0, a_1, \ldots, a_{n-1})$, where n is a power of 2.

```
RECURSIVE-FFT(a)
 1  n = a.length                    // n is a power of 2
 2  if n == 1
 3      return a
 4  ω_n = e^{2πi/n}
 5  ω = 1
 6  a^[0] = (a_0, a_2, ..., a_{n-2})
 7  a^[1] = (a_1, a_3, ..., a_{n-1})
 8  y^[0] = RECURSIVE-FFT(a^[0])
 9  y^[1] = RECURSIVE-FFT(a^[1])
10  for k = 0 to n/2 - 1
11      y_k = y_k^[0] + ω y_k^[1]
12      y_{k+(n/2)} = y_k^[0] - ω y_k^[1]
13      ω = ω ω_n
14  return y                        // y is assumed to be a column vector
```

The RECURSIVE-FFT procedure works as follows. Lines 2–3 represent the basis of the recursion; the DFT of one element is the element itself, since in this case

$$\begin{aligned} y_0 &= a_0 \omega_1^0 \\ &= a_0 \cdot 1 \\ &= a_0 \, . \end{aligned}$$

Lines 6–7 define the coefficient vectors for the polynomials $A^{[0]}$ and $A^{[1]}$. Lines 4, 5, and 13 guarantee that ω is updated properly so that whenever lines 11–12 are executed, we have $\omega = \omega_n^k$. (Keeping a running value of ω from iteration to iteration saves time over computing ω_n^k from scratch each time through the **for** loop.) Lines 8–9 perform the recursive $\mathrm{DFT}_{n/2}$ computations, setting, for $k = 0, 1, \ldots, n/2 - 1$,

$$\begin{aligned} y_k^{[0]} &= A^{[0]}(\omega_{n/2}^k) \, , \\ y_k^{[1]} &= A^{[1]}(\omega_{n/2}^k) \, , \end{aligned}$$

or, since $\omega_{n/2}^k = \omega_n^{2k}$ by the cancellation lemma,

$$\begin{aligned} y_k^{[0]} &= A^{[0]}(\omega_n^{2k}) \, , \\ y_k^{[1]} &= A^{[1]}(\omega_n^{2k}) \, . \end{aligned}$$

Lines 11–12 combine the results of the recursive $\text{DFT}_{n/2}$ calculations. For $y_0, y_1, \ldots, y_{n/2-1}$, line 11 yields

$$\begin{aligned} y_k &= y_k^{[0]} + \omega_n^k y_k^{[1]} \\ &= A^{[0]}(\omega_n^{2k}) + \omega_n^k A^{[1]}(\omega_n^{2k}) \\ &= A(\omega_n^k) \qquad \text{(by equation (30.9))} . \end{aligned}$$

For $y_{n/2}, y_{n/2+1}, \ldots, y_{n-1}$, letting $k = 0, 1, \ldots, n/2 - 1$, line 12 yields

$$\begin{aligned} y_{k+(n/2)} &= y_k^{[0]} - \omega_n^k y_k^{[1]} \\ &= y_k^{[0]} + \omega_n^{k+(n/2)} y_k^{[1]} && \text{(since } \omega_n^{k+(n/2)} = -\omega_n^k\text{)} \\ &= A^{[0]}(\omega_n^{2k}) + \omega_n^{k+(n/2)} A^{[1]}(\omega_n^{2k}) \\ &= A^{[0]}(\omega_n^{2k+n}) + \omega_n^{k+(n/2)} A^{[1]}(\omega_n^{2k+n}) && \text{(since } \omega_n^{2k+n} = \omega_n^{2k}\text{)} \\ &= A(\omega_n^{k+(n/2)}) && \text{(by equation (30.9))} . \end{aligned}$$

Thus, the vector y returned by RECURSIVE-FFT is indeed the DFT of the input vector a.

Lines 11 and 12 multiply each value $y_k^{[1]}$ by ω_n^k, for $k = 0, 1, \ldots, n/2 - 1$. Line 11 adds this product to $y_k^{[0]}$, and line 12 subtracts it. Because we use each factor ω_n^k in both its positive and negative forms, we call the factors ω_n^k ***twiddle factors***.

To determine the running time of procedure RECURSIVE-FFT, we note that exclusive of the recursive calls, each invocation takes time $\Theta(n)$, where n is the length of the input vector. The recurrence for the running time is therefore

$$\begin{aligned} T(n) &= 2T(n/2) + \Theta(n) \\ &= \Theta(n \lg n) . \end{aligned}$$

Thus, we can evaluate a polynomial of degree-bound n at the complex nth roots of unity in time $\Theta(n \lg n)$ using the fast Fourier transform.

