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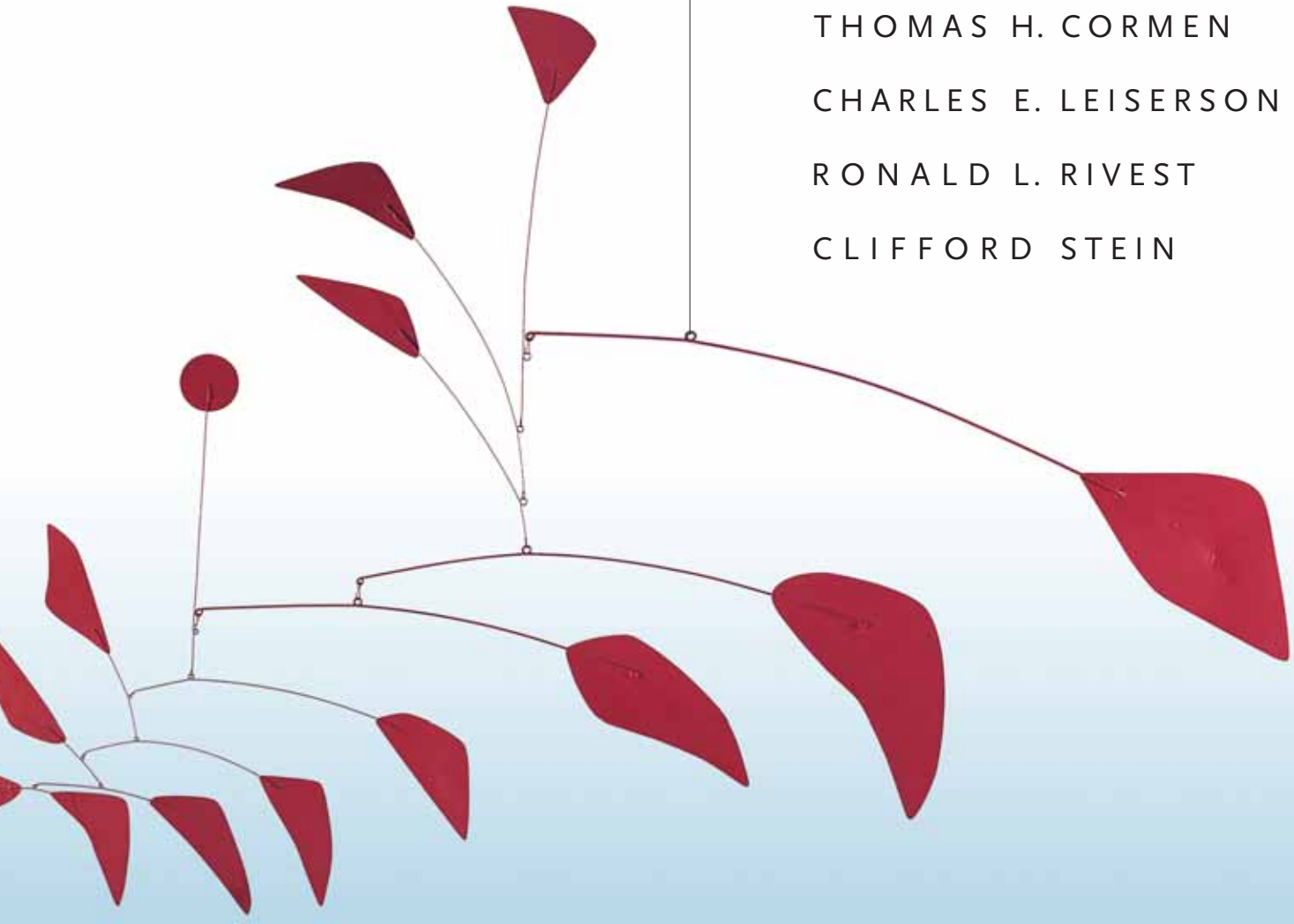

INTRODUCTION TO ALGORITHMS

THIRD EDITION

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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

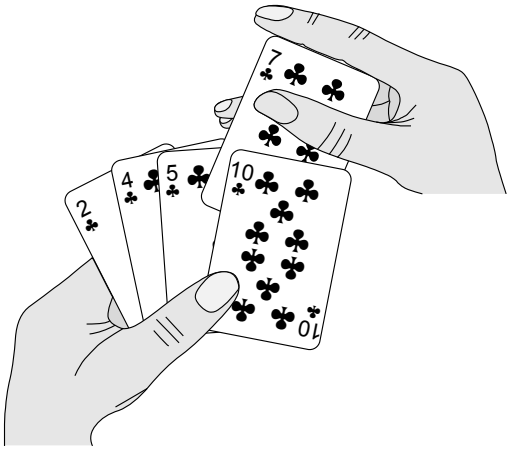

Figure 2.1 Sorting a hand of cards using insertion sort.

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.

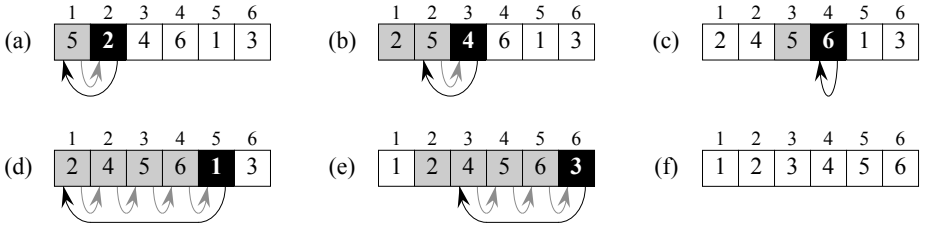

Figure 2.2 The operation of INSERTION-SORT on the array $A = \langle 5, 2, 4, 6, 1, 3 \rangle$. Array indices appear above the rectangles, and values stored in the array positions appear within the rectangles. **(a)–(e)** The iterations of the **for** loop of lines 1–8. In each iteration, the black rectangle 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

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[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 $A[1 \ldots j-1]$ to insert element $A[j]$? On average, half the elements in $A[1 \ldots j-1]$ are less than $A[j]$, and half the elements are greater. On average, therefore, we check half of the subarray $A[1 \ldots j-1]$, 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-

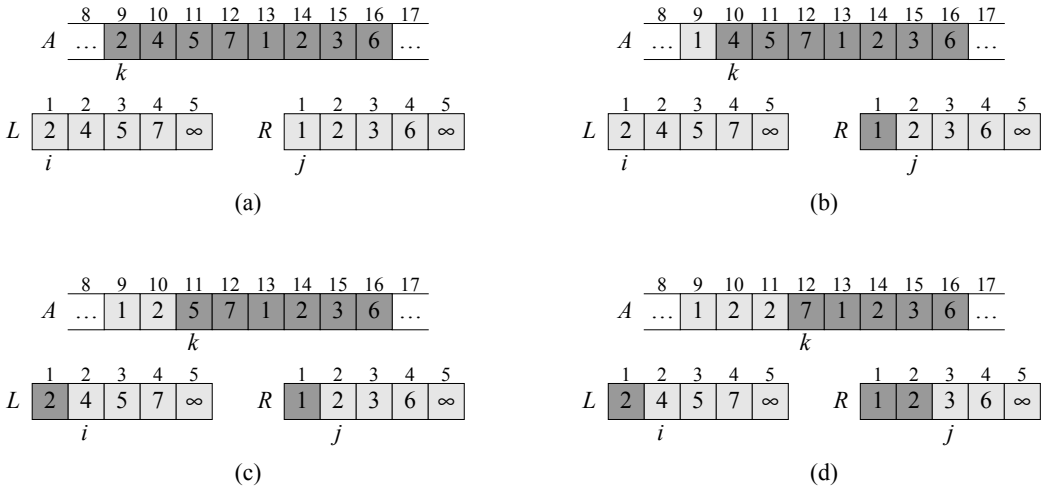

Figure 2.3 The operation of lines 10–17 in the call MERGE$(A, 9, 12, 16)$, when the subarray $A[9..16]$ contains the sequence $\langle 2, 4, 5, 7, 1, 2, 3, 6\rangle$. After copying and inserting sentinels, the array L contains $\langle 2, 4, 5, 7, \infty\rangle$, and the array R contains $\langle 1, 2, 3, 6, \infty\rangle$. 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.

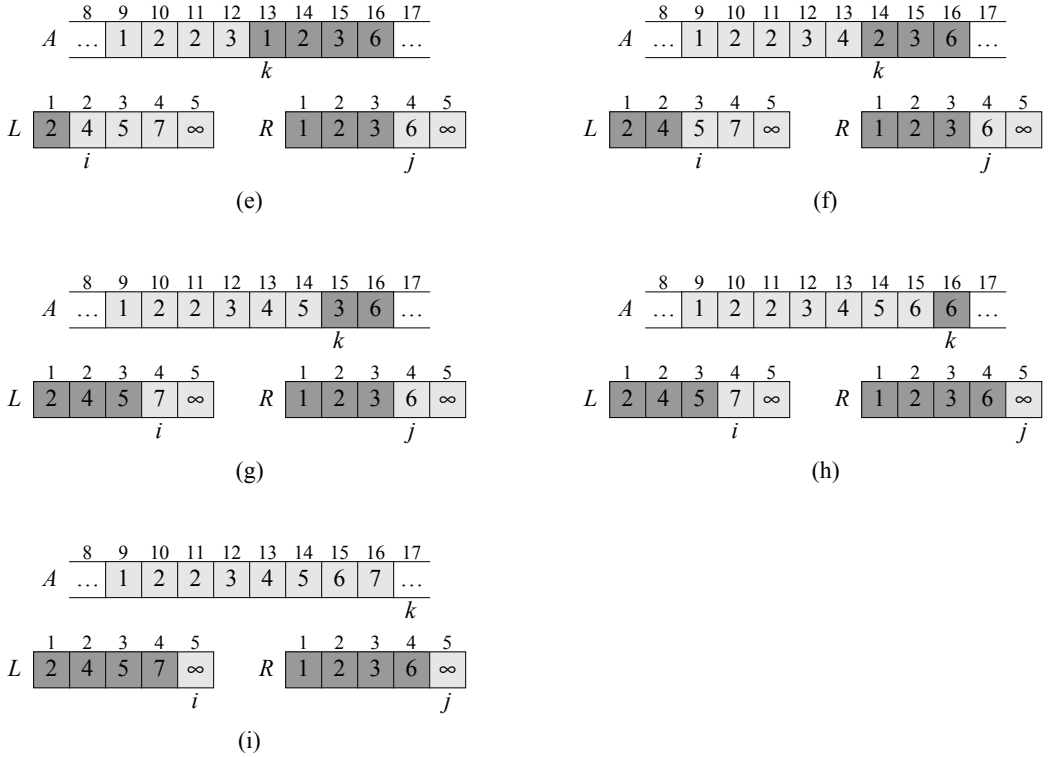

Figure 2.3, continued **(i)** The arrays and indices at termination. At this point, the subarray in $A[9\,..\,16]$ is sorted, and the two sentinels in L and R are the only two elements in these arrays that have not been copied into A.

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.

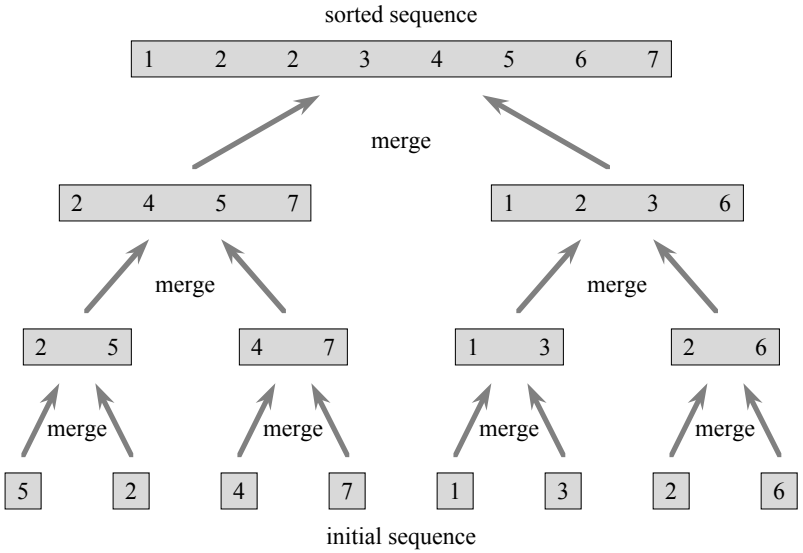

Figure 2.4 The operation of merge sort on the array $A = \langle 5, 2, 4, 7, 1, 3, 2, 6 \rangle$. The lengths of the sorted sequences being merged increase as the algorithm progresses from bottom to top.

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.

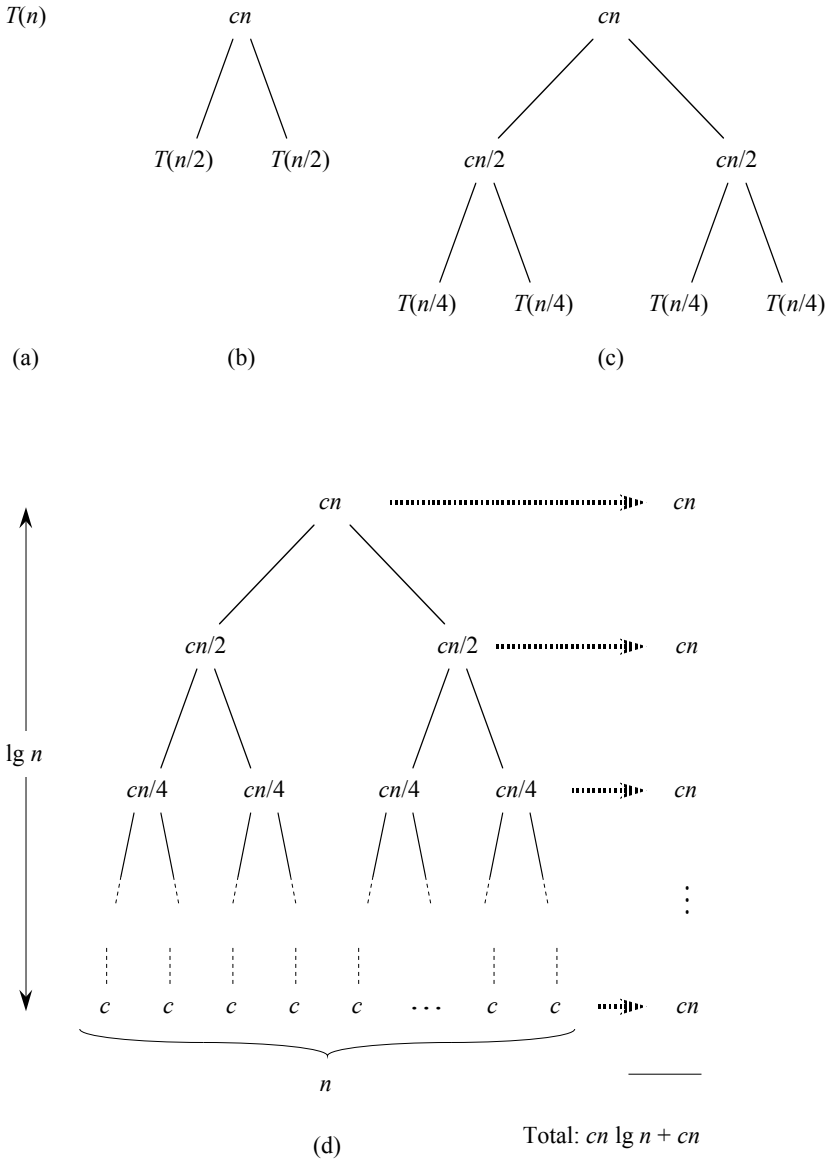

Figure 2.5 How to construct a recursion tree for the recurrence $T(n) = 2T(n/2) + cn$. Part **(a)** shows $T(n)$, which progressively expands in **(b)–(d)** to form the recursion tree. The fully expanded tree in part (d) has $\lg n + 1$ levels (i.e., it has height $\lg n$, as indicated), and each level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

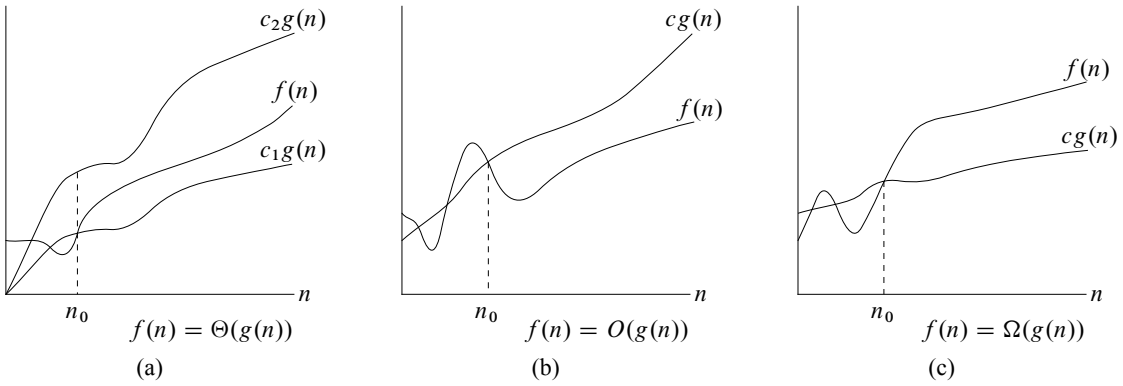

Figure 3.1 Graphic examples of the Θ, O, and Ω notations. In each part, the value of n_0 shown is the minimum possible value; any greater value would also work. **(a)** Θ-notation bounds a function to within constant factors. We write $f(n) = \Theta(g(n))$ if there exist positive constants n_0, c_1, 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

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[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 $\hat{\phi}$, 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):

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

Specifically, we have

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

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

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

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

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

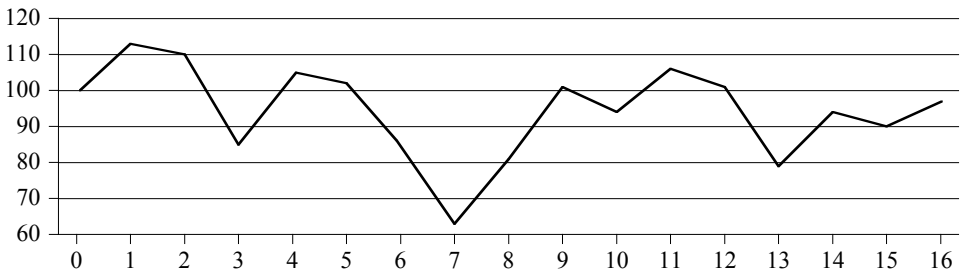
without explicitly giving values for small n. The reason is that although changing the value of $T(1)$ changes the exact solution to the recurrence, the solution typically doesn't change by more than a constant factor, and so the order of growth is unchanged.

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

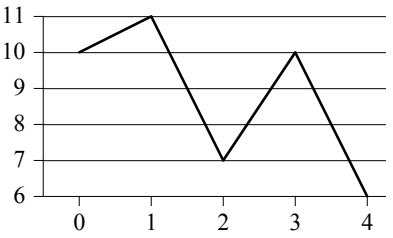
Suppose that you have been offered the opportunity to invest in the Volatile Chemical Corporation. Like the chemicals the company produces, the stock price of the Volatile Chemical Corporation is rather volatile. You are allowed to buy one unit of stock only one time and then sell it at a later date, 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

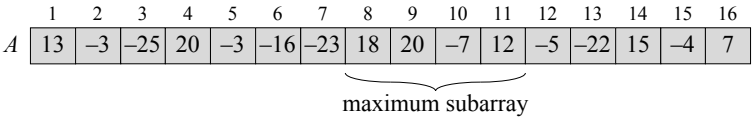


Figure 4.3 The change in stock prices as a maximum-subarray problem. Here, the subarray $A[8\,..\,11]$, with sum 43, has the greatest sum of any contiguous subarray of array A.

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

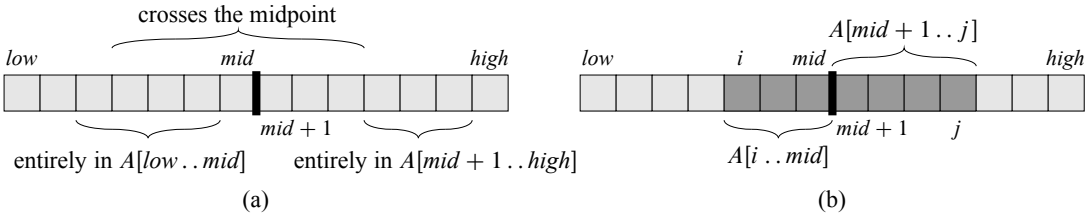


Figure 4.4 **(a)** Possible locations of subarrays of $A[low\,..\,high]$: entirely in $A[low\,..\,mid]$, entirely in $A[mid+1\,..\,high]$, or crossing the midpoint mid. **(b)** Any subarray of $A[low\,..\,high]$ crossing the midpoint comprises two subarrays $A[i\,..\,mid]$ and $A[mid+1\,..\,j]$, where $low \le i \le mid$ 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 $n/2 \times n/2$ 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

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

corresponding to equation (4.12).

Setting

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

makes C_{21} equal

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

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 $T(n) \le cn \lg n$ 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 $T(\lfloor n/2 \rfloor) \le c \lfloor n/2 \rfloor \lg(\lfloor n/2 \rfloor)$. Substituting into the recurrence yields

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

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

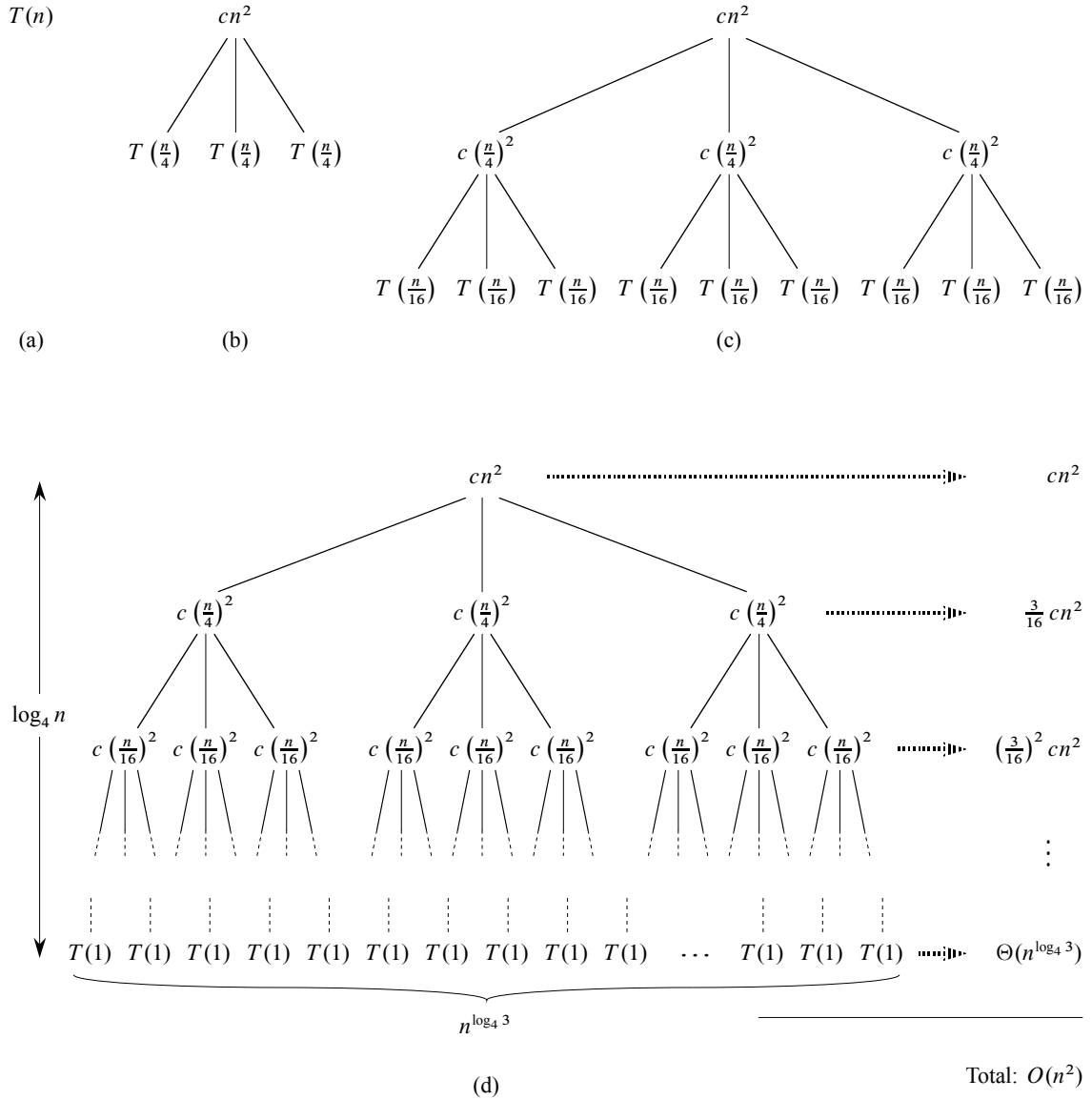


Figure 4.5 Constructing a recursion tree for the recurrence $T(n) = 3T(n/4) + cn^2$. Part **(a)** shows $T(n)$, which progressively expands in **(b)–(d)** to form the recursion tree. The fully expanded tree in part (d) has height $\log_4 n$ (it has $\log_4 n + 1$ levels).