Interpolation at the complex roots of unity

We now complete the polynomial multiplication scheme by showing how to interpolate the complex roots of unity by a polynomial, which enables us to convert from point-value form back to coefficient form. We interpolate by writing the DFT as a matrix equation and then looking at the form of the matrix inverse.

From equation (30.4), we can write the DFT as the matrix product $y = V_n a$, where V_n is a Vandermonde matrix containing the appropriate powers of ω_n:

$$\begin{pmatrix} y_0 \\ y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_{n-1} \end{pmatrix} = \begin{pmatrix} 1 & 1 & 1 & 1 & \cdots & 1 \\ 1 & \omega_n & \omega_n^2 & \omega_n^3 & \cdots & \omega_n^{n-1} \\ 1 & \omega_n^2 & \omega_n^4 & \omega_n^6 & \cdots & \omega_n^{2(n-1)} \\ 1 & \omega_n^3 & \omega_n^6 & \omega_n^9 & \cdots & \omega_n^{3(n-1)} \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & \omega_n^{n-1} & \omega_n^{2(n-1)} & \omega_n^{3(n-1)} & \cdots & \omega_n^{(n-1)(n-1)} \end{pmatrix} \begin{pmatrix} a_0 \\ a_1 \\ a_2 \\ a_3 \\ \vdots \\ a_{n-1} \end{pmatrix} .$$

The (k, j) entry of V_n is ω_n^{kj}, for $j, k = 0, 1, \ldots, n-1$. The exponents of the entries of V_n form a multiplication table.

For the inverse operation, which we write as $a = \mathrm{DFT}_n^{-1}(y)$, we proceed by multiplying y by the matrix V_n^{-1}, the inverse of V_n.

Theorem 30.7

For $j, k = 0, 1, \ldots, n-1$, the (j, k) entry of V_n^{-1} is ω_n^{-kj}/n.

Proof We show that $V_n^{-1} V_n = I_n$, the $n \times n$ identity matrix. Consider the (j, j') entry of $V_n^{-1} V_n$:

$$\begin{aligned} [V_n^{-1} V_n]_{jj'} &= \sum_{k=0}^{n-1} (\omega_n^{-kj}/n)(\omega_n^{kj'}) \\ &= \sum_{k=0}^{n-1} \omega_n^{k(j'-j)}/n \ . \end{aligned}$$

This summation equals 1 if $j' = j$, and it is 0 otherwise by the summation lemma (Lemma 30.6). Note that we rely on $-(n-1) \le j' - j \le n-1$, so that $j' - j$ is not divisible by n, in order for the summation lemma to apply. ■

Given the inverse matrix V_n^{-1}, we have that $\mathrm{DFT}_n^{-1}(y)$ is given by

$$a_j = \frac{1}{n} \sum_{k=0}^{n-1} y_k \omega_n^{-kj} \tag{30.11}$$

for $j = 0, 1, \ldots, n-1$. By comparing equations (30.8) and (30.11), we see that by modifying the FFT algorithm to switch the roles of a and y, replace ω_n by ω_n^{-1}, and divide each element of the result by n, we compute the inverse DFT (see Exercise 30.2-4). Thus, we can compute DFT_n^{-1} in $\Theta(n \lg n)$ time as well.

We see that, by using the FFT and the inverse FFT, we can transform a polynomial of degree-bound n back and forth between its coefficient representation and a point-value representation in time $\Theta(n \lg n)$. In the context of polynomial multiplication, we have shown the following.

Theorem 30.8 (Convolution theorem)
For any two vectors a and b of length n, where n is a power of 2,

$$a \otimes b = \mathrm{DFT}_{2n}^{-1}(\mathrm{DFT}_{2n}(a) \cdot \mathrm{DFT}_{2n}(b)) ,$$

where the vectors a and b are padded with 0s to length $2n$ and $\cdot$ denotes the componentwise product of two $2n$-element vectors. ■

Exercises

30.2-1
Prove Corollary 30.4.

30.2-2
Compute the DFT of the vector $(0, 1, 2, 3)$.

30.2-3
Do Exercise 30.1-1 by using the $\Theta(n \lg n)$-time scheme.