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

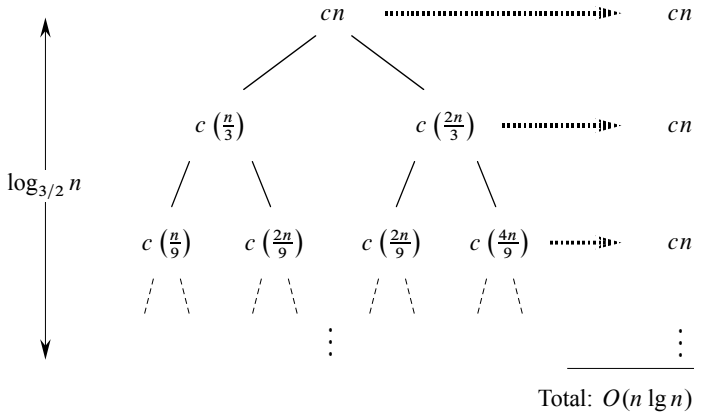


Figure 4.6 A recursion tree for the recurrence $T(n) = T(n/3) + T(2n/3) + cn$.

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

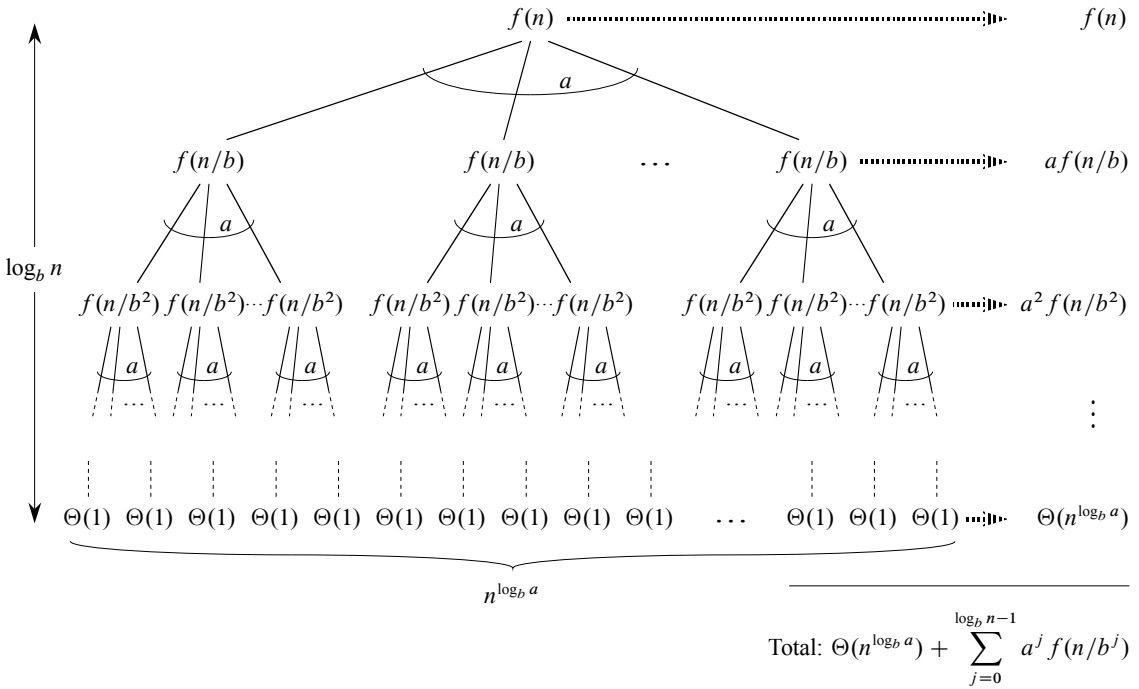


Figure 4.7 The recursion tree generated by $T(n) = aT(n/b) + f(n)$. The tree is a complete a-ary tree with $n^{\log_b a}$ leaves and height $\log_b n$. The cost of the nodes at each depth is shown at the right, and their sum is given in equation (4.21).

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:

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

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

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. This inequality holds for all but at most a constant number of terms with the smallest such values n/b^j, for which $a^j f(n/b^j) = O(1)$.

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

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

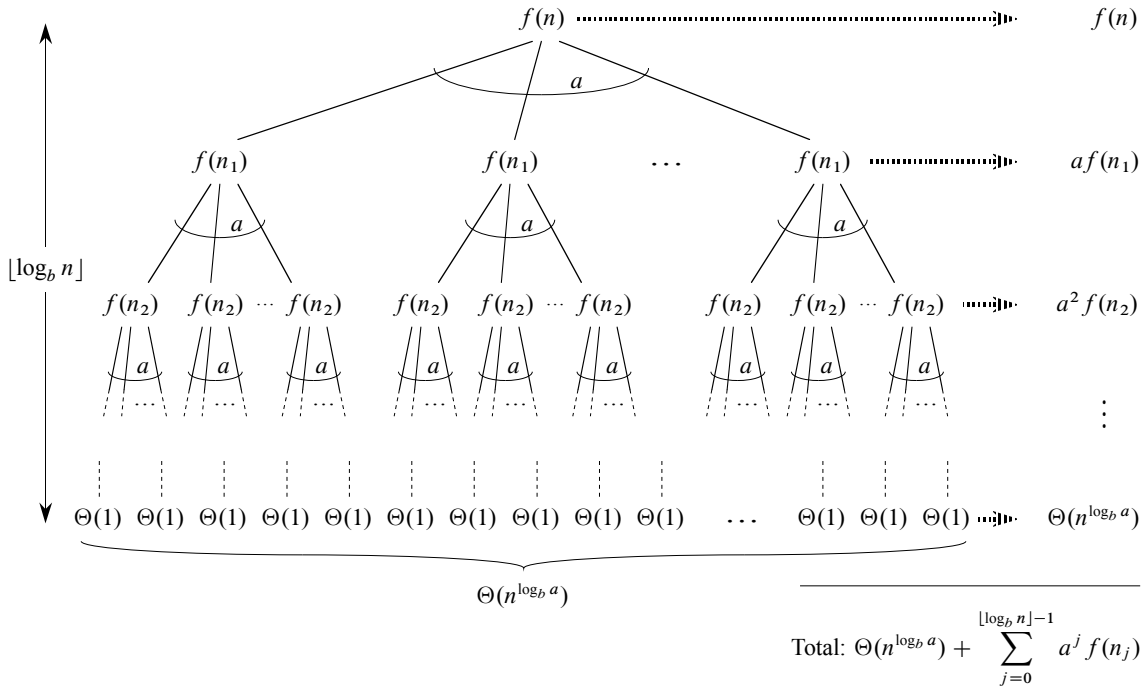


Figure 4.8 The recursion tree generated by $T(n) = aT(\lceil n/b \rceil) + f(n)$. The recursive argument n_j is given by equation (4.27).

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 $f(n_j) = O((n/b^j)^{\log_b a - \epsilon})$, 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 at least $n/2$ 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.

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 $A[1..A.length]$ may contain numbers, only the elements in $A[1..A.heap\text{-}size]$, where $0 \le A.heap\text{-}size \le A.length$, 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:

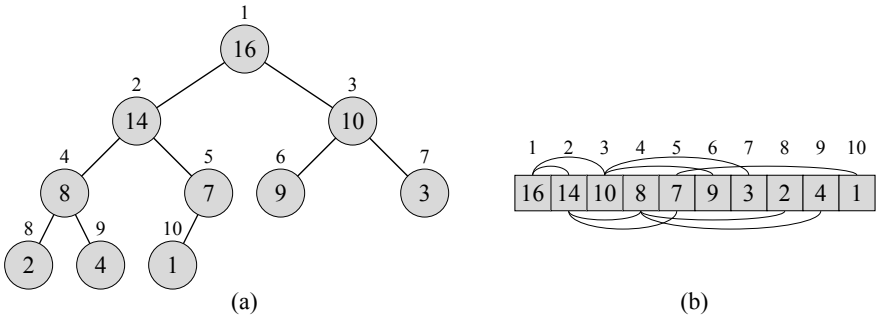


Figure 6.1 A max-heap viewed as **(a)** a binary tree and **(b)** an array. The number within the circle at each node in the tree is the value stored at that node. The number above a node is the corresponding index in the array. Above and below the array are lines showing parent-child relationships; 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

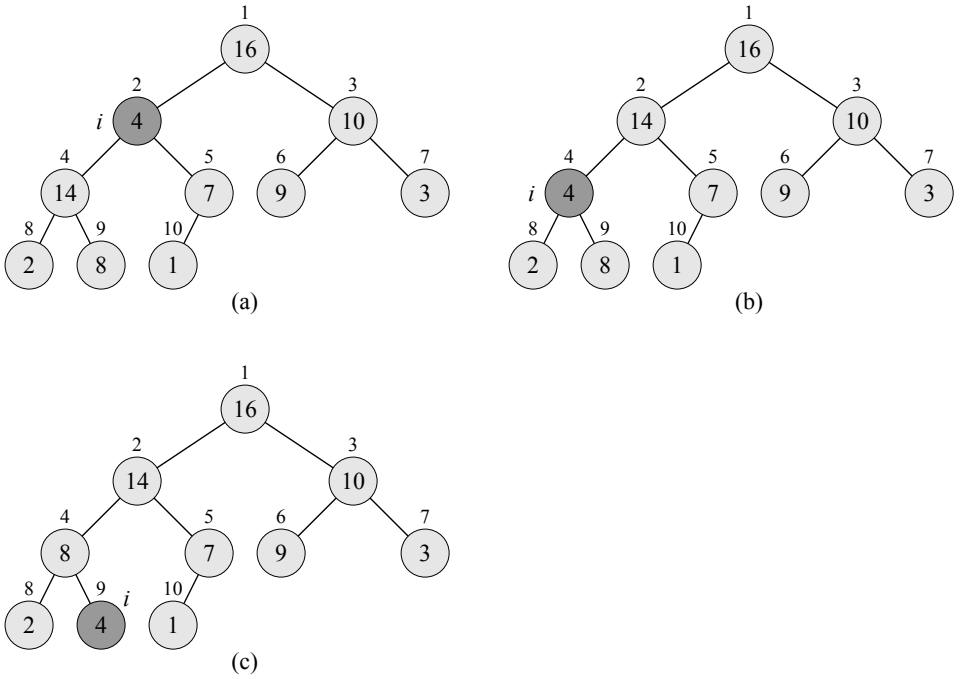


Figure 6.2 The action of MAX-HEAPIFY$(A, 2)$, where $A.heap\text{-}size = 10$. **(a)** The initial configuration, with $A[2]$ at node $i = 2$ violating the max-heap property since it is not larger than both children. The max-heap property is restored for node 2 in **(b)** by exchanging $A[2]$ with $A[4]$, 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

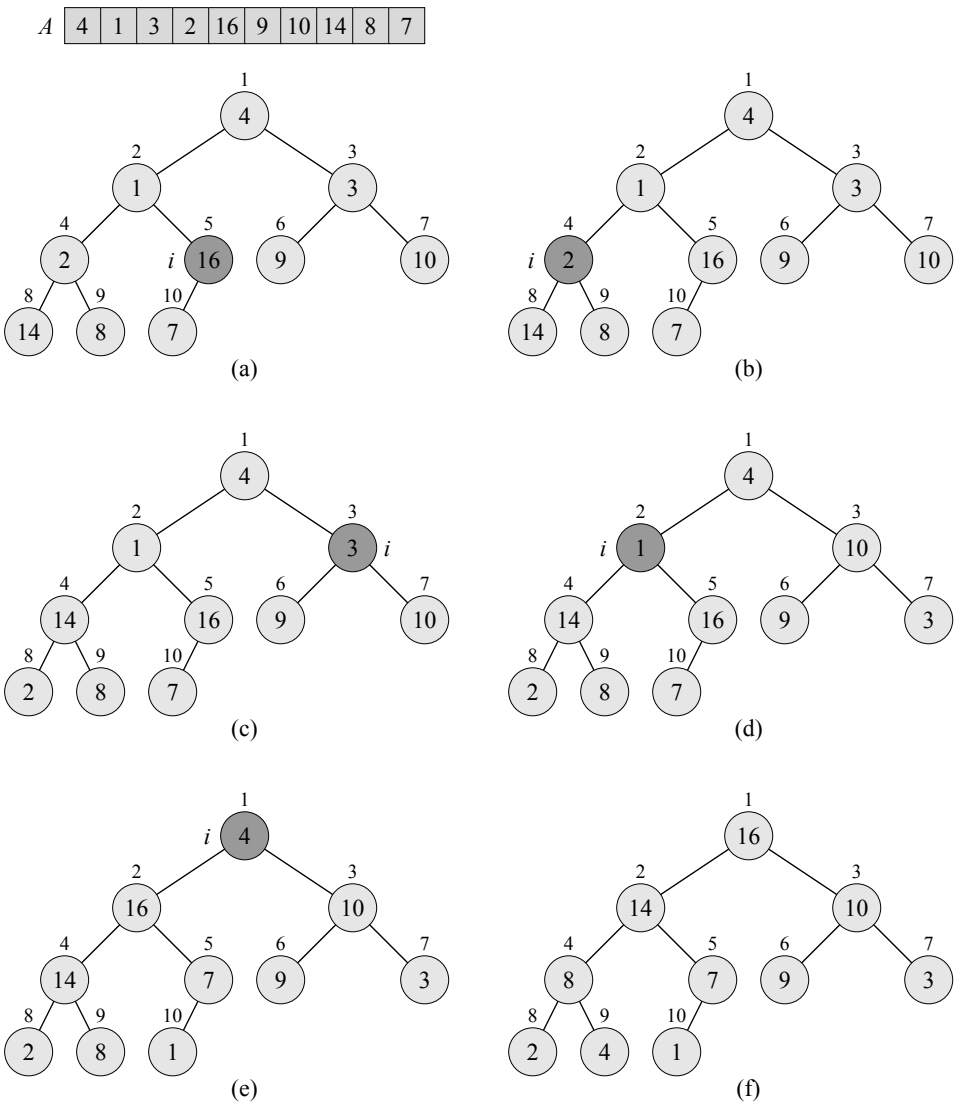


Figure 6.3 The operation of BUILD-MAX-HEAP, showing the data structure before the call to MAX-HEAPIFY in line 3 of BUILD-MAX-HEAP. **(a)** A 10-element input array A and the binary tree it represents. The figure shows that the loop index i refers to node 5 before the call MAX-HEAPIFY(A, i). **(b)** The 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 evaluate 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 $\Omega(n \lg n)$.

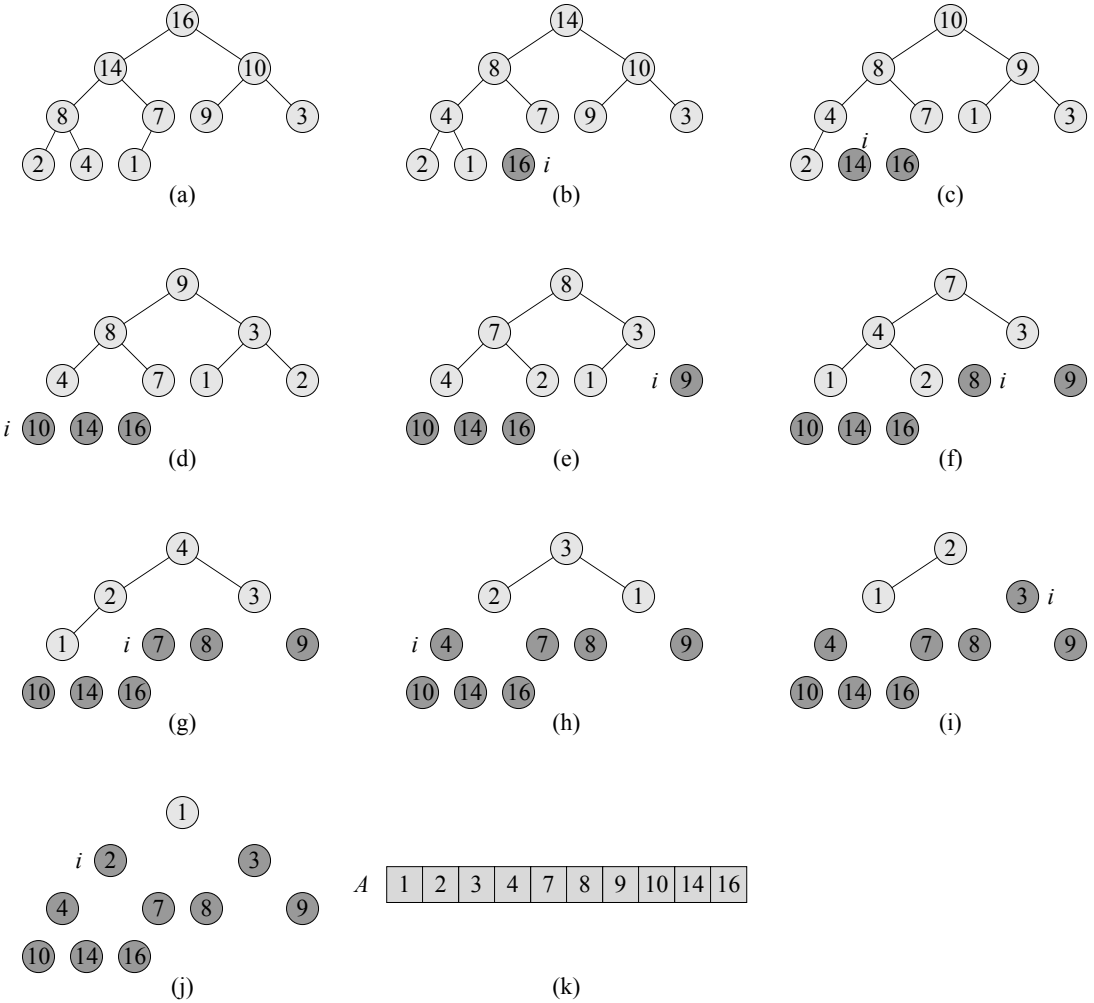


Figure 6.4 The operation of HEAPSORT. **(a)** The max-heap data structure just after BUILD-MAX-HEAP has built it in line 1. **(b)–(j)** The max-heap just after each call of MAX-HEAPIFY in line 5, showing the value of i at that time. Only lightly shaded nodes remain in the heap. **(k)** The resulting 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 $A = \langle 15, 13, 9, 5, 12, 8, 7, 4, 0, 6, 2, 1 \rangle$.

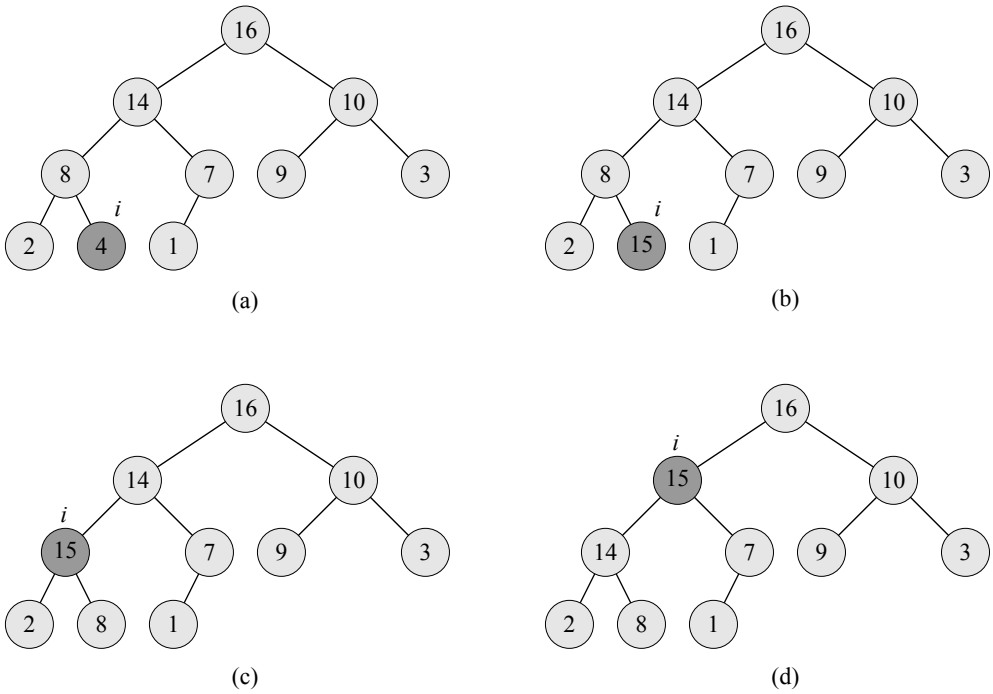


Figure 6.5 The operation of HEAP-INCREASE-KEY. **(a)** The max-heap of Figure 6.4(a) with a node whose index is i heavily shaded. **(b)** This node has its key increased to 15. **(c)** After one iteration of the **while** loop of lines 4–6, the node and its parent have exchanged keys, and the index i 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, $A[\text{PARENT}(i)] \geq A[\text{LEFT}(i)]$ and $A[\text{PARENT}(i)] \geq A[\text{RIGHT}(i)]$, if these nodes exist, and the subarray $A[1\,..\,A.\textit{heap-size}]$ 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 $A[1\,..\,A.\textit{heap-size}]$ 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 $A.heap\text{-}size = 1$
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 $r \leq mn$ 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 $A[k] = x$.

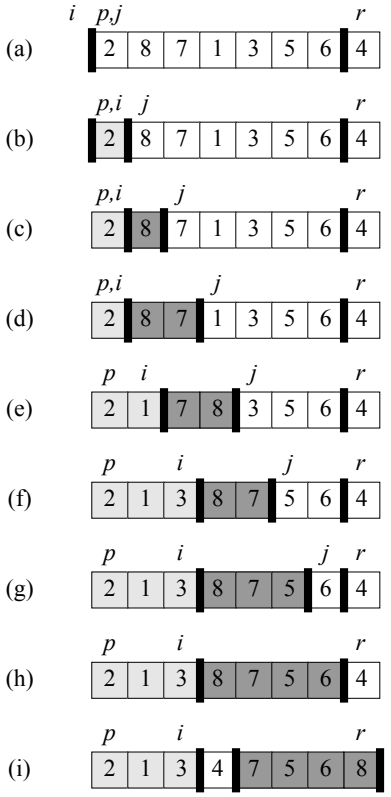


Figure 7.1 The operation of PARTITION on a sample array. Array entry $A[r]$ becomes the pivot element x. Lightly shaded array elements are all in the first partition with values no greater than x. Heavily shaded elements are in the second partition with values greater than x. The unshaded elements have 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.

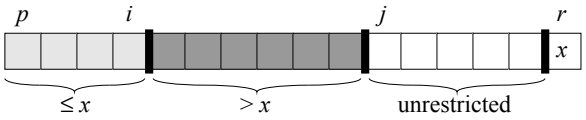


Figure 7.2 The four regions maintained by the procedure PARTITION on a subarray $A[p\,..\,r]$. The values in $A[p\,..\,i]$ are all less than or equal to x, the values in $A[i+1\,..\,j-1]$ are all greater than x, and $A[r] = x$. The subarray $A[j\,..\,r-1]$ can take on any values.

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 $A = \langle 13, 19, 9, 5, 12, 8, 7, 4, 21, 2, 6, 11 \rangle$.

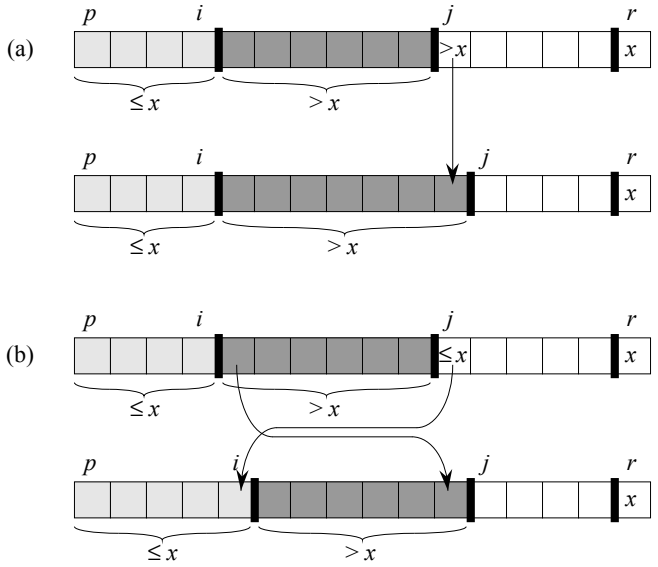


Figure 7.3 The two cases for one iteration of procedure PARTITION. **(a)** If $A[j] > x$, the only action is to increment j, which maintains the loop invariant. **(b)** If $A[j] \le x$, index i is incremented, $A[i]$ and $A[j]$ are swapped, and then j is incremented. Again, the loop invariant is maintained.

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-

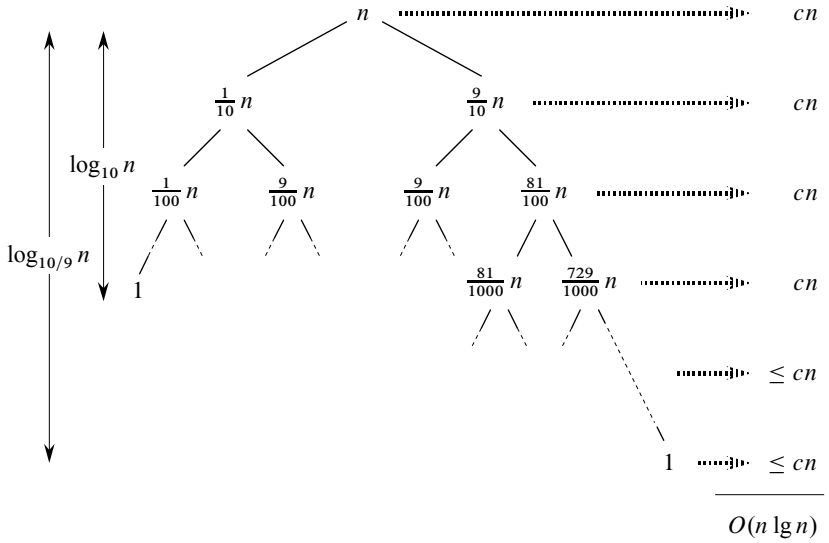


Figure 7.4 A recursion tree for QUICKSORT in which PARTITION always produces a 9-to-1 split, yielding a running time of $O(n \lg n)$. Nodes show subproblem sizes, with per-level costs on the right. The per-level costs include the constant c implicit in the $\Theta(n)$ term.

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.

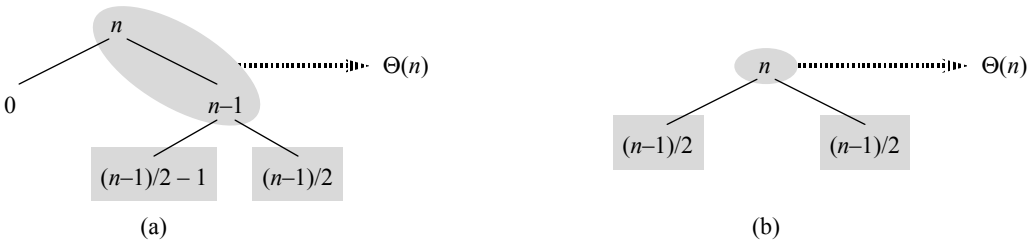


Figure 7.5 **(a)** Two levels of a recursion tree for quicksort. The partitioning at the root costs n and produces a "bad" split: two subarrays of sizes 0 and $n - 1$. The partitioning of the subarray of size $n - 1$ costs $n - 1$ and produces a "good" split: subarrays of size $(n - 1)/2 - 1$ and $(n - 1)/2$. **(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 $0<\alpha\le 1/2$ 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

$$\mathrm{E}[X] = \mathrm{E}\left[\sum_{i=1}^{n-1} \sum_{j=i+1}^{n} X_{ij}\right]$$

$$= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \mathrm{E}[X_{ij}]$$

$$= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \Pr\{z_i \text{ is compared to } z_j\} \ . \tag{7.2}$$

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

$$\begin{aligned}
\Pr\{z_i \text{ is compared to } z_j\} &= \Pr\{z_i \text{ or } z_j \text{ is first pivot chosen from } Z_{ij}\} \\
&= \Pr\{z_i \text{ is first pivot chosen from } Z_{ij}\} \\
&\quad + \Pr\{z_j \text{ is first pivot chosen from } Z_{ij}\} \\
&= \frac{1}{j-i+1} + \frac{1}{j-i+1} \\
&= \frac{2}{j-i+1} \ .
\end{aligned} \tag{7.3}$$

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-PARTITION procedure to call PARTITION$'$, and name the new procedure RANDOMIZED-PARTITION$'$. Then modify the QUICKSORT procedure to produce a procedure QUICKSORT$'(A, p, r)$ 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

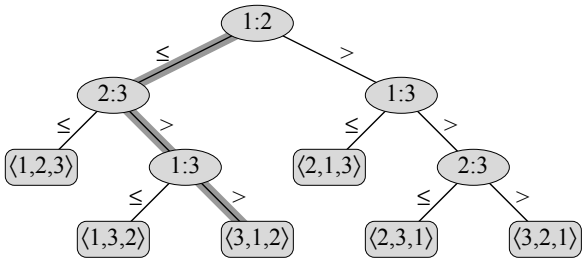


Figure 8.1 The decision tree for insertion sort operating on three elements. An internal node annotated by $i:j$ indicates a comparison between a_i and a_j. A leaf annotated by the permutation $\langle \pi(1), \pi(2), \ldots, \pi(n) \rangle$ indicates the ordering $a_{\pi(1)} \leq a_{\pi(2)} \leq \cdots \leq a_{\pi(n)}$. 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.

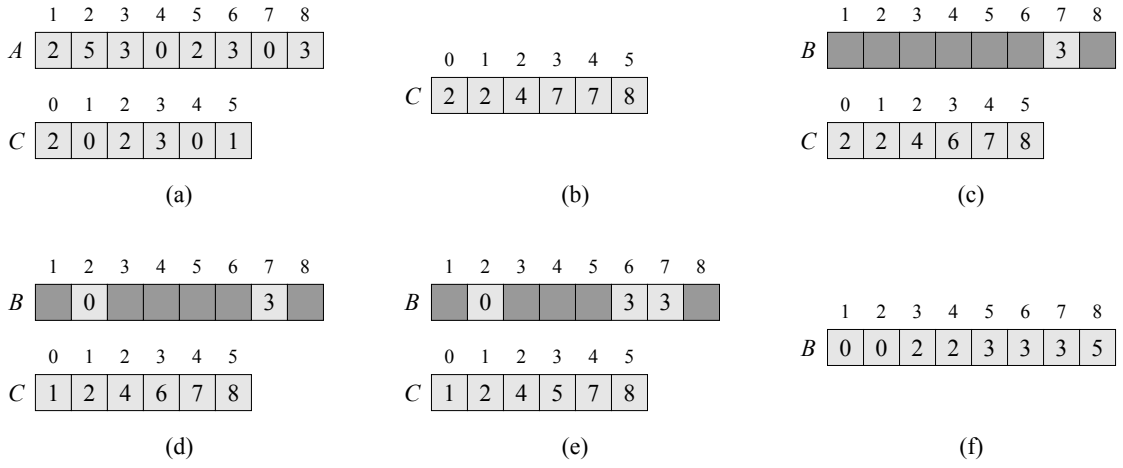


Figure 8.2 The operation of COUNTING-SORT on an input array $A[1..8]$, where each element of A is a nonnegative integer no larger than $k = 5$. **(a)** The array A and the auxiliary array C after line 5. **(b)** The array C after line 8. **(c)–(e)** The output array B and the auxiliary array C after 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.

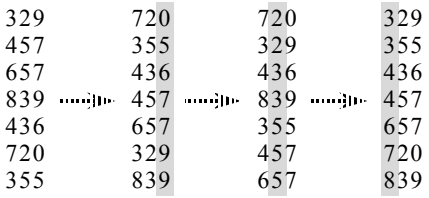


Figure 8.3 The operation of radix sort on a list of seven 3-digit numbers. The leftmost column is the input. The remaining columns show the list after successive sorts on increasingly significant digit positions. Shading indicates the digit position sorted on to produce each list from the previous one.

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.)

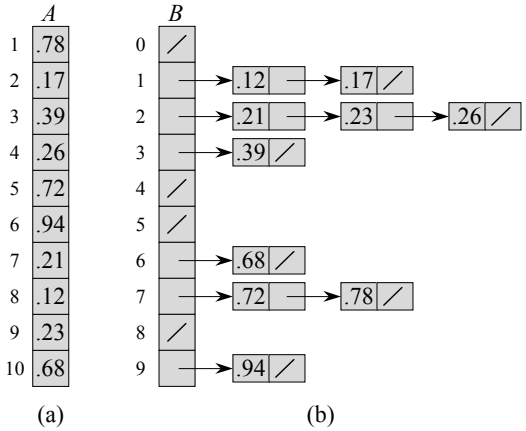


Figure 8.4 The operation of BUCKET-SORT for $n = 10$. **(a)** The input array $A[1..10]$. **(b)** The array $B[0..9]$ of sorted lists (buckets) after line 8 of the algorithm. Bucket i holds values in the half-open interval $[i/10, (i+1)/10)$. The sorted output consists of a concatenation in order of the lists $B[0], B[1], \ldots, B[9]$.

```
BUCKET-SORT(A)
1  n = A.length
2  let B[0..n − 1] be a new array
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.

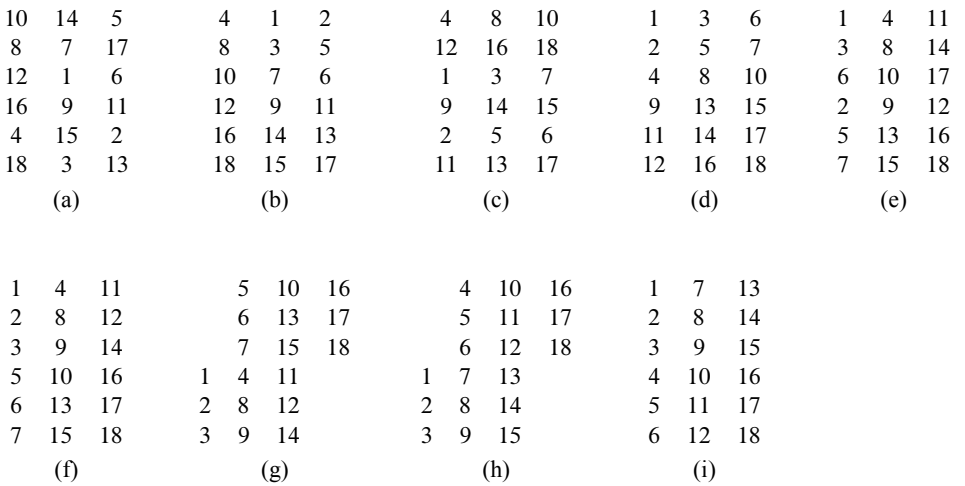


Figure 8.5 The steps of columnsort. **(a)** The input array with 6 rows and 3 columns. **(b)** After sorting each column in step 1. **(c)** After transposing and reshaping in step 2. **(d)** After sorting each column in step 3. **(e)** After performing step 4, which inverts the permutation from step 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 $1 \leq i \leq n$.

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

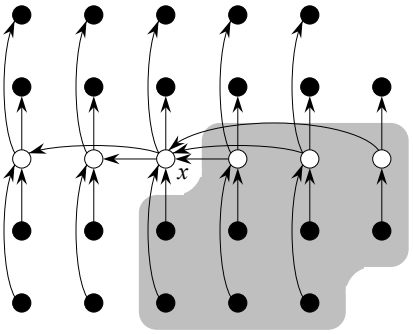


Figure 9.1 Analysis of the algorithm SELECT. The n elements are represented by small circles, and each group of 5 elements occupies a column. The medians of the groups are whitened, and the median-of-medians x is labeled. (When finding the median of an even number of elements, we use the lower median.) 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

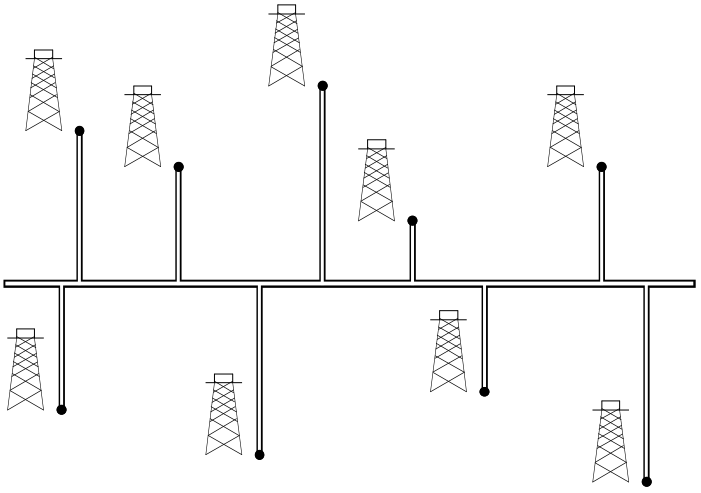


Figure 9.2 Professor Olay needs to determine the position of the east-west oil pipeline that minimizes the total length of the north-south spurs.

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.

15 Dynamic Programming

Dynamic programming, like the divide-and-conquer method, solves problems by combining the solutions to subproblems. ("Programming" in this context refers to a tabular method, not to writing computer code.) As we saw in Chapters 2 and 4, divide-and-conquer algorithms partition the problem into disjoint subproblems, solve the subproblems recursively, and then combine their solutions to solve the original problem. In contrast, dynamic programming applies when the subproblems overlap—that is, when subproblems share subsubproblems. In this context, a divide-and-conquer algorithm does more work than necessary, repeatedly solving the common subsubproblems. A dynamic-programming algorithm solves each subsubproblem just once and then saves its answer in a table, thereby avoiding the work of recomputing the answer every time it solves each subsubproblem.

We typically apply dynamic programming to ***optimization problems***. Such problems can have many possible solutions. Each solution has a value, and we wish to find a solution with the optimal (minimum or maximum) value. We call such a solution *an* optimal solution to the problem, as opposed to *the* optimal solution, since there may be several solutions that achieve the optimal value.

When developing a dynamic-programming algorithm, we follow a sequence of four steps:

1. Characterize the structure of an optimal solution.
2. Recursively define the value of an optimal solution.
3. Compute the value of an optimal solution, typically in a bottom-up fashion.
4. Construct an optimal solution from computed information.

Steps 1–3 form the basis of a dynamic-programming solution to a problem. If we need only the value of an optimal solution, and not the solution itself, then we can omit step 4. When we do perform step 4, we sometimes maintain additional information during step 3 so that we can easily construct an optimal solution.

The sections that follow use the dynamic-programming method to solve some optimization problems. Section 15.1 examines the problem of cutting a rod into

rods of smaller length in way that maximizes their total value. Section 15.2 asks how we can multiply a chain of matrices while performing the fewest total scalar multiplications. Given these examples of dynamic programming, Section 15.3 discusses two key characteristics that a problem must have for dynamic programming to be a viable solution technique. Section 15.4 then shows how to find the longest common subsequence of two sequences via dynamic programming. Finally, Section 15.5 uses dynamic programming to construct binary search trees that are optimal, given a known distribution of keys to be looked up.

15.1 Rod cutting

Our first example uses dynamic programming to solve a simple problem in deciding where to cut steel rods. Serling Enterprises buys long steel rods and cuts them into shorter rods, which it then sells. Each cut is free. The management of Serling Enterprises wants to know the best way to cut up the rods.

We assume that we know, for $i = 1, 2, \ldots$, the price p_i in dollars that Serling Enterprises charges for a rod of length i inches. Rod lengths are always an integral number of inches. Figure 15.1 gives a sample price table.

The ***rod-cutting problem*** is the following. Given a rod of length n inches and a table of prices p_i for $i = 1, 2, \ldots, n$, determine the maximum revenue r_n obtainable by cutting up the rod and selling the pieces. Note that if the price p_n for a rod of length n is large enough, an optimal solution may require no cutting at all.

Consider the case when $n = 4$. Figure 15.2 shows all the ways to cut up a rod of 4 inches in length, including the way with no cuts at all. We see that cutting a 4-inch rod into two 2-inch pieces produces revenue $p_2 + p_2 = 5 + 5 = 10$, which is optimal.

We can cut up a rod of length n in 2^{n-1} different ways, since we have an independent option of cutting, or not cutting, at distance i inches from the left end,

length i	1	2	3	4	5	6	7	8	9	10
price p_i	1	5	8	9	10	17	17	20	24	30

Figure 15.1 A sample price table for rods. Each rod of length i inches earns the company p_i dollars of revenue.

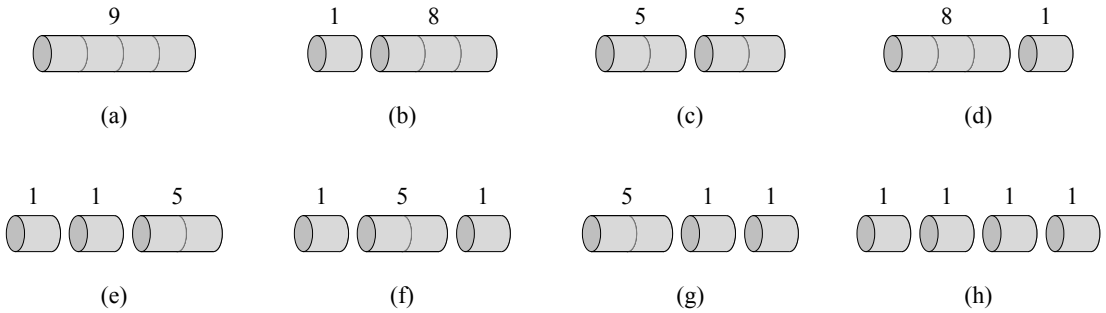


Figure 15.2 The 8 possible ways of cutting up a rod of length 4. Above each piece is the value of that piece, according to the sample price chart of Figure 15.1. The optimal strategy is part (c)—cutting the rod into two pieces of length 2—which has total value 10.

for $i = 1, 2, \ldots, n-1$.[1] We denote a decomposition into pieces using ordinary additive notation, so that $7 = 2 + 2 + 3$ indicates that a rod of length 7 is cut into three pieces—two of length 2 and one of length 3. If an optimal solution cuts the rod into k pieces, for some $1 \le k \le n$, then an optimal decomposition

$$n = i_1 + i_2 + \cdots + i_k$$

of the rod into pieces of lengths i_1, i_2, ..., i_k provides maximum corresponding revenue

$$r_n = p_{i_1} + p_{i_2} + \cdots + p_{i_k} .$$

For our sample problem, we can determine the optimal revenue figures r_i, for $i = 1, 2, \ldots, 10$, by inspection, with the corresponding optimal decompositions

[1] If we required the pieces to be cut in order of nondecreasing size, there would be fewer ways to consider. For $n = 4$, we would consider only 5 such ways: parts (a), (b), (c), (e), and (h) in Figure 15.2. The number of ways is called the ***partition function***; it is approximately equal to $e^{\pi\sqrt{2n/3}}/4n\sqrt{3}$. This quantity is less than 2^{n-1}, but still much greater than any polynomial in n. We shall not pursue this line of inquiry further, however.

$$
\begin{aligned}
r_1 &= 1 \quad \text{from solution } 1 = 1 \quad \text{(no cuts)}\,, \\
r_2 &= 5 \quad \text{from solution } 2 = 2 \quad \text{(no cuts)}\,, \\
r_3 &= 8 \quad \text{from solution } 3 = 3 \quad \text{(no cuts)}\,, \\
r_4 &= 10 \quad \text{from solution } 4 = 2 + 2\,, \\
r_5 &= 13 \quad \text{from solution } 5 = 2 + 3\,, \\
r_6 &= 17 \quad \text{from solution } 6 = 6 \quad \text{(no cuts)}\,, \\
r_7 &= 18 \quad \text{from solution } 7 = 1 + 6 \text{ or } 7 = 2 + 2 + 3\,, \\
r_8 &= 22 \quad \text{from solution } 8 = 2 + 6\,, \\
r_9 &= 25 \quad \text{from solution } 9 = 3 + 6\,, \\
r_{10} &= 30 \quad \text{from solution } 10 = 10 \quad \text{(no cuts)}\,.
\end{aligned}
$$

More generally, we can frame the values r_n for $n \geq 1$ in terms of optimal revenues from shorter rods:

$$r_n = \max\left(p_n, r_1 + r_{n-1}, r_2 + r_{n-2}, \ldots, r_{n-1} + r_1\right)\,. \tag{15.1}$$

The first argument, p_n, corresponds to making no cuts at all and selling the rod of length n as is. The other $n-1$ arguments to max correspond to the maximum revenue obtained by making an initial cut of the rod into two pieces of size i and $n-i$, for each $i = 1, 2, \ldots, n-1$, and then optimally cutting up those pieces further, obtaining revenues r_i and r_{n-i} from those two pieces. Since we don't know ahead of time which value of i optimizes revenue, we have to consider all possible values for i and pick the one that maximizes revenue. We also have the option of picking no i at all if we can obtain more revenue by selling the rod uncut.

Note that to solve the original problem of size n, we solve smaller problems of the same type, but of smaller sizes. Once we make the first cut, we may consider the two pieces as independent instances of the rod-cutting problem. The overall optimal solution incorporates optimal solutions to the two related subproblems, maximizing revenue from each of those two pieces. We say that the rod-cutting problem exhibits ***optimal substructure***: optimal solutions to a problem incorporate optimal solutions to related subproblems, which we may solve independently.

In a related, but slightly simpler, way to arrange a recursive structure for the rod-cutting problem, we view a decomposition as consisting of a first piece of length i cut off the left-hand end, and then a right-hand remainder of length $n-i$. Only the remainder, and not the first piece, may be further divided. We may view every decomposition of a length-n rod in this way: as a first piece followed by some decomposition of the remainder. When doing so, we can couch the solution with no cuts at all as saying that the first piece has size $i = n$ and revenue p_n and that the remainder has size 0 with corresponding revenue $r_0 = 0$. We thus obtain the following simpler version of equation (15.1):

$$r_n = \max_{1 \leq i \leq n} \left(p_i + r_{n-i}\right)\,. \tag{15.2}$$

In this formulation, an optimal solution embodies the solution to only *one* related subproblem—the remainder—rather than two.

Recursive top-down implementation

The following procedure implements the computation implicit in equation (15.2) in a straightforward, top-down, recursive manner.