30.2-4
Write pseudocode to compute DFT_n^{-1} in $\Theta(n \lg n)$ time.

30.2-5
Describe the generalization of the FFT procedure to the case in which n is a power of 3. Give a recurrence for the running time, and solve the recurrence.

30.2-6 ★
Suppose that instead of performing an n-element FFT over the field of complex numbers (where n is even), we use the ring $\mathbb{Z}_m$ of integers modulo m, where $m = 2^{tn/2} + 1$ and t is an arbitrary positive integer. Use $\omega = 2^t$ instead of ω_n as a principal nth root of unity, modulo m. Prove that the DFT and the inverse DFT are well defined in this system.

30.2-7
Given a list of values $z_0, z_1, \ldots, z_{n-1}$ (possibly with repetitions), show how to find the coefficients of a polynomial $P(x)$ of degree-bound $n + 1$ that has zeros only at $z_0, z_1, \ldots, z_{n-1}$ (possibly with repetitions). Your procedure should run in time $O(n \lg^2 n)$. (*Hint:* The polynomial $P(x)$ has a zero at z_j if and only if $P(x)$ is a multiple of $(x - z_j)$.)

30.2-8 ★
The ***chirp transform*** of a vector $a = (a_0, a_1, \ldots, a_{n-1})$ is the vector $y = (y_0, y_1, \ldots, y_{n-1})$, where $y_k = \sum_{j=0}^{n-1} a_j z^{kj}$ and z is any complex number. The

DFT is therefore a special case of the chirp transform, obtained by taking $z = \omega_n$. Show how to evaluate the chirp transform in time $O(n \lg n)$ for any complex number z. (*Hint:* Use the equation

$$y_k = z^{k^2/2} \sum_{j=0}^{n-1} \left(a_j z^{j^2/2}\right)\left(z^{-(k-j)^2/2}\right)$$

to view the chirp transform as a convolution.)

30.3 Efficient FFT implementations

Since the practical applications of the DFT, such as signal processing, demand the utmost speed, this section examines two efficient FFT implementations. First, we shall examine an iterative version of the FFT algorithm that runs in $\Theta(n \lg n)$ time but can have a lower constant hidden in the Θ-notation than the recursive version in Section 30.2. (Depending on the exact implementation, the recursive version may use the hardware cache more efficiently.) Then, we shall use the insights that led us to the iterative implementation to design an efficient parallel FFT circuit.

An iterative FFT implementation

We first note that the **for** loop of lines 10–13 of RECURSIVE-FFT involves computing the value $\omega_n^k\, y_k^{[1]}$ twice. In compiler terminology, we call such a value a ***common subexpression***. We can change the loop to compute it only once, storing it in a temporary variable t.

```
for k = 0 to n/2 − 1
    t = ω y_k^[1]
    y_k = y_k^[0] + t
    y_{k+(n/2)} = y_k^[0] − t
    ω = ω ω_n
```

The operation in this loop, multiplying the twiddle factor $\omega = \omega_n^k$ by $y_k^{[1]}$, storing the product into t, and adding and subtracting t from $y_k^{[0]}$, is known as a ***butterfly operation*** and is shown schematically in Figure 30.3.

We now show how to make the FFT algorithm iterative rather than recursive in structure. In Figure 30.4, we have arranged the input vectors to the recursive calls in an invocation of RECURSIVE-FFT in a tree structure, where the initial call is for $n = 8$. The tree has one node for each call of the procedure, labeled

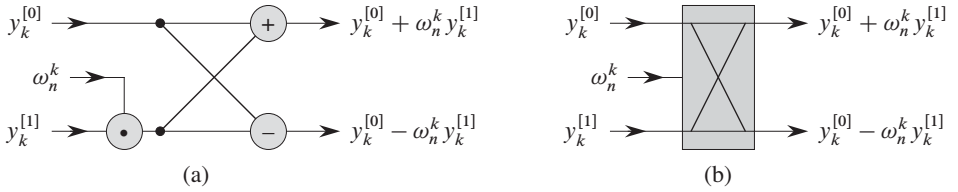


Figure 30.3 A butterfly operation. **(a)** The two input values enter from the left, the twiddle factor ω_n^k is multiplied by $y_k^{[1]}$, and the sum and difference are output on the right. **(b)** A simplified drawing of a butterfly operation. We will use this representation in a parallel FFT circuit.