```
CUT-ROD(p, n)
1  if n == 0
2       return 0
3  q = -∞
4  for i = 1 to n
5       q = max(q, p[i] + CUT-ROD(p, n - i))
6  return q
```

Procedure CUT-ROD takes as input an array $p[1..n]$ of prices and an integer n, and it returns the maximum revenue possible for a rod of length n. If $n = 0$, no revenue is possible, and so CUT-ROD returns 0 in line 2. Line 3 initializes the maximum revenue q to $-\infty$, so that the **for** loop in lines 4–5 correctly computes $q = \max_{1 \le i \le n}(p_i + \text{CUT-ROD}(p, n-i))$; line 6 then returns this value. A simple induction on n proves that this answer is equal to the desired answer r_n, using equation (15.2).

If you were to code up CUT-ROD in your favorite programming language and run it on your computer, you would find that once the input size becomes moderately large, your program would take a long time to run. For $n = 40$, you would find that your program takes at least several minutes, and most likely more than an hour. In fact, you would find that each time you increase n by 1, your program's running time would approximately double.

Why is CUT-ROD so inefficient? The problem is that CUT-ROD calls itself recursively over and over again with the same parameter values; it solves the same subproblems repeatedly. Figure 15.3 illustrates what happens for $n = 4$: CUT-ROD(p, n) calls CUT-ROD$(p, n-i)$ for $i = 1, 2, \ldots, n$. Equivalently, CUT-ROD(p, n) calls CUT-ROD(p, j) for each $j = 0, 1, \ldots, n-1$. When this process unfolds recursively, the amount of work done, as a function of n, grows explosively.

To analyze the running time of CUT-ROD, let $T(n)$ denote the total number of calls made to CUT-ROD when called with its second parameter equal to n. This expression equals the number of nodes in a subtree whose root is labeled n in the recursion tree. The count includes the initial call at its root. Thus, $T(0) = 1$ and

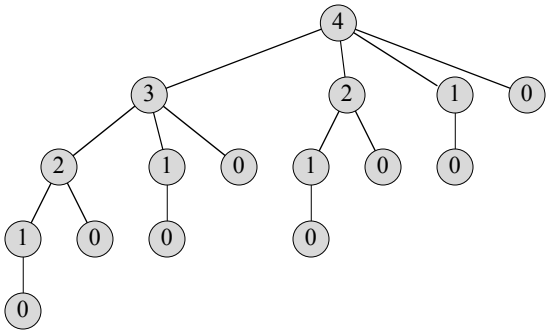


Figure 15.3 The recursion tree showing recursive calls resulting from a call CUT-ROD(p, n) for $n = 4$. Each node label gives the size n of the corresponding subproblem, so that an edge from a parent with label s to a child with label t corresponds to cutting off an initial piece of size $s - t$ and leaving a remaining subproblem of size t. A path from the root to a leaf corresponds to one of the 2^{n-1} ways of cutting up a rod of length n. In general, this recursion tree has 2^n nodes and 2^{n-1} leaves.

$$T(n) = 1 + \sum_{j=0}^{n-1} T(j) \,. \tag{15.3}$$

The initial 1 is for the call at the root, and the term $T(j)$ counts the number of calls (including recursive calls) due to the call CUT-ROD$(p, n - i)$, where $j = n - i$. As Exercise 15.1-1 asks you to show,

$$T(n) = 2^n \,, \tag{15.4}$$

and so the running time of CUT-ROD is exponential in n.

In retrospect, this exponential running time is not so surprising. CUT-ROD explicitly considers all the 2^{n-1} possible ways of cutting up a rod of length n. The tree of recursive calls has 2^{n-1} leaves, one for each possible way of cutting up the rod. The labels on the simple path from the root to a leaf give the sizes of each remaining right-hand piece before making each cut. That is, the labels give the corresponding cut points, measured from the right-hand end of the rod.

Using dynamic programming for optimal rod cutting

We now show how to convert CUT-ROD into an efficient algorithm, using dynamic programming.

The dynamic-programming method works as follows. Having observed that a naive recursive solution is inefficient because it solves the same subproblems repeatedly, we arrange for each subproblem to be solved only *once*, saving its solution. If we need to refer to this subproblem's solution again later, we can just look it

up, rather than recompute it. Dynamic programming thus uses additional memory to save computation time; it serves an example of a ***time-memory trade-off***. The savings may be dramatic: an exponential-time solution may be transformed into a polynomial-time solution. A dynamic-programming approach runs in polynomial time when the number of *distinct* subproblems involved is polynomial in the input size and we can solve each such subproblem in polynomial time.

There are usually two equivalent ways to implement a dynamic-programming approach. We shall illustrate both of them with our rod-cutting example.

The first approach is ***top-down with memoization***.[2] In this approach, we write the procedure recursively in a natural manner, but modified to save the result of each subproblem (usually in an array or hash table). The procedure now first checks to see whether it has previously solved this subproblem. If so, it returns the saved value, saving further computation at this level; if not, the procedure computes the value in the usual manner. We say that the recursive procedure has been ***memoized***; it "remembers" what results it has computed previously.

The second approach is the ***bottom-up method***. This approach typically depends on some natural notion of the "size" of a subproblem, such that solving any particular subproblem depends only on solving "smaller" subproblems. We sort the subproblems by size and solve them in size order, smallest first. When solving a particular subproblem, we have already solved all of the smaller subproblems its solution depends upon, and we have saved their solutions. We solve each subproblem only once, and when we first see it, we have already solved all of its prerequisite subproblems.

These two approaches yield algorithms with the same asymptotic running time, except in unusual circumstances where the top-down approach does not actually recurse to examine all possible subproblems. The bottom-up approach often has much better constant factors, since it has less overhead for procedure calls.

Here is the the pseudocode for the top-down CUT-ROD procedure, with memoization added:

```
MEMOIZED-CUT-ROD(p, n)
1  let r[0..n] be a new array
2  for i = 0 to n
3      r[i] = -∞
4  return MEMOIZED-CUT-ROD-AUX(p, n, r)
```

[2]This is not a misspelling. The word really is *memoization*, not *memorization*. *Memoization* comes from *memo*, since the technique consists of recording a value so that we can look it up later.

```
MEMOIZED-CUT-ROD-AUX(p, n, r)
1  if r[n] ≥ 0
2      return r[n]
3  if n == 0
4      q = 0
5  else q = −∞
6      for i = 1 to n
7          q = max(q, p[i] + MEMOIZED-CUT-ROD-AUX(p, n − i, r))
8  r[n] = q
9  return q
```

Here, the main procedure MEMOIZED-CUT-ROD initializes a new auxiliary array $r[0..n]$ with the value $-\infty$, a convenient choice with which to denote "unknown." (Known revenue values are always nonnegative.) It then calls its helper routine, MEMOIZED-CUT-ROD-AUX.

The procedure MEMOIZED-CUT-ROD-AUX is just the memoized version of our previous procedure, CUT-ROD. It first checks in line 1 to see whether the desired value is already known and, if it is, then line 2 returns it. Otherwise, lines 3–7 compute the desired value q in the usual manner, line 8 saves it in $r[n]$, and line 9 returns it.

The bottom-up version is even simpler:

```
BOTTOM-UP-CUT-ROD(p, n)
1  let r[0..n] be a new array
2  r[0] = 0
3  for j = 1 to n
4      q = −∞
5      for i = 1 to j
6          q = max(q, p[i] + r[j − i])
7      r[j] = q
8  return r[n]
```

For the bottom-up dynamic-programming approach, BOTTOM-UP-CUT-ROD uses the natural ordering of the subproblems: a subproblem of size i is "smaller" than a subproblem of size j if $i < j$. Thus, the procedure solves subproblems of sizes $j = 0, 1, \ldots, n$, in that order.

Line 1 of procedure BOTTOM-UP-CUT-ROD creates a new array $r[0..n]$ in which to save the results of the subproblems, and line 2 initializes $r[0]$ to 0, since a rod of length 0 earns no revenue. Lines 3–6 solve each subproblem of size j, for $j = 1, 2, \ldots, n$, in order of increasing size. The approach used to solve a problem of a particular size j is the same as that used by CUT-ROD, except that line 6 now

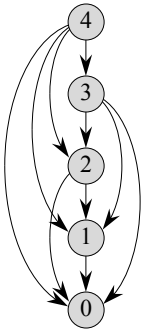


Figure 15.4 The subproblem graph for the rod-cutting problem with $n = 4$. The vertex labels give the sizes of the corresponding subproblems. A directed edge (x, y) indicates that we need a solution to subproblem y when solving subproblem x. This graph is a reduced version of the tree of Figure 15.3, in which all nodes with the same label are collapsed into a single vertex and all edges go from parent to child.

directly references array entry $r[j - i]$ instead of making a recursive call to solve the subproblem of size $j - i$. Line 7 saves in $r[j]$ the solution to the subproblem of size j. Finally, line 8 returns $r[n]$, which equals the optimal value r_n.

The bottom-up and top-down versions have the same asymptotic running time. The running time of procedure BOTTOM-UP-CUT-ROD is $\Theta(n^2)$, due to its doubly-nested loop structure. The number of iterations of its inner **for** loop, in lines 5–6, forms an arithmetic series. The running time of its top-down counterpart, MEMOIZED-CUT-ROD, is also $\Theta(n^2)$, although this running time may be a little harder to see. Because a recursive call to solve a previously solved subproblem returns immediately, MEMOIZED-CUT-ROD solves each subproblem just once. It solves subproblems for sizes $0, 1, \ldots, n$. To solve a subproblem of size n, the **for** loop of lines 6–7 iterates n times. Thus, the total number of iterations of this **for** loop, over all recursive calls of MEMOIZED-CUT-ROD, forms an arithmetic series, giving a total of $\Theta(n^2)$ iterations, just like the inner **for** loop of BOTTOM-UP-CUT-ROD. (We actually are using a form of aggregate analysis here. We shall see aggregate analysis in detail in Section 17.1.)

Subproblem graphs

When we think about a dynamic-programming problem, we should understand the set of subproblems involved and how subproblems depend on one another.

The ***subproblem graph*** for the problem embodies exactly this information. Figure 15.4 shows the subproblem graph for the rod-cutting problem with $n = 4$. It is a directed graph, containing one vertex for each distinct subproblem. The sub-

problem graph has a directed edge from the vertex for subproblem x to the vertex for subproblem y if determining an optimal solution for subproblem x involves directly considering an optimal solution for subproblem y. For example, the subproblem graph contains an edge from x to y if a top-down recursive procedure for solving x directly calls itself to solve y. We can think of the subproblem graph as a "reduced" or "collapsed" version of the recursion tree for the top-down recursive method, in which we coalesce all nodes for the same subproblem into a single vertex and direct all edges from parent to child.

The bottom-up method for dynamic programming considers the vertices of the subproblem graph in such an order that we solve the subproblems y adjacent to a given subproblem x before we solve subproblem x. (Recall from Section B.4 that the adjacency relation is not necessarily symmetric.) Using the terminology from Chapter 22, in a bottom-up dynamic-programming algorithm, we consider the vertices of the subproblem graph in an order that is a "reverse topological sort," or a "topological sort of the transpose" (see Section 22.4) of the subproblem graph. In other words, no subproblem is considered until all of the subproblems it depends upon have been solved. Similarly, using notions from the same chapter, we can view the top-down method (with memoization) for dynamic programming as a "depth-first search" of the subproblem graph (see Section 22.3).

The size of the subproblem graph $G = (V, E)$ can help us determine the running time of the dynamic programming algorithm. Since we solve each subproblem just once, the running time is the sum of the times needed to solve each subproblem. Typically, the time to compute the solution to a subproblem is proportional to the degree (number of outgoing edges) of the corresponding vertex in the subproblem graph, and the number of subproblems is equal to the number of vertices in the subproblem graph. In this common case, the running time of dynamic programming is linear in the number of vertices and edges.

Reconstructing a solution

Our dynamic-programming solutions to the rod-cutting problem return the value of an optimal solution, but they do not return an actual solution: a list of piece sizes. We can extend the dynamic-programming approach to record not only the optimal *value* computed for each subproblem, but also a *choice* that led to the optimal value. With this information, we can readily print an optimal solution.

Here is an extended version of BOTTOM-UP-CUT-ROD that computes, for each rod size j, not only the maximum revenue r_j, but also s_j, the optimal size of the first piece to cut off:

```
EXTENDED-BOTTOM-UP-CUT-ROD(p, n)
 1  let r[0..n] and s[0..n] be new arrays
 2  r[0] = 0
 3  for j = 1 to n
 4      q = -∞
 5      for i = 1 to j
 6          if q < p[i] + r[j - i]
 7              q = p[i] + r[j - i]
 8              s[j] = i
 9      r[j] = q
10  return r and s
```

This procedure is similar to BOTTOM-UP-CUT-ROD, except that it creates the array s in line 1, and it updates $s[j]$ in line 8 to hold the optimal size i of the first piece to cut off when solving a subproblem of size j.

The following procedure takes a price table p and a rod size n, and it calls EXTENDED-BOTTOM-UP-CUT-ROD to compute the array $s[1..n]$ of optimal first-piece sizes and then prints out the complete list of piece sizes in an optimal decomposition of a rod of length n:

```
PRINT-CUT-ROD-SOLUTION(p, n)
1  (r, s) = EXTENDED-BOTTOM-UP-CUT-ROD(p, n)
2  while n > 0
3      print s[n]
4      n = n - s[n]
```

In our rod-cutting example, the call EXTENDED-BOTTOM-UP-CUT-ROD$(p, 10)$ would return the following arrays:

i	0	1	2	3	4	5	6	7	8	9	10
$r[i]$	0	1	5	8	10	13	17	18	22	25	30
$s[i]$	0	1	2	3	2	2	6	1	2	3	10

A call to PRINT-CUT-ROD-SOLUTION$(p, 10)$ would print just 10, but a call with $n = 7$ would print the cuts 1 and 6, corresponding to the first optimal decomposition for r_7 given earlier.

Exercises

15.1-1

Show that equation (15.4) follows from equation (15.3) and the initial condition $T(0) = 1$.

15.1-2
Show, by means of a counterexample, that the following "greedy" strategy does not always determine an optimal way to cut rods. Define the ***density*** of a rod of length i to be p_i/i, that is, its value per inch. The greedy strategy for a rod of length n cuts off a first piece of length i, where $1 \le i \le n$, having maximum density. It then continues by applying the greedy strategy to the remaining piece of length $n - i$.

15.1-3
Consider a modification of the rod-cutting problem in which, in addition to a price p_i for each rod, each cut incurs a fixed cost of c. The revenue associated with a solution is now the sum of the prices of the pieces minus the costs of making the cuts. Give a dynamic-programming algorithm to solve this modified problem.

15.1-4
Modify MEMOIZED-CUT-ROD to return not only the value but the actual solution, too.

15.1-5
The Fibonacci numbers are defined by recurrence (3.22). Give an $O(n)$-time dynamic-programming algorithm to compute the nth Fibonacci number. Draw the subproblem graph. How many vertices and edges are in the graph?

15.2 Matrix-chain multiplication

Our next example of dynamic programming is an algorithm that solves the problem of matrix-chain multiplication. We are given a sequence (chain) $\langle A_1, A_2, \ldots, A_n \rangle$ of n matrices to be multiplied, and we wish to compute the product

$$A_1 A_2 \cdots A_n \,. \tag{15.5}$$

We can evaluate the expression (15.5) using the standard algorithm for multiplying pairs of matrices as a subroutine once we have parenthesized it to resolve all ambiguities in how the matrices are multiplied together. Matrix multiplication is associative, and so all parenthesizations yield the same product. A product of matrices is ***fully parenthesized*** if it is either a single matrix or the product of two fully parenthesized matrix products, surrounded by parentheses. For example, if the chain of matrices is $\langle A_1, A_2, A_3, A_4 \rangle$, then we can fully parenthesize the product $A_1 A_2 A_3 A_4$ in five distinct ways:

$(A_1(A_2(A_3A_4)))$,
$(A_1((A_2A_3)A_4))$,
$((A_1A_2)(A_3A_4))$,
$((A_1(A_2A_3))A_4)$,
$(((A_1A_2)A_3)A_4)$.

How we parenthesize a chain of matrices can have a dramatic impact on the cost of evaluating the product. Consider first the cost of multiplying two matrices. The standard algorithm is given by the following pseudocode, which generalizes the SQUARE-MATRIX-MULTIPLY procedure from Section 4.2. The attributes *rows* and *columns* are the numbers of rows and columns in a matrix.

```
MATRIX-MULTIPLY(A, B)
1  if A.columns ≠ B.rows
2      error "incompatible dimensions"
3  else let C be a new A.rows × B.columns matrix
4      for i = 1 to A.rows
5          for j = 1 to B.columns
6              c_ij = 0
7              for k = 1 to A.columns
8                  c_ij = c_ij + a_ik · b_kj
9      return C
```

We can multiply two matrices A and B only if they are ***compatible***: the number of columns of A must equal the number of rows of B. If A is a $p \times q$ matrix and B is a $q \times r$ matrix, the resulting matrix C is a $p \times r$ matrix. The time to compute C is dominated by the number of scalar multiplications in line 8, which is pqr. In what follows, we shall express costs in terms of the number of scalar multiplications.

To illustrate the different costs incurred by different parenthesizations of a matrix product, consider the problem of a chain $\langle A_1, A_2, A_3 \rangle$ of three matrices. Suppose that the dimensions of the matrices are 10×100, 100×5, and 5×50, respectively. If we multiply according to the parenthesization $((A_1A_2)A_3)$, we perform $10 \cdot 100 \cdot 5 = 5000$ scalar multiplications to compute the 10×5 matrix product A_1A_2, plus another $10 \cdot 5 \cdot 50 = 2500$ scalar multiplications to multiply this matrix by A_3, for a total of 7500 scalar multiplications. If instead we multiply according to the parenthesization $(A_1(A_2A_3))$, we perform $100 \cdot 5 \cdot 50 = 25{,}000$ scalar multiplications to compute the 100×50 matrix product A_2A_3, plus another $10 \cdot 100 \cdot 50 = 50{,}000$ scalar multiplications to multiply A_1 by this matrix, for a total of 75,000 scalar multiplications. Thus, computing the product according to the first parenthesization is 10 times faster.

We state the ***matrix-chain multiplication problem*** as follows: given a chain $\langle A_1, A_2, \ldots, A_n \rangle$ of n matrices, where for $i = 1, 2, \ldots, n$, matrix A_i has dimension

$p_{i-1} \times p_i$, fully parenthesize the product $A_1 A_2 \cdots A_n$ in a way that minimizes the number of scalar multiplications.

Note that in the matrix-chain multiplication problem, we are not actually multiplying matrices. Our goal is only to determine an order for multiplying matrices that has the lowest cost. Typically, the time invested in determining this optimal order is more than paid for by the time saved later on when actually performing the matrix multiplications (such as performing only 7500 scalar multiplications instead of 75,000).

Counting the number of parenthesizations

Before solving the matrix-chain multiplication problem by dynamic programming, let us convince ourselves that exhaustively checking all possible parenthesizations does not yield an efficient algorithm. Denote the number of alternative parenthesizations of a sequence of n matrices by $P(n)$. When $n = 1$, we have just one matrix and therefore only one way to fully parenthesize the matrix product. When $n \geq 2$, a fully parenthesized matrix product is the product of two fully parenthesized matrix subproducts, and the split between the two subproducts may occur between the kth and $(k+1)$st matrices for any $k = 1, 2, \ldots, n-1$. Thus, we obtain the recurrence

$$P(n) = \begin{cases} 1 & \text{if } n = 1 , \\ \displaystyle\sum_{k=1}^{n-1} P(k) P(n-k) & \text{if } n \geq 2 . \end{cases} \tag{15.6}$$

Problem 12-4 asked you to show that the solution to a similar recurrence is the sequence of ***Catalan numbers***, which grows as $\Omega(4^n / n^{3/2})$. A simpler exercise (see Exercise 15.2-3) is to show that the solution to the recurrence (15.6) is $\Omega(2^n)$. The number of solutions is thus exponential in n, and the brute-force method of exhaustive search makes for a poor strategy when determining how to optimally parenthesize a matrix chain.

Applying dynamic programming

We shall use the dynamic-programming method to determine how to optimally parenthesize a matrix chain. In so doing, we shall follow the four-step sequence that we stated at the beginning of this chapter:

1. Characterize the structure of an optimal solution.
2. Recursively define the value of an optimal solution.
3. Compute the value of an optimal solution.

4. Construct an optimal solution from computed information.

We shall go through these steps in order, demonstrating clearly how we apply each step to the problem.

Step 1: The structure of an optimal parenthesization

For our first step in the dynamic-programming paradigm, we find the optimal substructure and then use it to construct an optimal solution to the problem from optimal solutions to subproblems. In the matrix-chain multiplication problem, we can perform this step as follows. For convenience, let us adopt the notation $A_{i..j}$, where $i \le j$, for the matrix that results from evaluating the product $A_i A_{i+1} \cdots A_j$. Observe that if the problem is nontrivial, i.e., $i < j$, then to parenthesize the product $A_i A_{i+1} \cdots A_j$, we must split the product between A_k and A_{k+1} for some integer k in the range $i \le k < j$. That is, for some value of k, we first compute the matrices $A_{i..k}$ and $A_{k+1..j}$ and then multiply them together to produce the final product $A_{i..j}$. The cost of parenthesizing this way is the cost of computing the matrix $A_{i..k}$, plus the cost of computing $A_{k+1..j}$, plus the cost of multiplying them together.

The optimal substructure of this problem is as follows. Suppose that to optimally parenthesize $A_i A_{i+1} \cdots A_j$, we split the product between A_k and A_{k+1}. Then the way we parenthesize the "prefix" subchain $A_i A_{i+1} \cdots A_k$ within this optimal parenthesization of $A_i A_{i+1} \cdots A_j$ must be an optimal parenthesization of $A_i A_{i+1} \cdots A_k$. Why? If there were a less costly way to parenthesize $A_i A_{i+1} \cdots A_k$, then we could substitute that parenthesization in the optimal parenthesization of $A_i A_{i+1} \cdots A_j$ to produce another way to parenthesize $A_i A_{i+1} \cdots A_j$ whose cost was lower than the optimum: a contradiction. A similar observation holds for how we parenthesize the subchain $A_{k+1} A_{k+2} \cdots A_j$ in the optimal parenthesization of $A_i A_{i+1} \cdots A_j$: it must be an optimal parenthesization of $A_{k+1} A_{k+2} \cdots A_j$.

Now we use our optimal substructure to show that we can construct an optimal solution to the problem from optimal solutions to subproblems. We have seen that any solution to a nontrivial instance of the matrix-chain multiplication problem requires us to split the product, and that any optimal solution contains within it optimal solutions to subproblem instances. Thus, we can build an optimal solution to an instance of the matrix-chain multiplication problem by splitting the problem into two subproblems (optimally parenthesizing $A_i A_{i+1} \cdots A_k$ and $A_{k+1} A_{k+2} \cdots A_j$), finding optimal solutions to subproblem instances, and then combining these optimal subproblem solutions. We must ensure that when we search for the correct place to split the product, we have considered all possible places, so that we are sure of having examined the optimal one.

Step 2: A recursive solution

Next, we define the cost of an optimal solution recursively in terms of the optimal solutions to subproblems. For the matrix-chain multiplication problem, we pick as our subproblems the problems of determining the minimum cost of parenthesizing $A_i A_{i+1} \cdots A_j$ for $1 \le i \le j \le n$. Let $m[i, j]$ be the minimum number of scalar multiplications needed to compute the matrix $A_{i..j}$; for the full problem, the lowest-cost way to compute $A_{1..n}$ would thus be $m[1, n]$.

We can define $m[i, j]$ recursively as follows. If $i = j$, the problem is trivial; the chain consists of just one matrix $A_{i..i} = A_i$, so that no scalar multiplications are necessary to compute the product. Thus, $m[i, i] = 0$ for $i = 1, 2, \ldots, n$. To compute $m[i, j]$ when $i < j$, we take advantage of the structure of an optimal solution from step 1. Let us assume that to optimally parenthesize, we split the product $A_i A_{i+1} \cdots A_j$ between A_k and A_{k+1}, where $i \le k < j$. Then, $m[i, j]$ equals the minimum cost for computing the subproducts $A_{i..k}$ and $A_{k+1..j}$, plus the cost of multiplying these two matrices together. Recalling that each matrix A_i is $p_{i-1} \times p_i$, we see that computing the matrix product $A_{i..k} A_{k+1..j}$ takes $p_{i-1} p_k p_j$ scalar multiplications. Thus, we obtain

$$m[i, j] = m[i, k] + m[k + 1, j] + p_{i-1} p_k p_j \ .$$

This recursive equation assumes that we know the value of k, which we do not. There are only $j - i$ possible values for k, however, namely $k = i, i + 1, \ldots, j - 1$. Since the optimal parenthesization must use one of these values for k, we need only check them all to find the best. Thus, our recursive definition for the minimum cost of parenthesizing the product $A_i A_{i+1} \cdots A_j$ becomes

$$m[i, j] = \begin{cases} 0 & \text{if } i = j \ , \\ \min\limits_{i \le k < j} \{m[i, k] + m[k + 1, j] + p_{i-1} p_k p_j\} & \text{if } i < j \ . \end{cases} \tag{15.7}$$

The $m[i, j]$ values give the costs of optimal solutions to subproblems, but they do not provide all the information we need to construct an optimal solution. To help us do so, we define $s[i, j]$ to be a value of k at which we split the product $A_i A_{i+1} \cdots A_j$ in an optimal parenthesization. That is, $s[i, j]$ equals a value k such that $m[i, j] = m[i, k] + m[k + 1, j] + p_{i-1} p_k p_j$.

Step 3: Computing the optimal costs

At this point, we could easily write a recursive algorithm based on recurrence (15.7) to compute the minimum cost $m[1, n]$ for multiplying $A_1 A_2 \cdots A_n$. As we saw for the rod-cutting problem, and as we shall see in Section 15.3, this recursive algorithm takes exponential time, which is no better than the brute-force method of checking each way of parenthesizing the product.

Observe that we have relatively few distinct subproblems: one subproblem for each choice of i and j satisfying $1 \le i \le j \le n$, or $\binom{n}{2} + n = \Theta(n^2)$ in all. A recursive algorithm may encounter each subproblem many times in different branches of its recursion tree. This property of overlapping subproblems is the second hallmark of when dynamic programming applies (the first hallmark being optimal substructure).

Instead of computing the solution to recurrence (15.7) recursively, we compute the optimal cost by using a tabular, bottom-up approach. (We present the corresponding top-down approach using memoization in Section 15.3.)

We shall implement the tabular, bottom-up method in the procedure MATRIX-CHAIN-ORDER, which appears below. This procedure assumes that matrix A_i has dimensions $p_{i-1} \times p_i$ for $i = 1, 2, \ldots, n$. Its input is a sequence $p = \langle p_0, p_1, \ldots, p_n \rangle$, where $p.length = n + 1$. The procedure uses an auxiliary table $m[1..n, 1..n]$ for storing the $m[i, j]$ costs and another auxiliary table $s[1..n-1, 2..n]$ that records which index of k achieved the optimal cost in computing $m[i, j]$. We shall use the table s to construct an optimal solution.

In order to implement the bottom-up approach, we must determine which entries of the table we refer to when computing $m[i, j]$. Equation (15.7) shows that the cost $m[i, j]$ of computing a matrix-chain product of $j - i + 1$ matrices depends only on the costs of computing matrix-chain products of fewer than $j - i + 1$ matrices. That is, for $k = i, i + 1, \ldots, j - 1$, the matrix $A_{i..k}$ is a product of $k - i + 1 < j - i + 1$ matrices and the matrix $A_{k+1..j}$ is a product of $j - k < j - i + 1$ matrices. Thus, the algorithm should fill in the table m in a manner that corresponds to solving the parenthesization problem on matrix chains of increasing length. For the subproblem of optimally parenthesizing the chain $A_i A_{i+1} \cdots A_j$, we consider the subproblem size to be the length $j - i + 1$ of the chain.

```
MATRIX-CHAIN-ORDER(p)
 1  n = p.length − 1
 2  let m[1..n, 1..n] and s[1..n − 1, 2..n] be new tables
 3  for i = 1 to n
 4      m[i, i] = 0
 5  for l = 2 to n                  // l is the chain length
 6      for i = 1 to n − l + 1
 7          j = i + l − 1
 8          m[i, j] = ∞
 9          for k = i to j − 1
10              q = m[i, k] + m[k + 1, j] + p_{i−1} p_k p_j
11              if q < m[i, j]
12                  m[i, j] = q
13                  s[i, j] = k
14  return m and s
```

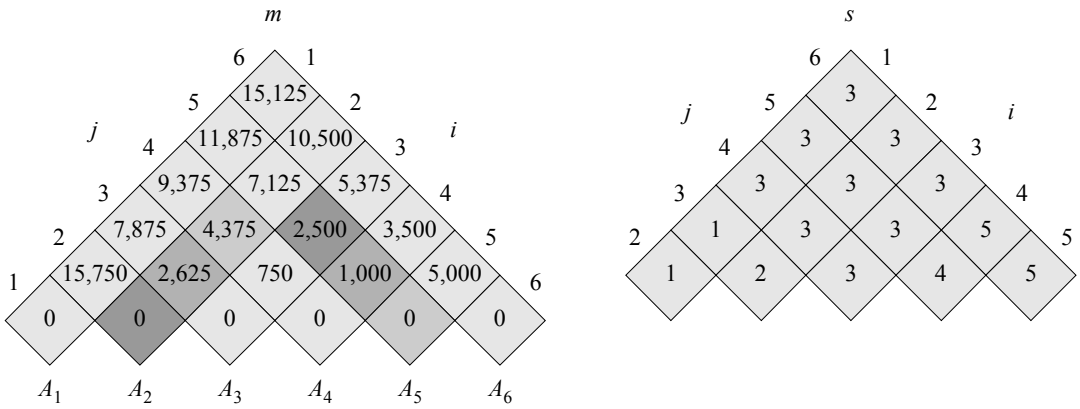


Figure 15.5 The m and s tables computed by MATRIX-CHAIN-ORDER for $n = 6$ and the following matrix dimensions:

matrix	A_1	A_2	A_3	A_4	A_5	A_6
dimension	30×35	35×15	15×5	5×10	10×20	20×25

The tables are rotated so that the main diagonal runs horizontally. The m table uses only the main diagonal and upper triangle, and the s table uses only the upper triangle. The minimum number of scalar multiplications to multiply the 6 matrices is $m[1, 6] = 15{,}125$. Of the darker entries, the pairs that have the same shading are taken together in line 10 when computing

$$
\begin{aligned}
m[2,5] &= \min \begin{cases} m[2,2] + m[3,5] + p_1 p_2 p_5 &= 0 + 2500 + 35 \cdot 15 \cdot 20 &= 13{,}000\,, \\ m[2,3] + m[4,5] + p_1 p_3 p_5 &= 2625 + 1000 + 35 \cdot 5 \cdot 20 &= 7125\,, \\ m[2,4] + m[5,5] + p_1 p_4 p_5 &= 4375 + 0 + 35 \cdot 10 \cdot 20 &= 11{,}375 \end{cases} \\
&= 7125\,.
\end{aligned}
$$

The algorithm first computes $m[i, i] = 0$ for $i = 1, 2, \ldots, n$ (the minimum costs for chains of length 1) in lines 3–4. It then uses recurrence (15.7) to compute $m[i, i + 1]$ for $i = 1, 2, \ldots, n - 1$ (the minimum costs for chains of length $l = 2$) during the first execution of the **for** loop in lines 5–13. The second time through the loop, it computes $m[i, i+2]$ for $i = 1, 2, \ldots, n-2$ (the minimum costs for chains of length $l = 3$), and so forth. At each step, the $m[i, j]$ cost computed in lines 10–13 depends only on table entries $m[i, k]$ and $m[k + 1, j]$ already computed.

Figure 15.5 illustrates this procedure on a chain of $n = 6$ matrices. Since we have defined $m[i, j]$ only for $i \le j$, only the portion of the table m strictly above the main diagonal is used. The figure shows the table rotated to make the main diagonal run horizontally. The matrix chain is listed along the bottom. Using this layout, we can find the minimum cost $m[i, j]$ for multiplying a subchain $A_i A_{i+1} \cdots A_j$ of matrices at the intersection of lines running northeast from A_i and

northwest from A_j. Each horizontal row in the table contains the entries for matrix chains of the same length. MATRIX-CHAIN-ORDER computes the rows from bottom to top and from left to right within each row. It computes each entry $m[i, j]$ using the products $p_{i-1} p_k p_j$ for $k = i, i+1, \ldots, j-1$ and all entries southwest and southeast from $m[i, j]$.

A simple inspection of the nested loop structure of MATRIX-CHAIN-ORDER yields a running time of $O(n^3)$ for the algorithm. The loops are nested three deep, and each loop index (l, i, and k) takes on at most $n-1$ values. Exercise 15.2-5 asks you to show that the running time of this algorithm is in fact also $\Omega(n^3)$. The algorithm requires $\Theta(n^2)$ space to store the m and s tables. Thus, MATRIX-CHAIN-ORDER is much more efficient than the exponential-time method of enumerating all possible parenthesizations and checking each one.

Step 4: Constructing an optimal solution

Although MATRIX-CHAIN-ORDER determines the optimal number of scalar multiplications needed to compute a matrix-chain product, it does not directly show how to multiply the matrices. The table $s[1..n-1, 2..n]$ gives us the information we need to do so. Each entry $s[i, j]$ records a value of k such that an optimal parenthesization of $A_i A_{i+1} \cdots A_j$ splits the product between A_k and A_{k+1}. Thus, we know that the final matrix multiplication in computing $A_{1..n}$ optimally is $A_{1..s[1,n]} A_{s[1,n]+1..n}$. We can determine the earlier matrix multiplications recursively, since $s[1, s[1, n]]$ determines the last matrix multiplication when computing $A_{1..s[1,n]}$ and $s[s[1, n] + 1, n]$ determines the last matrix multiplication when computing $A_{s[1,n]+1..n}$. The following recursive procedure prints an optimal parenthesization of $\langle A_i, A_{i+1}, \ldots, A_j \rangle$, given the s table computed by MATRIX-CHAIN-ORDER and the indices i and j. The initial call PRINT-OPTIMAL-PARENS$(s, 1, n)$ prints an optimal parenthesization of $\langle A_1, A_2, \ldots, A_n \rangle$.

```
PRINT-OPTIMAL-PARENS(s, i, j)
1  if i == j
2       print "A"_i
3  else print "("
4       PRINT-OPTIMAL-PARENS(s, i, s[i, j])
5       PRINT-OPTIMAL-PARENS(s, s[i, j] + 1, j)
6       print ")"
```

In the example of Figure 15.5, the call PRINT-OPTIMAL-PARENS$(s, 1, 6)$ prints the parenthesization $((A_1(A_2A_3))((A_4A_5)A_6))$.

Exercises

15.2-1
Find an optimal parenthesization of a matrix-chain product whose sequence of dimensions is $\langle 5, 10, 3, 12, 5, 50, 6 \rangle$.

15.2-2
Give a recursive algorithm MATRIX-CHAIN-MULTIPLY(A, s, i, j) that actually performs the optimal matrix-chain multiplication, given the sequence of matrices $\langle A_1, A_2, \ldots, A_n \rangle$, the s table computed by MATRIX-CHAIN-ORDER, and the indices i and j. (The initial call would be MATRIX-CHAIN-MULTIPLY$(A, s, 1, n)$.)

15.2-3
Use the substitution method to show that the solution to the recurrence (15.6) is $\Omega(2^n)$.

15.2-4
Describe the subproblem graph for matrix-chain multiplication with an input chain of length n. How many vertices does it have? How many edges does it have, and which edges are they?

15.2-5
Let $R(i, j)$ be the number of times that table entry $m[i, j]$ is referenced while computing other table entries in a call of MATRIX-CHAIN-ORDER. Show that the total number of references for the entire table is

$$\sum_{i=1}^{n} \sum_{j=i}^{n} R(i, j) = \frac{n^3 - n}{3} .$$

(*Hint:* You may find equation (A.3) useful.)

15.2-6
Show that a full parenthesization of an n-element expression has exactly $n - 1$ pairs of parentheses.

15.3 Elements of dynamic programming

Although we have just worked through two examples of the dynamic-programming method, you might still be wondering just when the method applies. From an engineering perspective, when should we look for a dynamic-programming solution to a problem? In this section, we examine the two key ingredients that an opti-

mization problem must have in order for dynamic programming to apply: optimal substructure and overlapping subproblems. We also revisit and discuss more fully how memoization might help us take advantage of the overlapping-subproblems property in a top-down recursive approach.

Optimal substructure

The first step in solving an optimization problem by dynamic programming is to characterize the structure of an optimal solution. Recall that a problem exhibits ***optimal substructure*** if an optimal solution to the problem contains within it optimal solutions to subproblems. Whenever a problem exhibits optimal substructure, we have a good clue that dynamic programming might apply. (As Chapter 16 discusses, it also might mean that a greedy strategy applies, however.) In dynamic programming, we build an optimal solution to the problem from optimal solutions to subproblems. Consequently, we must take care to ensure that the range of subproblems we consider includes those used in an optimal solution.

We discovered optimal substructure in both of the problems we have examined in this chapter so far. In Section 15.1, we observed that the optimal way of cutting up a rod of length n (if we make any cuts at all) involves optimally cutting up the two pieces resulting from the first cut. In Section 15.2, we observed that an optimal parenthesization of $A_i A_{i+1} \cdots A_j$ that splits the product between A_k and A_{k+1} contains within it optimal solutions to the problems of parenthesizing $A_i A_{i+1} \cdots A_k$ and $A_{k+1} A_{k+2} \cdots A_j$.

You will find yourself following a common pattern in discovering optimal substructure:

1. You show that a solution to the problem consists of making a choice, such as choosing an initial cut in a rod or choosing an index at which to split the matrix chain. Making this choice leaves one or more subproblems to be solved.
2. You suppose that for a given problem, you are given the choice that leads to an optimal solution. You do not concern yourself yet with how to determine this choice. You just assume that it has been given to you.
3. Given this choice, you determine which subproblems ensue and how to best characterize the resulting space of subproblems.
4. You show that the solutions to the subproblems used within an optimal solution to the problem must themselves be optimal by using a "cut-and-paste" technique. You do so by supposing that each of the subproblem solutions is not optimal and then deriving a contradiction. In particular, by "cutting out" the nonoptimal solution to each subproblem and "pasting in" the optimal one, you show that you can get a better solution to the original problem, thus contradicting your supposition that you already had an optimal solution. If an optimal

solution gives rise to more than one subproblem, they are typically so similar that you can modify the cut-and-paste argument for one to apply to the others with little effort.

To characterize the space of subproblems, a good rule of thumb says to try to keep the space as simple as possible and then expand it as necessary. For example, the space of subproblems that we considered for the rod-cutting problem contained the problems of optimally cutting up a rod of length i for each size i. This subproblem space worked well, and we had no need to try a more general space of subproblems.

Conversely, suppose that we had tried to constrain our subproblem space for matrix-chain multiplication to matrix products of the form $A_1 A_2 \cdots A_j$. As before, an optimal parenthesization must split this product between A_k and A_{k+1} for some $1 \le k < j$. Unless we could guarantee that k always equals $j - 1$, we would find that we had subproblems of the form $A_1 A_2 \cdots A_k$ and $A_{k+1} A_{k+2} \cdots A_j$, and that the latter subproblem is not of the form $A_1 A_2 \cdots A_j$. For this problem, we needed to allow our subproblems to vary at "both ends," that is, to allow both i and j to vary in the subproblem $A_i A_{i+1} \cdots A_j$.

Optimal substructure varies across problem domains in two ways:

1. how many subproblems an optimal solution to the original problem uses, and
2. how many choices we have in determining which subproblem(s) to use in an optimal solution.

In the rod-cutting problem, an optimal solution for cutting up a rod of size n uses just one subproblem (of size $n - i$), but we must consider n choices for i in order to determine which one yields an optimal solution. Matrix-chain multiplication for the subchain $A_i A_{i+1} \cdots A_j$ serves as an example with two subproblems and $j - i$ choices. For a given matrix A_k at which we split the product, we have two subproblems—parenthesizing $A_i A_{i+1} \cdots A_k$ and parenthesizing $A_{k+1} A_{k+2} \cdots A_j$—and we must solve *both* of them optimally. Once we determine the optimal solutions to subproblems, we choose from among $j - i$ candidates for the index k.

Informally, the running time of a dynamic-programming algorithm depends on the product of two factors: the number of subproblems overall and how many choices we look at for each subproblem. In rod cutting, we had $\Theta(n)$ subproblems overall, and at most n choices to examine for each, yielding an $O(n^2)$ running time. Matrix-chain multiplication had $\Theta(n^2)$ subproblems overall, and in each we had at most $n - 1$ choices, giving an $O(n^3)$ running time (actually, a $\Theta(n^3)$ running time, by Exercise 15.2-5).

Usually, the subproblem graph gives an alternative way to perform the same analysis. Each vertex corresponds to a subproblem, and the choices for a sub-

problem are the edges incident to that subproblem. Recall that in rod cutting, the subproblem graph had n vertices and at most n edges per vertex, yielding an $O(n^2)$ running time. For matrix-chain multiplication, if we were to draw the subproblem graph, it would have $\Theta(n^2)$ vertices and each vertex would have degree at most $n - 1$, giving a total of $O(n^3)$ vertices and edges.

Dynamic programming often uses optimal substructure in a bottom-up fashion. That is, we first find optimal solutions to subproblems and, having solved the subproblems, we find an optimal solution to the problem. Finding an optimal solution to the problem entails making a choice among subproblems as to which we will use in solving the problem. The cost of the problem solution is usually the subproblem costs plus a cost that is directly attributable to the choice itself. In rod cutting, for example, first we solved the subproblems of determining optimal ways to cut up rods of length i for $i = 0, 1, \ldots, n - 1$, and then we determined which such subproblem yielded an optimal solution for a rod of length n, using equation (15.2). The cost attributable to the choice itself is the term p_i in equation (15.2). In matrix-chain multiplication, we determined optimal parenthesizations of subchains of $A_i A_{i+1} \cdots A_j$, and then we chose the matrix A_k at which to split the product. The cost attributable to the choice itself is the term $p_{i-1} p_k p_j$.

In Chapter 16, we shall examine "greedy algorithms," which have many similarities to dynamic programming. In particular, problems to which greedy algorithms apply have optimal substructure. One major difference between greedy algorithms and dynamic programming is that instead of first finding optimal solutions to subproblems and then making an informed choice, greedy algorithms first make a "greedy" choice—the choice that looks best at the time—and then solve a resulting subproblem, without bothering to solve all possible related smaller subproblems. Surprisingly, in some cases this strategy works!

Subtleties

You should be careful not to assume that optimal substructure applies when it does not. Consider the following two problems in which we are given a directed graph $G = (V, E)$ and vertices $u, v \in V$.

Unweighted shortest path:[3] Find a path from u to v consisting of the fewest edges. Such a path must be simple, since removing a cycle from a path produces a path with fewer edges.

---

[3]We use the term "unweighted" to distinguish this problem from that of finding shortest paths with weighted edges, which we shall see in Chapters 24 and 25. We can use the breadth-first search technique of Chapter 22 to solve the unweighted problem.

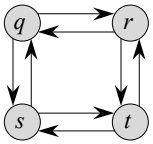


Figure 15.6 A directed graph showing that the problem of finding a longest simple path in an unweighted directed graph does not have optimal substructure. The path $q \to r \to t$ is a longest simple path from q to t, but the subpath $q \to r$ is not a longest simple path from q to r, nor is the subpath $r \to t$ a longest simple path from r to t.

Unweighted longest simple path: Find a simple path from u to v consisting of the most edges. We need to include the requirement of simplicity because otherwise we can traverse a cycle as many times as we like to create paths with an arbitrarily large number of edges.

The unweighted shortest-path problem exhibits optimal substructure, as follows. Suppose that $u \neq v$, so that the problem is nontrivial. Then, any path p from u to v must contain an intermediate vertex, say w. (Note that w may be u or v.) Thus, we can decompose the path $u \overset{p}{\rightsquigarrow} v$ into subpaths $u \overset{p_1}{\rightsquigarrow} w \overset{p_2}{\rightsquigarrow} v$. Clearly, the number of edges in p equals the number of edges in p_1 plus the number of edges in p_2. We claim that if p is an optimal (i.e., shortest) path from u to v, then p_1 must be a shortest path from u to w. Why? We use a "cut-and-paste" argument: if there were another path, say p_1', from u to w with fewer edges than p_1, then we could cut out p_1 and paste in p_1' to produce a path $u \overset{p_1'}{\rightsquigarrow} w \overset{p_2}{\rightsquigarrow} v$ with fewer edges than p, thus contradicting p's optimality. Symmetrically, p_2 must be a shortest path from w to v. Thus, we can find a shortest path from u to v by considering all intermediate vertices w, finding a shortest path from u to w and a shortest path from w to v, and choosing an intermediate vertex w that yields the overall shortest path. In Section 25.2, we use a variant of this observation of optimal substructure to find a shortest path between every pair of vertices on a weighted, directed graph.

You might be tempted to assume that the problem of finding an unweighted longest simple path exhibits optimal substructure as well. After all, if we decompose a longest simple path $u \overset{p}{\rightsquigarrow} v$ into subpaths $u \overset{p_1}{\rightsquigarrow} w \overset{p_2}{\rightsquigarrow} v$, then mustn't p_1 be a longest simple path from u to w, and mustn't p_2 be a longest simple path from w to v? The answer is no! Figure 15.6 supplies an example. Consider the path $q \to r \to t$, which is a longest simple path from q to t. Is $q \to r$ a longest simple path from q to r? No, for the path $q \to s \to t \to r$ is a simple path that is longer. Is $r \to t$ a longest simple path from r to t? No again, for the path $r \to q \to s \to t$ is a simple path that is longer.

This example shows that for longest simple paths, not only does the problem lack optimal substructure, but we cannot necessarily assemble a "legal" solution to the problem from solutions to subproblems. If we combine the longest simple paths $q \to s \to t \to r$ and $r \to q \to s \to t$, we get the path $q \to s \to t \to r \to q \to s \to t$, which is not simple. Indeed, the problem of finding an unweighted longest simple path does not appear to have any sort of optimal substructure. No efficient dynamic-programming algorithm for this problem has ever been found. In fact, this problem is NP-complete, which—as we shall see in Chapter 34—means that we are unlikely to find a way to solve it in polynomial time.

Why is the substructure of a longest simple path so different from that of a shortest path? Although a solution to a problem for both longest and shortest paths uses two subproblems, the subproblems in finding the longest simple path are not ***independent***, whereas for shortest paths they are. What do we mean by subproblems being independent? We mean that the solution to one subproblem does not affect the solution to another subproblem of the same problem. For the example of Figure 15.6, we have the problem of finding a longest simple path from q to t with two subproblems: finding longest simple paths from q to r and from r to t. For the first of these subproblems, we choose the path $q \to s \to t \to r$, and so we have also used the vertices s and t. We can no longer use these vertices in the second subproblem, since the combination of the two solutions to subproblems would yield a path that is not simple. If we cannot use vertex t in the second problem, then we cannot solve it at all, since t is required to be on the path that we find, and it is not the vertex at which we are "splicing" together the subproblem solutions (that vertex being r). Because we use vertices s and t in one subproblem solution, we cannot use them in the other subproblem solution. We must use at least one of them to solve the other subproblem, however, and we must use both of them to solve it optimally. Thus, we say that these subproblems are not independent. Looked at another way, using resources in solving one subproblem (those resources being vertices) renders them unavailable for the other subproblem.

Why, then, are the subproblems independent for finding a shortest path? The answer is that by nature, the subproblems do not share resources. We claim that if a vertex w is on a shortest path p from u to v, then we can splice together *any* shortest path $u \overset{p_1}{\rightsquigarrow} w$ and *any* shortest path $w \overset{p_2}{\rightsquigarrow} v$ to produce a shortest path from u to v. We are assured that, other than w, no vertex can appear in both paths p_1 and p_2. Why? Suppose that some vertex $x \neq w$ appears in both p_1 and p_2, so that we can decompose p_1 as $u \overset{p_{ux}}{\rightsquigarrow} x \rightsquigarrow w$ and p_2 as $w \rightsquigarrow x \overset{p_{xv}}{\rightsquigarrow} v$. By the optimal substructure of this problem, path p has as many edges as p_1 and p_2 together; let's say that p has e edges. Now let us construct a path $p' = u \overset{p_{ux}}{\rightsquigarrow} x \overset{p_{xv}}{\rightsquigarrow} v$ from u to v. Because we have excised the paths from x to w and from w to x, each of which contains at least one edge, path p' contains at most $e - 2$ edges, which contradicts

the assumption that p is a shortest path. Thus, we are assured that the subproblems for the shortest-path problem are independent.

Both problems examined in Sections 15.1 and 15.2 have independent subproblems. In matrix-chain multiplication, the subproblems are multiplying subchains $A_i A_{i+1} \cdots A_k$ and $A_{k+1} A_{k+2} \cdots A_j$. These subchains are disjoint, so that no matrix could possibly be included in both of them. In rod cutting, to determine the best way to cut up a rod of length n, we look at the best ways of cutting up rods of length i for $i = 0, 1, \ldots, n-1$. Because an optimal solution to the length-n problem includes just one of these subproblem solutions (after we have cut off the first piece), independence of subproblems is not an issue.

Overlapping subproblems

The second ingredient that an optimization problem must have for dynamic programming to apply is that the space of subproblems must be "small" in the sense that a recursive algorithm for the problem solves the same subproblems over and over, rather than always generating new subproblems. Typically, the total number of distinct subproblems is a polynomial in the input size. When a recursive algorithm revisits the same problem repeatedly, we say that the optimization problem has ***overlapping subproblems***.[4] In contrast, a problem for which a divide-and-conquer approach is suitable usually generates brand-new problems at each step of the recursion. Dynamic-programming algorithms typically take advantage of overlapping subproblems by solving each subproblem once and then storing the solution in a table where it can be looked up when needed, using constant time per lookup.

In Section 15.1, we briefly examined how a recursive solution to rod cutting makes exponentially many calls to find solutions of smaller subproblems. Our dynamic-programming solution takes an exponential-time recursive algorithm down to quadratic time.

To illustrate the overlapping-subproblems property in greater detail, let us reexamine the matrix-chain multiplication problem. Referring back to Figure 15.5, observe that MATRIX-CHAIN-ORDER repeatedly looks up the solution to subproblems in lower rows when solving subproblems in higher rows. For example, it references entry $m[3, 4]$ four times: during the computations of $m[2, 4]$, $m[1, 4]$,

[4] It may seem strange that dynamic programming relies on subproblems being both independent and overlapping. Although these requirements may sound contradictory, they describe two different notions, rather than two points on the same axis. Two subproblems of the same problem are independent if they do not share resources. Two subproblems are overlapping if they are really the same subproblem that occurs as a subproblem of different problems.

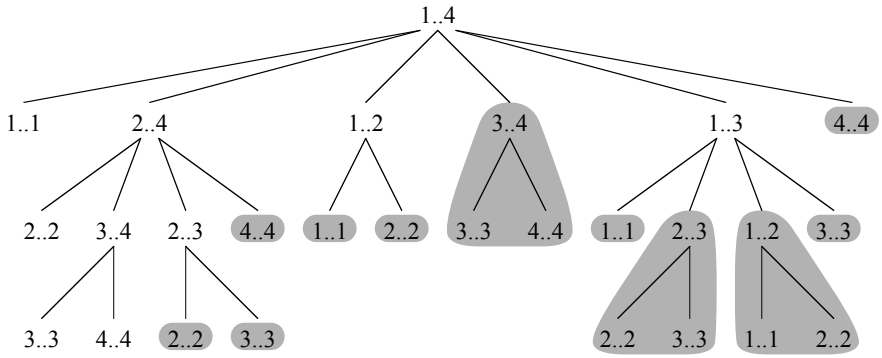


Figure 15.7 The recursion tree for the computation of RECURSIVE-MATRIX-CHAIN$(p, 1, 4)$. Each node contains the parameters i and j. The computations performed in a shaded subtree are replaced by a single table lookup in MEMOIZED-MATRIX-CHAIN.

$m[3, 5]$, and $m[3, 6]$. If we were to recompute $m[3, 4]$ each time, rather than just looking it up, the running time would increase dramatically. To see how, consider the following (inefficient) recursive procedure that determines $m[i, j]$, the minimum number of scalar multiplications needed to compute the matrix-chain product $A_{i..j} = A_i A_{i+1} \cdots A_j$. The procedure is based directly on the recurrence (15.7).