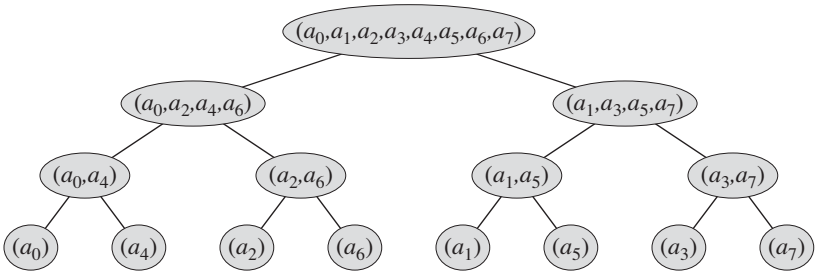


Figure 30.4 The tree of input vectors to the recursive calls of the RECURSIVE-FFT procedure. The initial invocation is for $n = 8$.

by the corresponding input vector. Each RECURSIVE-FFT invocation makes two recursive calls, unless it has received a 1-element vector. The first call appears in the left child, and the second call appears in the right child.

Looking at the tree, we observe that if we could arrange the elements of the initial vector a into the order in which they appear in the leaves, we could trace the execution of the RECURSIVE-FFT procedure, but bottom up instead of top down. First, we take the elements in pairs, compute the DFT of each pair using one butterfly operation, and replace the pair with its DFT. The vector then holds $n/2$ 2-element DFTs. Next, we take these $n/2$ DFTs in pairs and compute the DFT of the four vector elements they come from by executing two butterfly operations, replacing two 2-element DFTs with one 4-element DFT. The vector then holds $n/4$ 4-element DFTs. We continue in this manner until the vector holds two $(n/2)$-element DFTs, which we combine using $n/2$ butterfly operations into the final n-element DFT.

To turn this bottom-up approach into code, we use an array $A[0\,..\,n-1]$ that initially holds the elements of the input vector a in the order in which they appear

in the leaves of the tree of Figure 30.4. (We shall show later how to determine this order, which is known as a bit-reversal permutation.) Because we have to combine DFTs on each level of the tree, we introduce a variable s to count the levels, ranging from 1 (at the bottom, when we are combining pairs to form 2-element DFTs) to $\lg n$ (at the top, when we are combining two $(n/2)$-element DFTs to produce the final result). The algorithm therefore has the following structure:

```
1  for s = 1 to lg n
2      for k = 0 to n − 1 by 2^s
3          combine the two 2^(s−1)-element DFTs in
               A[k . . k + 2^(s−1) − 1] and A[k + 2^(s−1) . . k + 2^s − 1]
               into one 2^s-element DFT in A[k . . k + 2^s − 1]
```

We can express the body of the loop (line 3) as more precise pseudocode. We copy the **for** loop from the RECURSIVE-FFT procedure, identifying $y^{[0]}$ with $A[k \,..\, k + 2^{s-1} - 1]$ and $y^{[1]}$ with $A[k + 2^{s-1} \,..\, k + 2^s - 1]$. The twiddle factor used in each butterfly operation depends on the value of s; it is a power of ω_m, where $m = 2^s$. (We introduce the variable m solely for the sake of readability.) We introduce another temporary variable u that allows us to perform the butterfly operation in place. When we replace line 3 of the overall structure by the loop body, we get the following pseudocode, which forms the basis of the parallel implementation we shall present later. The code first calls the auxiliary procedure BIT-REVERSE-COPY(a, A) to copy vector a into array A in the initial order in which we need the values.

ITERATIVE-FFT(a)

```
 1  BIT-REVERSE-COPY(a, A)
 2  n = a.length                    // n is a power of 2
 3  for s = 1 to lg n
 4      m = 2^s
 5      ω_m = e^(2πi/m)
 6      for k = 0 to n − 1 by m
 7          ω = 1
 8          for j = 0 to m/2 − 1
 9              t = ω A[k + j + m/2]
10              u = A[k + j]
11              A[k + j] = u + t
12              A[k + j + m/2] = u − t
13              ω = ω ω_m
14  return A
```

How does BIT-REVERSE-COPY get the elements of the input vector a into the desired order in the array A? The order in which the leaves appear in Figure 30.4

is a ***bit-reversal permutation***. That is, if we let $\text{rev}(k)$ be the $\lg n$-bit integer formed by reversing the bits of the binary representation of k, then we want to place vector element a_k in array position $A[\text{rev}(k)]$. In Figure 30.4, for example, the leaves appear in the order $0, 4, 2, 6, 1, 5, 3, 7$; this sequence in binary is $000, 100, 010, 110, 001, 101, 011, 111$, and when we reverse the bits of each value we get the sequence $000, 001, 010, 011, 100, 101, 110, 111$. To see that we want a bit-reversal permutation in general, we note that at the top level of the tree, indices whose low-order bit is 0 go into the left subtree and indices whose low-order bit is 1 go into the right subtree. Stripping off the low-order bit at each level, we continue this process down the tree, until we get the order given by the bit-reversal permutation at the leaves.