```
RECURSIVE-MATRIX-CHAIN(p, i, j)
1  if i == j
2      return 0
3  m[i, j] = ∞
4  for k = i to j − 1
5      q = RECURSIVE-MATRIX-CHAIN(p, i, k)
             + RECURSIVE-MATRIX-CHAIN(p, k + 1, j)
             + p_{i−1} p_k p_j
6      if q < m[i, j]
7          m[i, j] = q
8  return m[i, j]
```

Figure 15.7 shows the recursion tree produced by the call RECURSIVE-MATRIX-CHAIN$(p, 1, 4)$. Each node is labeled by the values of the parameters i and j. Observe that some pairs of values occur many times.

In fact, we can show that the time to compute $m[1, n]$ by this recursive procedure is at least exponential in n. Let $T(n)$ denote the time taken by RECURSIVE-MATRIX-CHAIN to compute an optimal parenthesization of a chain of n matrices. Because the execution of lines 1–2 and of lines 6–7 each take at least unit time, as

does the multiplication in line 5, inspection of the procedure yields the recurrence

$$\begin{aligned} T(1) &\geq 1 , \\ T(n) &\geq 1 + \sum_{k=1}^{n-1} (T(k) + T(n-k) + 1) \qquad \text{for } n > 1 . \end{aligned}$$

Noting that for $i = 1, 2, \ldots, n-1$, each term $T(i)$ appears once as $T(k)$ and once as $T(n-k)$, and collecting the $n-1$ 1s in the summation together with the 1 out front, we can rewrite the recurrence as

$$T(n) \geq 2 \sum_{i=1}^{n-1} T(i) + n . \tag{15.8}$$

We shall prove that $T(n) = \Omega(2^n)$ using the substitution method. Specifically, we shall show that $T(n) \geq 2^{n-1}$ for all $n \geq 1$. The basis is easy, since $T(1) \geq 1 = 2^0$. Inductively, for $n \geq 2$ we have

$$\begin{aligned} T(n) &\geq 2 \sum_{i=1}^{n-1} 2^{i-1} + n \\ &= 2 \sum_{i=0}^{n-2} 2^i + n \\ &= 2(2^{n-1} - 1) + n \quad \text{(by equation (A.5))} \\ &= 2^n - 2 + n \\ &\geq 2^{n-1} , \end{aligned}$$

which completes the proof. Thus, the total amount of work performed by the call RECURSIVE-MATRIX-CHAIN$(p, 1, n)$ is at least exponential in n.

Compare this top-down, recursive algorithm (without memoization) with the bottom-up dynamic-programming algorithm. The latter is more efficient because it takes advantage of the overlapping-subproblems property. Matrix-chain multiplication has only $\Theta(n^2)$ distinct subproblems, and the dynamic-programming algorithm solves each exactly once. The recursive algorithm, on the other hand, must again solve each subproblem every time it reappears in the recursion tree. Whenever a recursion tree for the natural recursive solution to a problem contains the same subproblem repeatedly, and the total number of distinct subproblems is small, dynamic programming can improve efficiency, sometimes dramatically.

Reconstructing an optimal solution

As a practical matter, we often store which choice we made in each subproblem in a table so that we do not have to reconstruct this information from the costs that we stored.

For matrix-chain multiplication, the table $s[i, j]$ saves us a significant amount of work when reconstructing an optimal solution. Suppose that we did not maintain the $s[i, j]$ table, having filled in only the table $m[i, j]$ containing optimal subproblem costs. We choose from among $j - i$ possibilities when we determine which subproblems to use in an optimal solution to parenthesizing $A_i A_{i+1} \cdots A_j$, and $j - i$ is not a constant. Therefore, it would take $\Theta(j - i) = \omega(1)$ time to reconstruct which subproblems we chose for a solution to a given problem. By storing in $s[i, j]$ the index of the matrix at which we split the product $A_i A_{i+1} \cdots A_j$, we can reconstruct each choice in $O(1)$ time.

Memoization

As we saw for the rod-cutting problem, there is an alternative approach to dynamic programming that often offers the efficiency of the bottom-up dynamic-programming approach while maintaining a top-down strategy. The idea is to ***memoize*** the natural, but inefficient, recursive algorithm. As in the bottom-up approach, we maintain a table with subproblem solutions, but the control structure for filling in the table is more like the recursive algorithm.

A memoized recursive algorithm maintains an entry in a table for the solution to each subproblem. Each table entry initially contains a special value to indicate that the entry has yet to be filled in. When the subproblem is first encountered as the recursive algorithm unfolds, its solution is computed and then stored in the table. Each subsequent time that we encounter this subproblem, we simply look up the value stored in the table and return it.[5]

Here is a memoized version of RECURSIVE-MATRIX-CHAIN. Note where it resembles the memoized top-down method for the rod-cutting problem.

---

[5] This approach presupposes that we know the set of all possible subproblem parameters and that we have established the relationship between table positions and subproblems. Another, more general, approach is to memoize by using hashing with the subproblem parameters as keys.

```
MEMOIZED-MATRIX-CHAIN(p)
1  n = p.length − 1
2  let m[1..n, 1..n] be a new table
3  for i = 1 to n
4      for j = i to n
5          m[i, j] = ∞
6  return LOOKUP-CHAIN(m, p, 1, n)

LOOKUP-CHAIN(m, p, i, j)
1  if m[i, j] < ∞
2      return m[i, j]
3  if i == j
4      m[i, j] = 0
5  else for k = i to j − 1
6          q = LOOKUP-CHAIN(m, p, i, k)
                + LOOKUP-CHAIN(m, p, k + 1, j) + p_{i−1} p_k p_j
7          if q < m[i, j]
8              m[i, j] = q
9  return m[i, j]
```

The MEMOIZED-MATRIX-CHAIN procedure, like MATRIX-CHAIN-ORDER, maintains a table $m[1..n, 1..n]$ of computed values of $m[i, j]$, the minimum number of scalar multiplications needed to compute the matrix $A_{i..j}$. Each table entry initially contains the value ∞ to indicate that the entry has yet to be filled in. Upon calling LOOKUP-CHAIN(m, p, i, j), if line 1 finds that $m[i, j] < \infty$, then the procedure simply returns the previously computed cost $m[i, j]$ in line 2. Otherwise, the cost is computed as in RECURSIVE-MATRIX-CHAIN, stored in $m[i, j]$, and returned. Thus, LOOKUP-CHAIN(m, p, i, j) always returns the value of $m[i, j]$, but it computes it only upon the first call of LOOKUP-CHAIN with these specific values of i and j.

Figure 15.7 illustrates how MEMOIZED-MATRIX-CHAIN saves time compared with RECURSIVE-MATRIX-CHAIN. Shaded subtrees represent values that it looks up rather than recomputes.

Like the bottom-up dynamic-programming algorithm MATRIX-CHAIN-ORDER, the procedure MEMOIZED-MATRIX-CHAIN runs in $O(n^3)$ time. Line 5 of MEMOIZED-MATRIX-CHAIN executes $\Theta(n^2)$ times. We can categorize the calls of LOOKUP-CHAIN into two types:

1. calls in which $m[i, j] = \infty$, so that lines 3–9 execute, and
2. calls in which $m[i, j] < \infty$, so that LOOKUP-CHAIN simply returns in line 2.

There are $\Theta(n^2)$ calls of the first type, one per table entry. All calls of the second type are made as recursive calls by calls of the first type. Whenever a given call of LOOKUP-CHAIN makes recursive calls, it makes $O(n)$ of them. Therefore, there are $O(n^3)$ calls of the second type in all. Each call of the second type takes $O(1)$ time, and each call of the first type takes $O(n)$ time plus the time spent in its recursive calls. The total time, therefore, is $O(n^3)$. Memoization thus turns an $\Omega(2^n)$-time algorithm into an $O(n^3)$-time algorithm.

In summary, we can solve the matrix-chain multiplication problem by either a top-down, memoized dynamic-programming algorithm or a bottom-up dynamic-programming algorithm in $O(n^3)$ time. Both methods take advantage of the overlapping-subproblems property. There are only $\Theta(n^2)$ distinct subproblems in total, and either of these methods computes the solution to each subproblem only once. Without memoization, the natural recursive algorithm runs in exponential time, since solved subproblems are repeatedly solved.

In general practice, if all subproblems must be solved at least once, a bottom-up dynamic-programming algorithm usually outperforms the corresponding top-down memoized algorithm by a constant factor, because the bottom-up algorithm has no overhead for recursion and less overhead for maintaining the table. Moreover, for some problems we can exploit the regular pattern of table accesses in the dynamic-programming algorithm to reduce time or space requirements even further. Alternatively, if some subproblems in the subproblem space need not be solved at all, the memoized solution has the advantage of solving only those subproblems that are definitely required.

Exercises

15.3-1

Which is a more efficient way to determine the optimal number of multiplications in a matrix-chain multiplication problem: enumerating all the ways of parenthesizing the product and computing the number of multiplications for each, or running RECURSIVE-MATRIX-CHAIN? Justify your answer.

15.3-2

Draw the recursion tree for the MERGE-SORT procedure from Section 2.3.1 on an array of 16 elements. Explain why memoization fails to speed up a good divide-and-conquer algorithm such as MERGE-SORT.

15.3-3

Consider a variant of the matrix-chain multiplication problem in which the goal is to parenthesize the sequence of matrices so as to maximize, rather than minimize,

the number of scalar multiplications. Does this problem exhibit optimal substructure?

15.3-4

As stated, in dynamic programming we first solve the subproblems and then choose which of them to use in an optimal solution to the problem. Professor Capulet claims that we do not always need to solve all the subproblems in order to find an optimal solution. She suggests that we can find an optimal solution to the matrix-chain multiplication problem by always choosing the matrix A_k at which to split the subproduct $A_i A_{i+1} \cdots A_j$ (by selecting k to minimize the quantity $p_{i-1} p_k p_j$) *before* solving the subproblems. Find an instance of the matrix-chain multiplication problem for which this greedy approach yields a suboptimal solution.

15.3-5

Suppose that in the rod-cutting problem of Section 15.1, we also had limit l_i on the number of pieces of length i that we are allowed to produce, for $i = 1, 2, \ldots, n$. Show that the optimal-substructure property described in Section 15.1 no longer holds.

15.3-6

Imagine that you wish to exchange one currency for another. You realize that instead of directly exchanging one currency for another, you might be better off making a series of trades through other currencies, winding up with the currency you want. Suppose that you can trade n different currencies, numbered $1, 2, \ldots, n$, where you start with currency 1 and wish to wind up with currency n. You are given, for each pair of currencies i and j, an exchange rate r_{ij}, meaning that if you start with d units of currency i, you can trade for $d r_{ij}$ units of currency j. A sequence of trades may entail a commission, which depends on the number of trades you make. Let c_k be the commission that you are charged when you make k trades. Show that, if $c_k = 0$ for all $k = 1, 2, \ldots, n$, then the problem of finding the best sequence of exchanges from currency 1 to currency n exhibits optimal substructure. Then show that if commissions c_k are arbitrary values, then the problem of finding the best sequence of exchanges from currency 1 to currency n does not necessarily exhibit optimal substructure.

15.4 Longest common subsequence

Biological applications often need to compare the DNA of two (or more) different organisms. A strand of DNA consists of a string of molecules called

bases, where the possible bases are adenine, guanine, cytosine, and thymine. Representing each of these bases by its initial letter, we can express a strand of DNA as a string over the finite set $\{\mathtt{A}, \mathtt{C}, \mathtt{G}, \mathtt{T}\}$. (See Appendix C for the definition of a string.) For example, the DNA of one organism may be $S_1 = \mathtt{ACCGGTCGAGTGCGCGGAAGCCGGCCGAA}$, and the DNA of another organism may be $S_2 = \mathtt{GTCGTTCGGAATGCCGTTGCTCTGTAAA}$. One reason to compare two strands of DNA is to determine how "similar" the two strands are, as some measure of how closely related the two organisms are. We can, and do, define similarity in many different ways. For example, we can say that two DNA strands are similar if one is a substring of the other. (Chapter 32 explores algorithms to solve this problem.) In our example, neither S_1 nor S_2 is a substring of the other. Alternatively, we could say that two strands are similar if the number of changes needed to turn one into the other is small. (Problem 15-5 looks at this notion.) Yet another way to measure the similarity of strands S_1 and S_2 is by finding a third strand S_3 in which the bases in S_3 appear in each of S_1 and S_2; these bases must appear in the same order, but not necessarily consecutively. The longer the strand S_3 we can find, the more similar S_1 and S_2 are. In our example, the longest strand S_3 is $\mathtt{GTCGTCGGAAGCCGGCCGAA}$.

We formalize this last notion of similarity as the longest-common-subsequence problem. A subsequence of a given sequence is just the given sequence with zero or more elements left out. Formally, given a sequence $X = \langle x_1, x_2, \ldots, x_m \rangle$, another sequence $Z = \langle z_1, z_2, \ldots, z_k \rangle$ is a ***subsequence*** of X if there exists a strictly increasing sequence $\langle i_1, i_2, \ldots, i_k \rangle$ of indices of X such that for all $j = 1, 2, \ldots, k$, we have $x_{i_j} = z_j$. For example, $Z = \langle B, C, D, B \rangle$ is a subsequence of $X = \langle A, B, C, B, D, A, B \rangle$ with corresponding index sequence $\langle 2, 3, 5, 7 \rangle$.

Given two sequences X and Y, we say that a sequence Z is a ***common subsequence*** of X and Y if Z is a subsequence of both X and Y. For example, if $X = \langle A, B, C, B, D, A, B \rangle$ and $Y = \langle B, D, C, A, B, A \rangle$, the sequence $\langle B, C, A \rangle$ is a common subsequence of both X and Y. The sequence $\langle B, C, A \rangle$ is not a *longest* common subsequence (LCS) of X and Y, however, since it has length 3 and the sequence $\langle B, C, B, A \rangle$, which is also common to both X and Y, has length 4. The sequence $\langle B, C, B, A \rangle$ is an LCS of X and Y, as is the sequence $\langle B, D, A, B \rangle$, since X and Y have no common subsequence of length 5 or greater.

In the ***longest-common-subsequence problem***, we are given two sequences $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Y = \langle y_1, y_2, \ldots, y_n \rangle$ and wish to find a maximum-length common subsequence of X and Y. This section shows how to efficiently solve the LCS problem using dynamic programming.

Step 1: Characterizing a longest common subsequence

In a brute-force approach to solving the LCS problem, we would enumerate all subsequences of X and check each subsequence to see whether it is also a subsequence of Y, keeping track of the longest subsequence we find. Each subsequence of X corresponds to a subset of the indices $\{1, 2, \ldots, m\}$ of X. Because X has 2^m subsequences, this approach requires exponential time, making it impractical for long sequences.

The LCS problem has an optimal-substructure property, however, as the following theorem shows. As we shall see, the natural classes of subproblems correspond to pairs of "prefixes" of the two input sequences. To be precise, given a sequence $X = \langle x_1, x_2, \ldots, x_m \rangle$, we define the ith ***prefix*** of X, for $i = 0, 1, \ldots, m$, as $X_i = \langle x_1, x_2, \ldots, x_i \rangle$. For example, if $X = \langle A, B, C, B, D, A, B \rangle$, then $X_4 = \langle A, B, C, B \rangle$ and X_0 is the empty sequence.

Theorem 15.1 (Optimal substructure of an LCS)
Let $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Y = \langle y_1, y_2, \ldots, y_n \rangle$ be sequences, and let $Z = \langle z_1, z_2, \ldots, z_k \rangle$ be any LCS of X and Y.

1. If $x_m = y_n$, then $z_k = x_m = y_n$ and Z_{k-1} is an LCS of X_{m-1} and Y_{n-1}.
2. If $x_m \neq y_n$, then $z_k \neq x_m$ implies that Z is an LCS of X_{m-1} and Y.
3. If $x_m \neq y_n$, then $z_k \neq y_n$ implies that Z is an LCS of X and Y_{n-1}.

Proof (1) If $z_k \neq x_m$, then we could append $x_m = y_n$ to Z to obtain a common subsequence of X and Y of length $k + 1$, contradicting the supposition that Z is a *longest* common subsequence of X and Y. Thus, we must have $z_k = x_m = y_n$. Now, the prefix Z_{k-1} is a length-$(k - 1)$ common subsequence of X_{m-1} and Y_{n-1}. We wish to show that it is an LCS. Suppose for the purpose of contradiction that there exists a common subsequence W of X_{m-1} and Y_{n-1} with length greater than $k - 1$. Then, appending $x_m = y_n$ to W produces a common subsequence of X and Y whose length is greater than k, which is a contradiction.

(2) If $z_k \neq x_m$, then Z is a common subsequence of X_{m-1} and Y. If there were a common subsequence W of X_{m-1} and Y with length greater than k, then W would also be a common subsequence of X_m and Y, contradicting the assumption that Z is an LCS of X and Y.

(3) The proof is symmetric to (2). ■

The way that Theorem 15.1 characterizes longest common subsequences tells us that an LCS of two sequences contains within it an LCS of prefixes of the two sequences. Thus, the LCS problem has an optimal-substructure property. A recur-

sive solution also has the overlapping-subproblems property, as we shall see in a moment.

Step 2: A recursive solution

Theorem 15.1 implies that we should examine either one or two subproblems when finding an LCS of $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Y = \langle y_1, y_2, \ldots, y_n \rangle$. If $x_m = y_n$, we must find an LCS of X_{m-1} and Y_{n-1}. Appending $x_m = y_n$ to this LCS yields an LCS of X and Y. If $x_m \neq y_n$, then we must solve two subproblems: finding an LCS of X_{m-1} and Y and finding an LCS of X and Y_{n-1}. Whichever of these two LCSs is longer is an LCS of X and Y. Because these cases exhaust all possibilities, we know that one of the optimal subproblem solutions must appear within an LCS of X and Y.

We can readily see the overlapping-subproblems property in the LCS problem. To find an LCS of X and Y, we may need to find the LCSs of X and Y_{n-1} and of X_{m-1} and Y. But each of these subproblems has the subsubproblem of finding an LCS of X_{m-1} and Y_{n-1}. Many other subproblems share subsubproblems.

As in the matrix-chain multiplication problem, our recursive solution to the LCS problem involves establishing a recurrence for the value of an optimal solution. Let us define $c[i, j]$ to be the length of an LCS of the sequences X_i and Y_j. If either $i = 0$ or $j = 0$, one of the sequences has length 0, and so the LCS has length 0. The optimal substructure of the LCS problem gives the recursive formula

$$c[i, j] = \begin{cases} 0 & \text{if } i = 0 \text{ or } j = 0 , \\ c[i-1, j-1] + 1 & \text{if } i, j > 0 \text{ and } x_i = y_j , \\ \max(c[i, j-1], c[i-1, j]) & \text{if } i, j > 0 \text{ and } x_i \neq y_j . \end{cases} \tag{15.9}$$

Observe that in this recursive formulation, a condition in the problem restricts which subproblems we may consider. When $x_i = y_j$, we can and should consider the subproblem of finding an LCS of X_{i-1} and Y_{j-1}. Otherwise, we instead consider the two subproblems of finding an LCS of X_i and Y_{j-1} and of X_{i-1} and Y_j. In the previous dynamic-programming algorithms we have examined—for rod cutting and matrix-chain multiplication—we ruled out no subproblems due to conditions in the problem. Finding an LCS is not the only dynamic-programming algorithm that rules out subproblems based on conditions in the problem. For example, the edit-distance problem (see Problem 15-5) has this characteristic.

Step 3: Computing the length of an LCS

Based on equation (15.9), we could easily write an exponential-time recursive algorithm to compute the length of an LCS of two sequences. Since the LCS problem

has only $\Theta(mn)$ distinct subproblems, however, we can use dynamic programming to compute the solutions bottom up.

Procedure LCS-LENGTH takes two sequences $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Y = \langle y_1, y_2, \ldots, y_n \rangle$ as inputs. It stores the $c[i, j]$ values in a table $c[0..m, 0..n]$, and it computes the entries in ***row-major*** order. (That is, the procedure fills in the first row of c from left to right, then the second row, and so on.) The procedure also maintains the table $b[1..m, 1..n]$ to help us construct an optimal solution. Intuitively, $b[i, j]$ points to the table entry corresponding to the optimal subproblem solution chosen when computing $c[i, j]$. The procedure returns the b and c tables; $c[m, n]$ contains the length of an LCS of X and Y.