Since we can easily compute the function $\text{rev}(k)$, the BIT-REVERSE-COPY procedure is simple:

```
BIT-REVERSE-COPY(a, A)
1  n = a.length
2  for k = 0 to n − 1
3      A[rev(k)] = a_k
```

The iterative FFT implementation runs in time $\Theta(n \lg n)$. The call to BIT-REVERSE-COPY(a, A) certainly runs in $O(n \lg n)$ time, since we iterate n times and can reverse an integer between 0 and $n - 1$, with $\lg n$ bits, in $O(\lg n)$ time. (In practice, because we usually know the initial value of n in advance, we would probably code a table mapping k to $\text{rev}(k)$, making BIT-REVERSE-COPY run in $\Theta(n)$ time with a low hidden constant. Alternatively, we could use the clever amortized reverse binary counter scheme described in Problem 17-1.) To complete the proof that ITERATIVE-FFT runs in time $\Theta(n \lg n)$, we show that $L(n)$, the number of times the body of the innermost loop (lines 8–13) executes, is $\Theta(n \lg n)$. The **for** loop of lines 6–13 iterates $n/m = n/2^s$ times for each value of s, and the innermost loop of lines 8–13 iterates $m/2 = 2^{s-1}$ times. Thus,

$$\begin{aligned} L(n) &= \sum_{s=1}^{\lg n} \frac{n}{2^s} \cdot 2^{s-1} \\ &= \sum_{s=1}^{\lg n} \frac{n}{2} \\ &= \Theta(n \lg n) \, . \end{aligned}$$

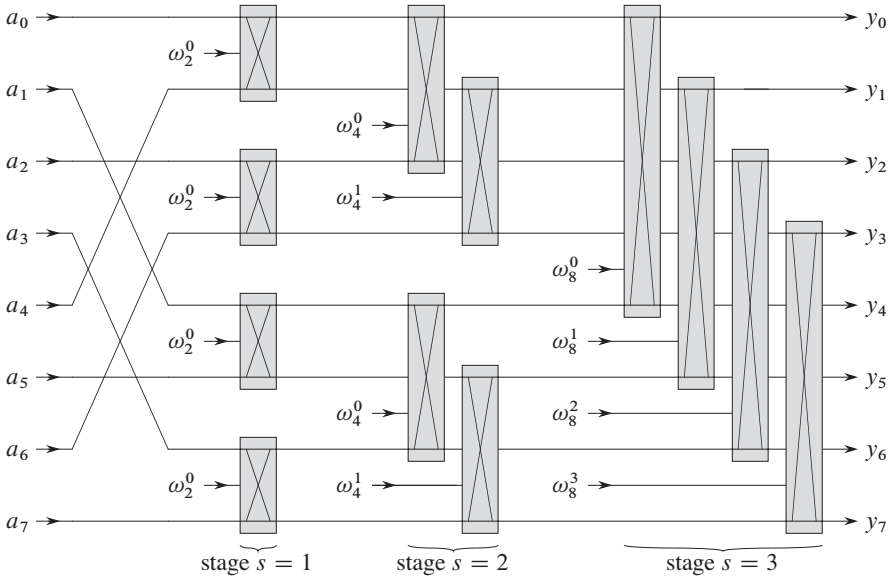


Figure 30.5 A circuit that computes the FFT in parallel, here shown on $n = 8$ inputs. Each butterfly operation takes as input the values on two wires, along with a twiddle factor, and it produces as outputs the values on two wires. The stages of butterflies are labeled to correspond to iterations of the outermost loop of the ITERATIVE-FFT procedure. Only the top and bottom wires passing through a butterfly interact with it; wires that pass through the middle of a butterfly do not affect that butterfly, nor are their values changed by that butterfly. For example, the top butterfly in stage 2 has nothing to do with wire 1 (the wire whose output is labeled y_1); its inputs and outputs are only on wires 0 and 2 (labeled y_0 and y_2, respectively). This circuit has depth $\Theta(\lg n)$ and performs $\Theta(n \lg n)$ butterfly operations altogether.

A parallel FFT circuit

We can exploit many of the properties that allowed us to implement an efficient iterative FFT algorithm to produce an efficient parallel algorithm for the FFT. We will express the parallel FFT algorithm as a circuit. Figure 30.5 shows a parallel FFT circuit, which computes the FFT on n inputs, for $n = 8$. The circuit begins with a bit-reverse permutation of the inputs, followed by $\lg n$ stages, each stage consisting of $n/2$ butterflies executed in parallel. The ***depth*** of the circuit—the maximum number of computational elements between any output and any input that can reach it—is therefore $\Theta(\lg n)$.

The leftmost part of the parallel FFT circuit performs the bit-reverse permutation, and the remainder mimics the iterative ITERATIVE-FFT procedure. Because each iteration of the outermost **for** loop performs $n/2$ independent butterfly operations, the circuit performs them in parallel. The value of s in each iteration within

ITERATIVE-FFT corresponds to a stage of butterflies shown in Figure 30.5. For $s = 1, 2, \ldots, \lg n$, stage s consists of $n/2^s$ groups of butterflies (corresponding to each value of k in ITERATIVE-FFT), with 2^{s-1} butterflies per group (corresponding to each value of j in ITERATIVE-FFT). The butterflies shown in Figure 30.5 correspond to the butterfly operations of the innermost loop (lines 9–12 of ITERATIVE-FFT). Note also that the twiddle factors used in the butterflies correspond to those used in ITERATIVE-FFT: in stage s, we use $\omega_m^0, \omega_m^1, \ldots, \omega_m^{m/2-1}$, where $m = 2^s$.

Exercises

30.3-1
Show how ITERATIVE-FFT computes the DFT of the input vector $(0, 2, 3, -1, 4, 5, 7, 9)$.

30.3-2
Show how to implement an FFT algorithm with the bit-reversal permutation occurring at the end, rather than at the beginning, of the computation. (*Hint:* Consider the inverse DFT.)

30.3-3
How many times does ITERATIVE-FFT compute twiddle factors in each stage? Rewrite ITERATIVE-FFT to compute twiddle factors only 2^{s-1} times in stage s.

30.3-4 ⋆
Suppose that the adders within the butterfly operations of the FFT circuit sometimes fail in such a manner that they always produce a zero output, independent of their inputs. Suppose that exactly one adder has failed, but that you don't know which one. Describe how you can identify the failed adder by supplying inputs to the overall FFT circuit and observing the outputs. How efficient is your method?

Problems

30-1 Divide-and-conquer multiplication

a. Show how to multiply two linear polynomials $ax + b$ and $cx + d$ using only three multiplications. (*Hint:* One of the multiplications is $(a + b) \cdot (c + d)$.)

b. Give two divide-and-conquer algorithms for multiplying two polynomials of degree-bound n in $\Theta(n^{\lg 3})$ time. The first algorithm should divide the input polynomial coefficients into a high half and a low half, and the second algorithm should divide them according to whether their index is odd or even.

c. Show how to multiply two n-bit integers in $O(n^{\lg 3})$ steps, where each step operates on at most a constant number of 1-bit values.

30-2 Toeplitz matrices

A ***Toeplitz matrix*** is an $n \times n$ matrix $A = (a_{ij})$ such that $a_{ij} = a_{i-1,j-1}$ for $i = 2, 3, \ldots, n$ and $j = 2, 3, \ldots, n$.

a. Is the sum of two Toeplitz matrices necessarily Toeplitz? What about the product?

b. Describe how to represent a Toeplitz matrix so that you can add two $n \times n$ Toeplitz matrices in $O(n)$ time.

c. Give an $O(n \lg n)$-time algorithm for multiplying an $n \times n$ Toeplitz matrix by a vector of length n. Use your representation from part (b).

d. Give an efficient algorithm for multiplying two $n \times n$ Toeplitz matrices. Analyze its running time.