```
LCS-LENGTH(X, Y)
 1  m = X.length
 2  n = Y.length
 3  let b[1..m, 1..n] and c[0..m, 0..n] be new tables
 4  for i = 1 to m
 5      c[i, 0] = 0
 6  for j = 0 to n
 7      c[0, j] = 0
 8  for i = 1 to m
 9      for j = 1 to n
10          if x_i == y_j
11              c[i, j] = c[i − 1, j − 1] + 1
12              b[i, j] = "↖"
13          elseif c[i − 1, j] ≥ c[i, j − 1]
14              c[i, j] = c[i − 1, j]
15              b[i, j] = "↑"
16          else c[i, j] = c[i, j − 1]
17              b[i, j] = "←"
18  return c and b
```

Figure 15.8 shows the tables produced by LCS-LENGTH on the sequences $X = \langle A, B, C, B, D, A, B \rangle$ and $Y = \langle B, D, C, A, B, A \rangle$. The running time of the procedure is $\Theta(mn)$, since each table entry takes $\Theta(1)$ time to compute.

Step 4: Constructing an LCS

The b table returned by LCS-LENGTH enables us to quickly construct an LCS of $X = \langle x_1, x_2, \ldots, x_m \rangle$ and $Y = \langle y_1, y_2, \ldots, y_n \rangle$. We simply begin at $b[m, n]$ and trace through the table by following the arrows. Whenever we encounter a "↖" in entry $b[i, j]$, it implies that $x_i = y_j$ is an element of the LCS that LCS-LENGTH

i	j	0	1	2	3	4	5	6
		y_j	B	D	C	A	B	A
0	x_i	0	0	0	0	0	0	0
1	A	0	↑ 0	↑ 0	↑ 0	↖ 1	← 1	↖ 1
2	B	0	↖ 1	← 1	← 1	↑ 1	↖ 2	← 2
3	C	0	↑ 1	↑ 1	↖ 2	← 2	↑ 2	↑ 2
4	B	0	↖ 1	↑ 1	↑ 2	↑ 2	↖ 3	← 3
5	D	0	↑ 1	↖ 2	↑ 2	↑ 2	↑ 3	↑ 3
6	A	0	↑ 1	↑ 2	↑ 2	↖ 3	↑ 3	↖ 4
7	B	0	↖ 1	↑ 2	↑ 2	↑ 3	↖ 4	↑ 4

Figure 15.8 The c and b tables computed by LCS-LENGTH on the sequences $X = \langle A, B, C, B, D, A, B\rangle$ and $Y = \langle B, D, C, A, B, A\rangle$. The square in row i and column j contains the value of $c[i, j]$ and the appropriate arrow for the value of $b[i, j]$. The entry 4 in $c[7, 6]$—the lower right-hand corner of the table—is the length of an LCS $\langle B, C, B, A\rangle$ of X and Y. For $i, j > 0$, entry $c[i, j]$ depends only on whether $x_i = y_j$ and the values in entries $c[i - 1, j]$, $c[i, j - 1]$, and $c[i - 1, j - 1]$, which are computed before $c[i, j]$. To reconstruct the elements of an LCS, follow the $b[i, j]$ arrows from the lower right-hand corner; the sequence is shaded. Each "↖" on the shaded sequence corresponds to an entry (highlighted) for which $x_i = y_j$ is a member of an LCS.

found. With this method, we encounter the elements of this LCS in reverse order. The following recursive procedure prints out an LCS of X and Y in the proper, forward order. The initial call is PRINT-LCS$(b, X, X.length, Y.length)$.

```
PRINT-LCS(b, X, i, j)
1  if i == 0 or j == 0
2      return
3  if b[i, j] == "↖"
4      PRINT-LCS(b, X, i − 1, j − 1)
5      print x_i
6  elseif b[i, j] == "↑"
7      PRINT-LCS(b, X, i − 1, j)
8  else PRINT-LCS(b, X, i, j − 1)
```

For the b table in Figure 15.8, this procedure prints $BCBA$. The procedure takes time $O(m + n)$, since it decrements at least one of i and j in each recursive call.

Improving the code

Once you have developed an algorithm, you will often find that you can improve on the time or space it uses. Some changes can simplify the code and improve constant factors but otherwise yield no asymptotic improvement in performance. Others can yield substantial asymptotic savings in time and space.

In the LCS algorithm, for example, we can eliminate the b table altogether. Each $c[i, j]$ entry depends on only three other c table entries: $c[i-1, j-1]$, $c[i-1, j]$, and $c[i, j-1]$. Given the value of $c[i, j]$, we can determine in $O(1)$ time which of these three values was used to compute $c[i, j]$, without inspecting table b. Thus, we can reconstruct an LCS in $O(m+n)$ time using a procedure similar to PRINT-LCS. (Exercise 15.4-2 asks you to give the pseudocode.) Although we save $\Theta(mn)$ space by this method, the auxiliary space requirement for computing an LCS does not asymptotically decrease, since we need $\Theta(mn)$ space for the c table anyway.

We can, however, reduce the asymptotic space requirements for LCS-LENGTH, since it needs only two rows of table c at a time: the row being computed and the previous row. (In fact, as Exercise 15.4-4 asks you to show, we can use only slightly more than the space for one row of c to compute the length of an LCS.) This improvement works if we need only the length of an LCS; if we need to reconstruct the elements of an LCS, the smaller table does not keep enough information to retrace our steps in $O(m+n)$ time.

Exercises

15.4-1
Determine an LCS of $\langle 1, 0, 0, 1, 0, 1, 0, 1\rangle$ and $\langle 0, 1, 0, 1, 1, 0, 1, 1, 0\rangle$.

15.4-2
Give pseudocode to reconstruct an LCS from the completed c table and the original sequences $X = \langle x_1, x_2, \ldots, x_m\rangle$ and $Y = \langle y_1, y_2, \ldots, y_n\rangle$ in $O(m+n)$ time, without using the b table.

15.4-3
Give a memoized version of LCS-LENGTH that runs in $O(mn)$ time.

15.4-4
Show how to compute the length of an LCS using only $2 \cdot \min(m, n)$ entries in the c table plus $O(1)$ additional space. Then show how to do the same thing, but using $\min(m, n)$ entries plus $O(1)$ additional space.

15.4-5
Give an $O(n^2)$-time algorithm to find the longest monotonically increasing subsequence of a sequence of n numbers.

15.4-6 ⋆
Give an $O(n \lg n)$-time algorithm to find the longest monotonically increasing subsequence of a sequence of n numbers. (*Hint:* Observe that the last element of a candidate subsequence of length i is at least as large as the last element of a candidate subsequence of length $i - 1$. Maintain candidate subsequences by linking them through the input sequence.)

15.5 Optimal binary search trees

Suppose that we are designing a program to translate text from English to French. For each occurrence of each English word in the text, we need to look up its French equivalent. We could perform these lookup operations by building a binary search tree with n English words as keys and their French equivalents as satellite data. Because we will search the tree for each individual word in the text, we want the total time spent searching to be as low as possible. We could ensure an $O(\lg n)$ search time per occurrence by using a red-black tree or any other balanced binary search tree. Words appear with different frequencies, however, and a frequently used word such as *the* may appear far from the root while a rarely used word such as *machicolation* appears near the root. Such an organization would slow down the translation, since the number of nodes visited when searching for a key in a binary search tree equals one plus the depth of the node containing the key. We want words that occur frequently in the text to be placed nearer the root.[6] Moreover, some words in the text might have no French translation,[7] and such words would not appear in the binary search tree at all. How do we organize a binary search tree so as to minimize the number of nodes visited in all searches, given that we know how often each word occurs?

What we need is known as an ***optimal binary search tree***. Formally, we are given a sequence $K = \langle k_1, k_2, \ldots, k_n \rangle$ of n distinct keys in sorted order (so that $k_1 < k_2 < \cdots < k_n$), and we wish to build a binary search tree from these keys. For each key k_i, we have a probability p_i that a search will be for k_i. Some searches may be for values not in K, and so we also have $n + 1$ "dummy keys"

[6] If the subject of the text is castle architecture, we might want *machicolation* to appear near the root.

[7] Yes, *machicolation* has a French counterpart: *mâchicoulis*.

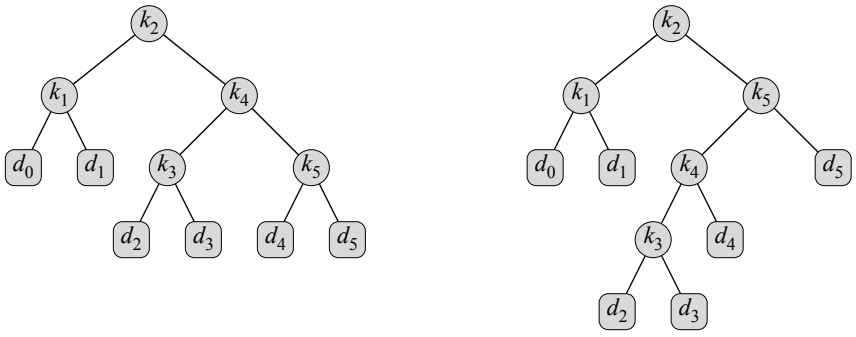


Figure 15.9 Two binary search trees for a set of $n = 5$ keys with the following probabilities:

i	0	1	2	3	4	5
p_i		0.15	0.10	0.05	0.10	0.20
q_i	0.05	0.10	0.05	0.05	0.05	0.10

(a) A binary search tree with expected search cost 2.80. **(b)** A binary search tree with expected search cost 2.75. This tree is optimal.

$d_0, d_1, d_2, \ldots, d_n$ representing values not in K. In particular, d_0 represents all values less than k_1, d_n represents all values greater than k_n, and for $i = 1, 2, \ldots, n-1$, the dummy key d_i represents all values between k_i and k_{i+1}. For each dummy key d_i, we have a probability q_i that a search will correspond to d_i. Figure 15.9 shows two binary search trees for a set of $n = 5$ keys. Each key k_i is an internal node, and each dummy key d_i is a leaf. Every search is either successful (finding some key k_i) or unsuccessful (finding some dummy key d_i), and so we have

$$\sum_{i=1}^{n} p_i + \sum_{i=0}^{n} q_i = 1 \, . \tag{15.10}$$

Because we have probabilities of searches for each key and each dummy key, we can determine the expected cost of a search in a given binary search tree T. Let us assume that the actual cost of a search equals the number of nodes examined, i.e., the depth of the node found by the search in T, plus 1. Then the expected cost of a search in T is

$$\begin{aligned} \mathrm{E}\,[\text{search cost in } T] &= \sum_{i=1}^{n} (\mathrm{depth}_T(k_i) + 1) \cdot p_i + \sum_{i=0}^{n} (\mathrm{depth}_T(d_i) + 1) \cdot q_i \\ &= 1 + \sum_{i=1}^{n} \mathrm{depth}_T(k_i) \cdot p_i + \sum_{i=0}^{n} \mathrm{depth}_T(d_i) \cdot q_i \, , \end{aligned} \tag{15.11}$$

where depth_T denotes a node's depth in the tree T. The last equality follows from equation (15.10). In Figure 15.9(a), we can calculate the expected search cost node by node:

node	depth	probability	contribution
k_1	1	0.15	0.30
k_2	0	0.10	0.10
k_3	2	0.05	0.15
k_4	1	0.10	0.20
k_5	2	0.20	0.60
d_0	2	0.05	0.15
d_1	2	0.10	0.30
d_2	3	0.05	0.20
d_3	3	0.05	0.20
d_4	3	0.05	0.20
d_5	3	0.10	0.40
Total			2.80

For a given set of probabilities, we wish to construct a binary search tree whose expected search cost is smallest. We call such a tree an ***optimal binary search tree***. Figure 15.9(b) shows an optimal binary search tree for the probabilities given in the figure caption; its expected cost is 2.75. This example shows that an optimal binary search tree is not necessarily a tree whose overall height is smallest. Nor can we necessarily construct an optimal binary search tree by always putting the key with the greatest probability at the root. Here, key k_5 has the greatest search probability of any key, yet the root of the optimal binary search tree shown is k_2. (The lowest expected cost of any binary search tree with k_5 at the root is 2.85.)

As with matrix-chain multiplication, exhaustive checking of all possibilities fails to yield an efficient algorithm. We can label the nodes of any n-node binary tree with the keys $k_1, k_2, \ldots, k_n$ to construct a binary search tree, and then add in the dummy keys as leaves. In Problem 12-4, we saw that the number of binary trees with n nodes is $\Omega(4^n/n^{3/2})$, and so we would have to examine an exponential number of binary search trees in an exhaustive search. Not surprisingly, we shall solve this problem with dynamic programming.

Step 1: The structure of an optimal binary search tree

To characterize the optimal substructure of optimal binary search trees, we start with an observation about subtrees. Consider any subtree of a binary search tree. It must contain keys in a contiguous range $k_i, \ldots, k_j$, for some $1 \le i \le j \le n$. In addition, a subtree that contains keys $k_i, \ldots, k_j$ must also have as its leaves the dummy keys $d_{i-1}, \ldots, d_j$.

Now we can state the optimal substructure: if an optimal binary search tree T has a subtree T' containing keys $k_i, \ldots, k_j$, then this subtree T' must be optimal as

well for the subproblem with keys $k_i, \ldots, k_j$ and dummy keys $d_{i-1}, \ldots, d_j$. The usual cut-and-paste argument applies. If there were a subtree T'' whose expected cost is lower than that of T', then we could cut T' out of T and paste in T'', resulting in a binary search tree of lower expected cost than T, thus contradicting the optimality of T.

We need to use the optimal substructure to show that we can construct an optimal solution to the problem from optimal solutions to subproblems. Given keys $k_i, \ldots, k_j$, one of these keys, say k_r ($i \le r \le j$), is the root of an optimal subtree containing these keys. The left subtree of the root k_r contains the keys $k_i, \ldots, k_{r-1}$ (and dummy keys $d_{i-1}, \ldots, d_{r-1}$), and the right subtree contains the keys $k_{r+1}, \ldots, k_j$ (and dummy keys $d_r, \ldots, d_j$). As long as we examine all candidate roots k_r, where $i \le r \le j$, and we determine all optimal binary search trees containing $k_i, \ldots, k_{r-1}$ and those containing $k_{r+1}, \ldots, k_j$, we are guaranteed that we will find an optimal binary search tree.

There is one detail worth noting about "empty" subtrees. Suppose that in a subtree with keys $k_i, \ldots, k_j$, we select k_i as the root. By the above argument, k_i's left subtree contains the keys $k_i, \ldots, k_{i-1}$. We interpret this sequence as containing no keys. Bear in mind, however, that subtrees also contain dummy keys. We adopt the convention that a subtree containing keys $k_i, \ldots, k_{i-1}$ has no actual keys but does contain the single dummy key d_{i-1}. Symmetrically, if we select k_j as the root, then k_j's right subtree contains the keys $k_{j+1}, \ldots, k_j$; this right subtree contains no actual keys, but it does contain the dummy key d_j.

Step 2: A recursive solution

We are ready to define the value of an optimal solution recursively. We pick our subproblem domain as finding an optimal binary search tree containing the keys $k_i, \ldots, k_j$, where $i \ge 1$, $j \le n$, and $j \ge i - 1$. (When $j = i - 1$, there are no actual keys; we have just the dummy key d_{i-1}.) Let us define $e[i, j]$ as the expected cost of searching an optimal binary search tree containing the keys $k_i, \ldots, k_j$. Ultimately, we wish to compute $e[1, n]$.

The easy case occurs when $j = i - 1$. Then we have just the dummy key d_{i-1}. The expected search cost is $e[i, i - 1] = q_{i-1}$.

When $j \ge i$, we need to select a root k_r from among $k_i, \ldots, k_j$ and then make an optimal binary search tree with keys $k_i, \ldots, k_{r-1}$ as its left subtree and an optimal binary search tree with keys $k_{r+1}, \ldots, k_j$ as its right subtree. What happens to the expected search cost of a subtree when it becomes a subtree of a node? The depth of each node in the subtree increases by 1. By equation (15.11), the expected search cost of this subtree increases by the sum of all the probabilities in the subtree. For a subtree with keys $k_i, \ldots, k_j$, let us denote this sum of probabilities as

$$w(i,j) = \sum_{l=i}^{j} p_l + \sum_{l=i-1}^{j} q_l \ . \tag{15.12}$$

Thus, if k_r is the root of an optimal subtree containing keys $k_i, \ldots, k_j$, we have

$$e[i,j] = p_r + (e[i,r-1] + w(i,r-1)) + (e[r+1,j] + w(r+1,j)) \ .$$

Noting that

$$w(i,j) = w(i,r-1) + p_r + w(r+1,j) \ ,$$

we rewrite $e[i,j]$ as

$$e[i,j] = e[i,r-1] + e[r+1,j] + w(i,j) \ . \tag{15.13}$$

The recursive equation (15.13) assumes that we know which node k_r to use as the root. We choose the root that gives the lowest expected search cost, giving us our final recursive formulation:

$$e[i,j] = \begin{cases} q_{i-1} & \text{if } j = i-1 \ , \\ \min\limits_{i \le r \le j} \{e[i,r-1] + e[r+1,j] + w(i,j)\} & \text{if } i \le j \ . \end{cases} \tag{15.14}$$

The $e[i,j]$ values give the expected search costs in optimal binary search trees. To help us keep track of the structure of optimal binary search trees, we define $root[i,j]$, for $1 \le i \le j \le n$, to be the index r for which k_r is the root of an optimal binary search tree containing keys $k_i, \ldots, k_j$. Although we will see how to compute the values of $root[i,j]$, we leave the construction of an optimal binary search tree from these values as Exercise 15.5-1.

Step 3: Computing the expected search cost of an optimal binary search tree

At this point, you may have noticed some similarities between our characterizations of optimal binary search trees and matrix-chain multiplication. For both problem domains, our subproblems consist of contiguous index subranges. A direct, recursive implementation of equation (15.14) would be as inefficient as a direct, recursive matrix-chain multiplication algorithm. Instead, we store the $e[i,j]$ values in a table $e[1\,..\,n+1, 0\,..\,n]$. The first index needs to run to $n+1$ rather than n because in order to have a subtree containing only the dummy key d_n, we need to compute and store $e[n+1,n]$. The second index needs to start from 0 because in order to have a subtree containing only the dummy key d_0, we need to compute and store $e[1,0]$. We use only the entries $e[i,j]$ for which $j \ge i-1$. We also use a table $root[i,j]$, for recording the root of the subtree containing keys $k_i, \ldots, k_j$. This table uses only the entries for which $1 \le i \le j \le n$.

We will need one other table for efficiency. Rather than compute the value of $w(i,j)$ from scratch every time we are computing $e[i,j]$—which would take

$\Theta(j - i)$ additions—we store these values in a table $w[1..n+1, 0..n]$. For the base case, we compute $w[i, i-1] = q_{i-1}$ for $1 \le i \le n+1$. For $j \ge i$, we compute

$$w[i, j] = w[i, j-1] + p_j + q_j \ . \tag{15.15}$$

Thus, we can compute the $\Theta(n^2)$ values of $w[i, j]$ in $\Theta(1)$ time each.

The pseudocode that follows takes as inputs the probabilities $p_1, \ldots, p_n$ and $q_0, \ldots, q_n$ and the size n, and it returns the tables e and *root*.