30-3 Multidimensional fast Fourier transform

We can generalize the 1-dimensional discrete Fourier transform defined by equation (30.8) to d dimensions. The input is a d-dimensional array $A = (a_{j_1, j_2, \ldots, j_d})$ whose dimensions are $n_1, n_2, \ldots, n_d$, where $n_1 n_2 \cdots n_d = n$. We define the d-dimensional discrete Fourier transform by the equation

$$y_{k_1,k_2,\ldots,k_d} = \sum_{j_1=0}^{n_1-1} \sum_{j_2=0}^{n_2-1} \cdots \sum_{j_d=0}^{n_d-1} a_{j_1,j_2,\ldots,j_d} \omega_{n_1}^{j_1 k_1} \omega_{n_2}^{j_2 k_2} \cdots \omega_{n_d}^{j_d k_d}$$

for $0 \le k_1 < n_1, 0 \le k_2 < n_2, \ldots, 0 \le k_d < n_d$.

a. Show that we can compute a d-dimensional DFT by computing 1-dimensional DFTs on each dimension in turn. That is, we first compute n/n_1 separate 1-dimensional DFTs along dimension 1. Then, using the result of the DFTs along dimension 1 as the input, we compute n/n_2 separate 1-dimensional DFTs along dimension 2. Using this result as the input, we compute n/n_3 separate 1-dimensional DFTs along dimension 3, and so on, through dimension d.

b. Show that the ordering of dimensions does not matter, so that we can compute a d-dimensional DFT by computing the 1-dimensional DFTs in any order of the d dimensions.

c. Show that if we compute each 1-dimensional DFT by computing the fast Fourier transform, the total time to compute a d-dimensional DFT is $O(n \lg n)$, independent of d.

30-4 Evaluating all derivatives of a polynomial at a point

Given a polynomial $A(x)$ of degree-bound n, we define its tth derivative by

$$A^{(t)}(x) = \begin{cases} A(x) & \text{if } t = 0 , \\ \frac{d}{dx} A^{(t-1)}(x) & \text{if } 1 \le t \le n-1 , \\ 0 & \text{if } t \ge n . \end{cases}$$

From the coefficient representation $(a_0, a_1, \ldots, a_{n-1})$ of $A(x)$ and a given point x_0, we wish to determine $A^{(t)}(x_0)$ for $t = 0, 1, \ldots, n-1$.

a. Given coefficients $b_0, b_1, \ldots, b_{n-1}$ such that

$$A(x) = \sum_{j=0}^{n-1} b_j (x - x_0)^j ,$$

show how to compute $A^{(t)}(x_0)$, for $t = 0, 1, \ldots, n-1$, in $O(n)$ time.

b. Explain how to find $b_0, b_1, \ldots, b_{n-1}$ in $O(n \lg n)$ time, given $A(x_0 + \omega_n^k)$ for $k = 0, 1, \ldots, n-1$.

c. Prove that

$$A(x_0 + \omega_n^k) = \sum_{r=0}^{n-1} \left(\frac{\omega_n^{kr}}{r!} \sum_{j=0}^{n-1} f(j) g(r-j) \right) ,$$

where $f(j) = a_j \cdot j!$ and

$$g(l) = \begin{cases} x_0^{-l}/(-l)! & \text{if } -(n-1) \le l \le 0 , \\ 0 & \text{if } 1 \le l \le n-1 . \end{cases}$$

d. Explain how to evaluate $A(x_0 + \omega_n^k)$ for $k = 0, 1, \ldots, n-1$ in $O(n \lg n)$ time. Conclude that we can evaluate all nontrivial derivatives of $A(x)$ at x_0 in $O(n \lg n)$ time.

30-5 Polynomial evaluation at multiple points

We have seen how to evaluate a polynomial of degree-bound n at a single point in $O(n)$ time using Horner's rule. We have also discovered how to evaluate such a polynomial at all n complex roots of unity in $O(n \lg n)$ time using the FFT. We shall now show how to evaluate a polynomial of degree-bound n at n arbitrary points in $O(n \lg^2 n)$ time.

To do so, we shall assume that we can compute the polynomial remainder when one such polynomial is divided by another in $O(n \lg n)$ time, a result that we state without proof. For example, the remainder of $3x^3 + x^2 - 3x + 1$ when divided by $x^2 + x + 2$ is

$$(3x^3 + x^2 - 3x + 1) \bmod (x^2 + x + 2) = -7x + 5 .$$

Given the coefficient representation of a polynomial $A(x) = \sum_{k=0}^{n-1} a_k x^k$ and n points $x_0, x_1, \ldots, x_{n-1}$, we wish to compute the n values $A(x_0), A(x_1), \ldots, A(x_{n-1})$. For $0 \le i \le j \le n-1$, define the polynomials $P_{ij}(x) = \prod_{k=i}^{j} (x - x_k)$ and $Q_{ij}(x) = A(x) \bmod P_{ij}(x)$. Note that $Q_{ij}(x)$ has degree at most $j - i$.

a. Prove that $A(x) \bmod (x - z) = A(z)$ for any point z.

b. Prove that $Q_{kk}(x) = A(x_k)$ and that $Q_{0,n-1}(x) = A(x)$.

c. Prove that for $i \le k \le j$, we have $Q_{ik}(x) = Q_{ij}(x) \bmod P_{ik}(x)$ and $Q_{kj}(x) = Q_{ij}(x) \bmod P_{kj}(x)$.

d. Give an $O(n \lg^2 n)$-time algorithm to evaluate $A(x_0), A(x_1), \ldots, A(x_{n-1})$.

30-6 FFT using modular arithmetic

As defined, the discrete Fourier transform requires us to compute with complex numbers, which can result in a loss of precision due to round-off errors. For some problems, the answer is known to contain only integers, and by using a variant of the FFT based on modular arithmetic, we can guarantee that the answer is calculated exactly. An example of such a problem is that of multiplying two polynomials with integer coefficients. Exercise 30.2-6 gives one approach, using a modulus of length $\Omega(n)$ bits to handle a DFT on n points. This problem gives another approach, which uses a modulus of the more reasonable length $O(\lg n)$; it requires that you understand the material of Chapter 31. Let n be a power of 2.

a. Suppose that we search for the smallest k such that $p = kn + 1$ is prime. Give a simple heuristic argument why we might expect k to be approximately $\ln n$. (The value of k might be much larger or smaller, but we can reasonably expect to examine $O(\lg n)$ candidate values of k on average.) How does the expected length of p compare to the length of n?

Let g be a generator of $\mathbb{Z}_p^*$, and let $w = g^k \bmod p$.

b. Argue that the DFT and the inverse DFT are well-defined inverse operations modulo p, where w is used as a principal nth root of unity.

c. Show how to make the FFT and its inverse work modulo p in time $O(n \lg n)$, where operations on words of $O(\lg n)$ bits take unit time. Assume that the algorithm is given p and w.

d. Compute the DFT modulo $p = 17$ of the vector $(0, 5, 3, 7, 7, 2, 1, 6)$. Note that $g = 3$ is a generator of $\mathbb{Z}_{17}^*$.

Chapter notes

Van Loan's book [343] provides an outstanding treatment of the fast Fourier transform. Press, Teukolsky, Vetterling, and Flannery [283, 284] have a good description of the fast Fourier transform and its applications. For an excellent introduction to signal processing, a popular FFT application area, see the texts by Oppenheim and Schafer [266] and Oppenheim and Willsky [267]. The Oppenheim and Schafer book also shows how to handle cases in which n is not an integer power of 2.

Fourier analysis is not limited to 1-dimensional data. It is widely used in image processing to analyze data in 2 or more dimensions. The books by Gonzalez and Woods [146] and Pratt [281] discuss multidimensional Fourier transforms and their use in image processing, and books by Tolimieri, An, and Lu [338] and Van Loan [343] discuss the mathematics of multidimensional fast Fourier transforms.

Cooley and Tukey [76] are widely credited with devising the FFT in the 1960s. The FFT had in fact been discovered many times previously, but its importance was not fully realized before the advent of modern digital computers. Although Press, Teukolsky, Vetterling, and Flannery attribute the origins of the method to Runge and König in 1924, an article by Heideman, Johnson, and Burrus [163] traces the history of the FFT as far back as C. F. Gauss in 1805.

Frigo and Johnson [117] developed a fast and flexible implementation of the FFT, called FFTW ("fastest Fourier transform in the West"). FFTW is designed for situations requiring multiple DFT computations on the same problem size. Before actually computing the DFTs, FFTW executes a "planner," which, by a series of trial runs, determines how best to decompose the FFT computation for the given problem size on the host machine. FFTW adapts to use the hardware cache efficiently, and once subproblems are small enough, FFTW solves them with optimized, straight-line code. Furthermore, FFTW has the unusual advantage of taking $\Theta(n \lg n)$ time for any problem size n, even when n is a large prime.

Although the standard Fourier transform assumes that the input represents points that are uniformly spaced in the time domain, other techniques can approximate the FFT on "nonequispaced" data. The article by Ware [348] provides an overview.