```
OPTIMAL-BST(p, q, n)
 1  let e[1..n+1, 0..n], w[1..n+1, 0..n],
          and root[1..n, 1..n] be new tables
 2  for i = 1 to n + 1
 3      e[i, i-1] = q_{i-1}
 4      w[i, i-1] = q_{i-1}
 5  for l = 1 to n
 6      for i = 1 to n - l + 1
 7          j = i + l - 1
 8          e[i, j] = ∞
 9          w[i, j] = w[i, j-1] + p_j + q_j
10          for r = i to j
11              t = e[i, r-1] + e[r+1, j] + w[i, j]
12              if t < e[i, j]
13                  e[i, j] = t
14                  root[i, j] = r
15  return e and root
```

From the description above and the similarity to the MATRIX-CHAIN-ORDER procedure in Section 15.2, you should find the operation of this procedure to be fairly straightforward. The **for** loop of lines 2–4 initializes the values of $e[i, i-1]$ and $w[i, i-1]$. The **for** loop of lines 5–14 then uses the recurrences (15.14) and (15.15) to compute $e[i, j]$ and $w[i, j]$ for all $1 \le i \le j \le n$. In the first iteration, when $l = 1$, the loop computes $e[i, i]$ and $w[i, i]$ for $i = 1, 2, \ldots, n$. The second iteration, with $l = 2$, computes $e[i, i+1]$ and $w[i, i+1]$ for $i = 1, 2, \ldots, n-1$, and so forth. The innermost **for** loop, in lines 10–14, tries each candidate index r to determine which key k_r to use as the root of an optimal binary search tree containing keys $k_i, \ldots, k_j$. This **for** loop saves the current value of the index r in $root[i, j]$ whenever it finds a better key to use as the root.

Figure 15.10 shows the tables $e[i, j]$, $w[i, j]$, and $root[i, j]$ computed by the procedure OPTIMAL-BST on the key distribution shown in Figure 15.9. As in the matrix-chain multiplication example of Figure 15.5, the tables are rotated to make

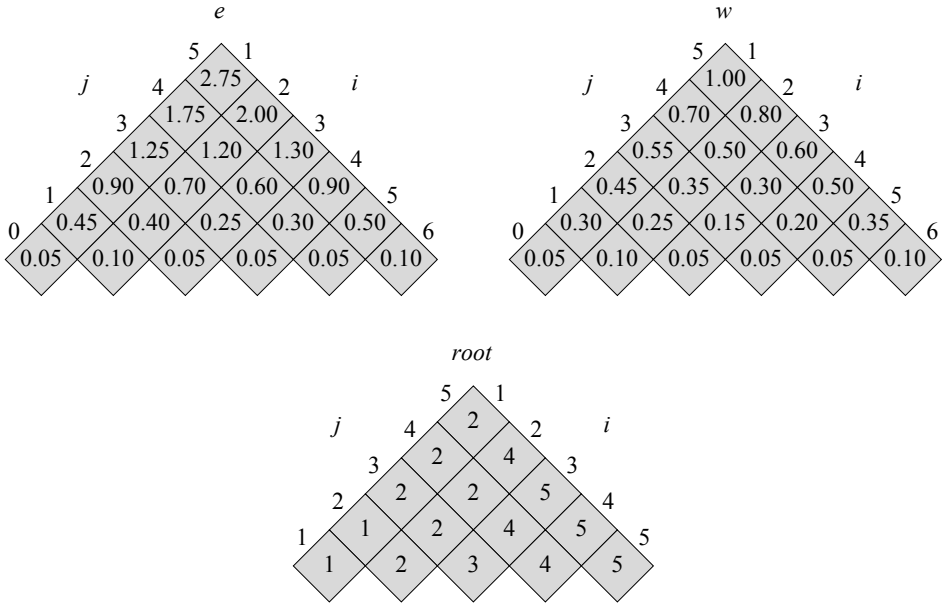


Figure 15.10 The tables $e[i, j]$, $w[i, j]$, and $root[i, j]$ computed by OPTIMAL-BST on the key distribution shown in Figure 15.9. The tables are rotated so that the diagonals run horizontally.

the diagonals run horizontally. OPTIMAL-BST computes the rows from bottom to top and from left to right within each row.

The OPTIMAL-BST procedure takes $\Theta(n^3)$ time, just like MATRIX-CHAIN-ORDER. We can easily see that its running time is $O(n^3)$, since its **for** loops are nested three deep and each loop index takes on at most n values. The loop indices in OPTIMAL-BST do not have exactly the same bounds as those in MATRIX-CHAIN-ORDER, but they are within at most 1 in all directions. Thus, like MATRIX-CHAIN-ORDER, the OPTIMAL-BST procedure takes $\Omega(n^3)$ time.

Exercises

15.5-1

Write pseudocode for the procedure CONSTRUCT-OPTIMAL-BST($root$) which, given the table $root$, outputs the structure of an optimal binary search tree. For the example in Figure 15.10, your procedure should print out the structure

k_2 is the root
k_1 is the left child of k_2
d_0 is the left child of k_1
d_1 is the right child of k_1
k_5 is the right child of k_2
k_4 is the left child of k_5
k_3 is the left child of k_4
d_2 is the left child of k_3
d_3 is the right child of k_3
d_4 is the right child of k_4
d_5 is the right child of k_5

corresponding to the optimal binary search tree shown in Figure 15.9(b).

15.5-2

Determine the cost and structure of an optimal binary search tree for a set of $n = 7$ keys with the following probabilities:

i	0	1	2	3	4	5	6	7
p_i		0.04	0.06	0.08	0.02	0.10	0.12	0.14
q_i	0.06	0.06	0.06	0.06	0.05	0.05	0.05	0.05

15.5-3

Suppose that instead of maintaining the table $w[i, j]$, we computed the value of $w(i, j)$ directly from equation (15.12) in line 9 of OPTIMAL-BST and used this computed value in line 11. How would this change affect the asymptotic running time of OPTIMAL-BST?

15.5-4 ⋆

Knuth [212] has shown that there are always roots of optimal subtrees such that $root[i, j-1] \le root[i, j] \le root[i+1, j]$ for all $1 \le i < j \le n$. Use this fact to modify the OPTIMAL-BST procedure to run in $\Theta(n^2)$ time.

Problems

15-1 Longest simple path in a directed acyclic graph

Suppose that we are given a directed acyclic graph $G = (V, E)$ with real-valued edge weights and two distinguished vertices s and t. Describe a dynamic-programming approach for finding a longest weighted simple path from s to t. What does the subproblem graph look like? What is the efficiency of your algorithm?

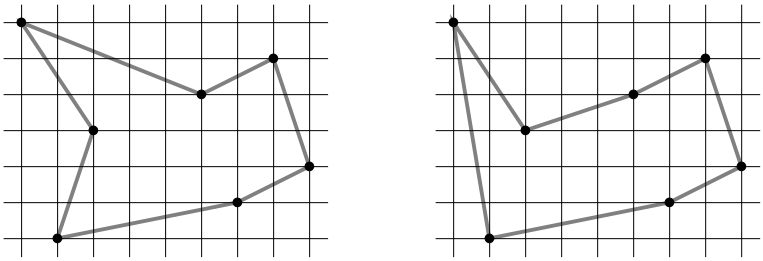


Figure 15.11 Seven points in the plane, shown on a unit grid. **(a)** The shortest closed tour, with length approximately 24.89. This tour is not bitonic. **(b)** The shortest bitonic tour for the same set of points. Its length is approximately 25.58.

15-2 Longest palindrome subsequence

A ***palindrome*** is a nonempty string over some alphabet that reads the same forward and backward. Examples of palindromes are all strings of length 1, `civic`, `racecar`, and `aibohphobia` (fear of palindromes).

Give an efficient algorithm to find the longest palindrome that is a subsequence of a given input string. For example, given the input `character`, your algorithm should return `carac`. What is the running time of your algorithm?

15-3 Bitonic euclidean traveling-salesman problem

In the ***euclidean traveling-salesman problem***, we are given a set of n points in the plane, and we wish to find the shortest closed tour that connects all n points. Figure 15.11(a) shows the solution to a 7-point problem. The general problem is NP-hard, and its solution is therefore believed to require more than polynomial time (see Chapter 34).

J. L. Bentley has suggested that we simplify the problem by restricting our attention to ***bitonic tours***, that is, tours that start at the leftmost point, go strictly rightward to the rightmost point, and then go strictly leftward back to the starting point. Figure 15.11(b) shows the shortest bitonic tour of the same 7 points. In this case, a polynomial-time algorithm is possible.

Describe an $O(n^2)$-time algorithm for determining an optimal bitonic tour. You may assume that no two points have the same x-coordinate and that all operations on real numbers take unit time. (*Hint:* Scan left to right, maintaining optimal possibilities for the two parts of the tour.)

15-4 Printing neatly

Consider the problem of neatly printing a paragraph with a monospaced font (all characters having the same width) on a printer. The input text is a sequence of n

words of lengths $l_1, l_2, \ldots, l_n$, measured in characters. We want to print this paragraph neatly on a number of lines that hold a maximum of M characters each. Our criterion of "neatness" is as follows. If a given line contains words i through j, where $i \le j$, and we leave exactly one space between words, the number of extra space characters at the end of the line is $M - j + i - \sum_{k=i}^{j} l_k$, which must be nonnegative so that the words fit on the line. We wish to minimize the sum, over all lines except the last, of the cubes of the numbers of extra space characters at the ends of lines. Give a dynamic-programming algorithm to print a paragraph of n words neatly on a printer. Analyze the running time and space requirements of your algorithm.

15-5 Edit distance

In order to transform one source string of text $x[1..m]$ to a target string $y[1..n]$, we can perform various transformation operations. Our goal is, given x and y, to produce a series of transformations that change x to y. We use an array z—assumed to be large enough to hold all the characters it will need—to hold the intermediate results. Initially, z is empty, and at termination, we should have $z[j] = y[j]$ for $j = 1, 2, \ldots, n$. We maintain current indices i into x and j into z, and the operations are allowed to alter z and these indices. Initially, $i = j = 1$. We are required to examine every character in x during the transformation, which means that at the end of the sequence of transformation operations, we must have $i = m + 1$.

We may choose from among six transformation operations:

Copy a character from x to z by setting $z[j] = x[i]$ and then incrementing both i and j. This operation examines $x[i]$.

Replace a character from x by another character c, by setting $z[j] = c$, and then incrementing both i and j. This operation examines $x[i]$.

Delete a character from x by incrementing i but leaving j alone. This operation examines $x[i]$.

Insert the character c into z by setting $z[j] = c$ and then incrementing j, but leaving i alone. This operation examines no characters of x.

Twiddle (i.e., exchange) the next two characters by copying them from x to z but in the opposite order; we do so by setting $z[j] = x[i+1]$ and $z[j+1] = x[i]$ and then setting $i = i + 2$ and $j = j + 2$. This operation examines $x[i]$ and $x[i+1]$.

Kill the remainder of x by setting $i = m + 1$. This operation examines all characters in x that have not yet been examined. This operation, if performed, must be the final operation.

As an example, one way to transform the source string `algorithm` to the target string `altruistic` is to use the following sequence of operations, where the underlined characters are $x[i]$ and $z[j]$ after the operation:

Operation	x	z
initial strings	a`lgorithm`	_
copy	al`gorithm`	a_
copy	alg`orithm`	al_
replace by `t`	alg`orithm`	alt_
delete	algo`rithm`	alt_
copy	algor`ithm`	altr_
insert `u`	algor`ithm`	altru_
insert `i`	algor`ithm`	altrui_
insert `s`	algor`ithm`	altruis_
twiddle	algorit`hm`	altruisti_
insert `c`	algorit`hm`	altruistic_
kill	`algorithm_`	altruistic_

Note that there are several other sequences of transformation operations that transform `algorithm` to `altruistic`.

Each of the transformation operations has an associated cost. The cost of an operation depends on the specific application, but we assume that each operation's cost is a constant that is known to us. We also assume that the individual costs of the copy and replace operations are less than the combined costs of the delete and insert operations; otherwise, the copy and replace operations would not be used. The cost of a given sequence of transformation operations is the sum of the costs of the individual operations in the sequence. For the sequence above, the cost of transforming `algorithm` to `altruistic` is

$$(3 \cdot \text{cost(copy)}) + \text{cost(replace)} + \text{cost(delete)} + (4 \cdot \text{cost(insert)}) + \text{cost(twiddle)} + \text{cost(kill)} .$$

a. Given two sequences $x[1 \,..\, m]$ and $y[1 \,..\, n]$ and set of transformation-operation costs, the ***edit distance*** from x to y is the cost of the least expensive operation sequence that transforms x to y. Describe a dynamic-programming algorithm that finds the edit distance from $x[1 \,..\, m]$ to $y[1 \,..\, n]$ and prints an optimal operation sequence. Analyze the running time and space requirements of your algorithm.

The edit-distance problem generalizes the problem of aligning two DNA sequences (see, for example, Setubal and Meidanis [310, Section 3.2]). There are several methods for measuring the similarity of two DNA sequences by aligning them. One such method to align two sequences x and y consists of inserting spaces at

arbitrary locations in the two sequences (including at either end) so that the resulting sequences x' and y' have the same length but do not have a space in the same position (i.e., for no position j are both $x'[j]$ and $y'[j]$ a space). Then we assign a "score" to each position. Position j receives a score as follows:

- $+1$ if $x'[j] = y'[j]$ and neither is a space,
- -1 if $x'[j] \neq y'[j]$ and neither is a space,
- -2 if either $x'[j]$ or $y'[j]$ is a space.

The score for the alignment is the sum of the scores of the individual positions. For example, given the sequences $x =$ `GATCGGCAT` and $y =$ `CAATGTGAATC`, one alignment is

```
G ATCG GCAT
CAAT GTGAATC
-*+++++*-+++*
```

A `+` under a position indicates a score of $+1$ for that position, a `-` indicates a score of -1, and a `*` indicates a score of -2, so that this alignment has a total score of $6 \cdot 1 - 2 \cdot 1 - 4 \cdot 2 = -4$.

b. Explain how to cast the problem of finding an optimal alignment as an edit distance problem using a subset of the transformation operations copy, replace, delete, insert, twiddle, and kill.

15-6 Planning a company party

Professor Stewart is consulting for the president of a corporation that is planning a company party. The company has a hierarchical structure; that is, the supervisor relation forms a tree rooted at the president. The personnel office has ranked each employee with a conviviality rating, which is a real number. In order to make the party fun for all attendees, the president does not want both an employee and his or her immediate supervisor to attend.

Professor Stewart is given the tree that describes the structure of the corporation, using the left-child, right-sibling representation described in Section 10.4. Each node of the tree holds, in addition to the pointers, the name of an employee and that employee's conviviality ranking. Describe an algorithm to make up a guest list that maximizes the sum of the conviviality ratings of the guests. Analyze the running time of your algorithm.

15-7 Viterbi algorithm

We can use dynamic programming on a directed graph $G = (V, E)$ for speech recognition. Each edge $(u, v) \in E$ is labeled with a sound $\sigma(u, v)$ from a finite set Σ of sounds. The labeled graph is a formal model of a person speaking

a restricted language. Each path in the graph starting from a distinguished vertex $v_0 \in V$ corresponds to a possible sequence of sounds produced by the model. We define the label of a directed path to be the concatenation of the labels of the edges on that path.

a. Describe an efficient algorithm that, given an edge-labeled graph G with distinguished vertex v_0 and a sequence $s = \langle \sigma_1, \sigma_2, \ldots, \sigma_k \rangle$ of sounds from Σ, returns a path in G that begins at v_0 and has s as its label, if any such path exists. Otherwise, the algorithm should return NO-SUCH-PATH. Analyze the running time of your algorithm. (*Hint:* You may find concepts from Chapter 22 useful.)

Now, suppose that every edge $(u, v) \in E$ has an associated nonnegative probability $p(u, v)$ of traversing the edge (u, v) from vertex u and thus producing the corresponding sound. The sum of the probabilities of the edges leaving any vertex equals 1. The probability of a path is defined to be the product of the probabilities of its edges. We can view the probability of a path beginning at v_0 as the probability that a "random walk" beginning at v_0 will follow the specified path, where we randomly choose which edge to take leaving a vertex u according to the probabilities of the available edges leaving u.

b. Extend your answer to part (a) so that if a path is returned, it is a *most probable path* starting at v_0 and having label s. Analyze the running time of your algorithm.

15-8 Image compression by seam carving

We are given a color picture consisting of an $m \times n$ array $A[1..m, 1..n]$ of pixels, where each pixel specifies a triple of red, green, and blue (RGB) intensities. Suppose that we wish to compress this picture slightly. Specifically, we wish to remove one pixel from each of the m rows, so that the whole picture becomes one pixel narrower. To avoid disturbing visual effects, however, we require that the pixels removed in two adjacent rows be in the same or adjacent columns; the pixels removed form a "seam" from the top row to the bottom row where successive pixels in the seam are adjacent vertically or diagonally.

a. Show that the number of such possible seams grows at least exponentially in m, assuming that $n > 1$.

b. Suppose now that along with each pixel $A[i, j]$, we have calculated a real-valued disruption measure $d[i, j]$, indicating how disruptive it would be to remove pixel $A[i, j]$. Intuitively, the lower a pixel's disruption measure, the more similar the pixel is to its neighbors. Suppose further that we define the disruption measure of a seam to be the sum of the disruption measures of its pixels.

Give an algorithm to find a seam with the lowest disruption measure. How efficient is your algorithm?

15-9 Breaking a string

A certain string-processing language allows a programmer to break a string into two pieces. Because this operation copies the string, it costs n time units to break a string of n characters into two pieces. Suppose a programmer wants to break a string into many pieces. The order in which the breaks occur can affect the total amount of time used. For example, suppose that the programmer wants to break a 20-character string after characters 2, 8, and 10 (numbering the characters in ascending order from the left-hand end, starting from 1). If she programs the breaks to occur in left-to-right order, then the first break costs 20 time units, the second break costs 18 time units (breaking the string from characters 3 to 20 at character 8), and the third break costs 12 time units, totaling 50 time units. If she programs the breaks to occur in right-to-left order, however, then the first break costs 20 time units, the second break costs 10 time units, and the third break costs 8 time units, totaling 38 time units. In yet another order, she could break first at 8 (costing 20), then break the left piece at 2 (costing 8), and finally the right piece at 10 (costing 12), for a total cost of 40.

Design an algorithm that, given the numbers of characters after which to break, determines a least-cost way to sequence those breaks. More formally, given a string S with n characters and an array $L[1\,..\,m]$ containing the break points, compute the lowest cost for a sequence of breaks, along with a sequence of breaks that achieves this cost.

15-10 Planning an investment strategy

Your knowledge of algorithms helps you obtain an exciting job with the Acme Computer Company, along with a $10,000 signing bonus. You decide to invest this money with the goal of maximizing your return at the end of 10 years. You decide to use the Amalgamated Investment Company to manage your investments. Amalgamated Investments requires you to observe the following rules. It offers n different investments, numbered 1 through n. In each year j, investment i provides a return rate of r_{ij}. In other words, if you invest d dollars in investment i in year j, then at the end of year j, you have dr_{ij} dollars. The return rates are guaranteed, that is, you are given all the return rates for the next 10 years for each investment. You make investment decisions only once per year. At the end of each year, you can leave the money made in the previous year in the same investments, or you can shift money to other investments, by either shifting money between existing investments or moving money to a new investement. If you do not move your money between two consecutive years, you pay a fee of f_1 dollars, whereas if you switch your money, you pay a fee of f_2 dollars, where $f_2 > f_1$.

a. The problem, as stated, allows you to invest your money in multiple investments in each year. Prove that there exists an optimal investment strategy that, in each year, puts all the money into a single investment. (Recall that an optimal investment strategy maximizes the amount of money after 10 years and is not concerned with any other objectives, such as minimizing risk.)

b. Prove that the problem of planning your optimal investment strategy exhibits optimal substructure.

c. Design an algorithm that plans your optimal investment strategy. What is the running time of your algorithm?

d. Suppose that Amalgamated Investments imposed the additional restriction that, at any point, you can have no more than \$15,000 in any one investment. Show that the problem of maximizing your income at the end of 10 years no longer exhibits optimal substructure.

15-11 Inventory planning

The Rinky Dink Company makes machines that resurface ice rinks. The demand for such products varies from month to month, and so the company needs to develop a strategy to plan its manufacturing given the fluctuating, but predictable, demand. The company wishes to design a plan for the next n months. For each month i, the company knows the demand d_i, that is, the number of machines that it will sell. Let $D = \sum_{i=1}^{n} d_i$ be the total demand over the next n months. The company keeps a full-time staff who provide labor to manufacture up to m machines per month. If the company needs to make more than m machines in a given month, it can hire additional, part-time labor, at a cost that works out to c dollars per machine. Furthermore, if, at the end of a month, the company is holding any unsold machines, it must pay inventory costs. The cost for holding j machines is given as a function $h(j)$ for $j = 1, 2, \ldots, D$, where $h(j) \geq 0$ for $1 \leq j \leq D$ and $h(j) \leq h(j+1)$ for $1 \leq j \leq D-1$.

Give an algorithm that calculates a plan for the company that minimizes its costs while fulfilling all the demand. The running time should be polynomial in n and D.

15-12 Signing free-agent baseball players

Suppose that you are the general manager for a major-league baseball team. During the off-season, you need to sign some free-agent players for your team. The team owner has given you a budget of $\$X$ to spend on free agents. You are allowed to spend less than $\$X$ altogether, but the owner will fire you if you spend any more than $\$X$.

You are considering N different positions, and for each position, P free-agent players who play that position are available.[8] Because you do not want to overload your roster with too many players at any position, for each position you may sign at most one free agent who plays that position. (If you do not sign any players at a particular position, then you plan to stick with the players you already have at that position.)

To determine how valuable a player is going to be, you decide to use a sabermetric statistic[9] known as "VORP," or "value over replacement player." A player with a higher VORP is more valuable than a player with a lower VORP. A player with a higher VORP is not necessarily more expensive to sign than a player with a lower VORP, because factors other than a player's value determine how much it costs to sign him.

For each available free-agent player, you have three pieces of information:

- the player's position,
- the amount of money it will cost to sign the player, and
- the player's VORP.

Devise an algorithm that maximizes the total VORP of the players you sign while spending no more than $\$X$ altogether. You may assume that each player signs for a multiple of \$100,000. Your algorithm should output the total VORP of the players you sign, the total amount of money you spend, and a list of which players you sign. Analyze the running time and space requirement of your algorithm.

Chapter notes

R. Bellman began the systematic study of dynamic programming in 1955. The word "programming," both here and in linear programming, refers to using a tabular solution method. Although optimization techniques incorporating elements of dynamic programming were known earlier, Bellman provided the area with a solid mathematical basis [37].

[8] Although there are nine positions on a baseball team, N is not necesarily equal to 9 because some general managers have particular ways of thinking about positions. For example, a general manager might consider right-handed pitchers and left-handed pitchers to be separate "positions," as well as starting pitchers, long relief pitchers (relief pitchers who can pitch several innings), and short relief pitchers (relief pitchers who normally pitch at most only one inning).

[9] ***Sabermetrics*** is the application of statistical analysis to baseball records. It provides several ways to compare the relative values of individual players.

Galil and Park [125] classify dynamic-programming algorithms according to the size of the table and the number of other table entries each entry depends on. They call a dynamic-programming algorithm tD/eD if its table size is $O(n^t)$ and each entry depends on $O(n^e)$ other entries. For example, the matrix-chain multiplication algorithm in Section 15.2 would be $2D/1D$, and the longest-common-subsequence algorithm in Section 15.4 would be $2D/0D$.

Hu and Shing [182, 183] give an $O(n \lg n)$-time algorithm for the matrix-chain multiplication problem.

The $O(mn)$-time algorithm for the longest-common-subsequence problem appears to be a folk algorithm. Knuth [70] posed the question of whether subquadratic algorithms for the LCS problem exist. Masek and Paterson [244] answered this question in the affirmative by giving an algorithm that runs in $O(mn/\lg n)$ time, where $n \leq m$ and the sequences are drawn from a set of bounded size. For the special case in which no element appears more than once in an input sequence, Szymanski [326] shows how to solve the problem in $O((n + m) \lg(n + m))$ time. Many of these results extend to the problem of computing string edit distances (Problem 15-5).

An early paper on variable-length binary encodings by Gilbert and Moore [133] had applications to constructing optimal binary search trees for the case in which all probabilities p_i are 0; this paper contains an $O(n^3)$-time algorithm. Aho, Hopcroft, and Ullman [5] present the algorithm from Section 15.5. Exercise 15.5-4 is due to Knuth [212]. Hu and Tucker [184] devised an algorithm for the case in which all probabilities p_i are 0 that uses $O(n^2)$ time and $O(n)$ space; subsequently, Knuth [211] reduced the time to $O(n \lg n)$.

Problem 15-8 is due to Avidan and Shamir [27], who have posted on the Web a wonderful video illustrating this image-compression technique.

16 Greedy Algorithms

Algorithms for optimization problems typically go through a sequence of steps, with a set of choices at each step. For many optimization problems, using dynamic programming to determine the best choices is overkill; simpler, more efficient algorithms will do. A ***greedy algorithm*** always makes the choice that looks best at the moment. That is, it makes a locally optimal choice in the hope that this choice will lead to a globally optimal solution. This chapter explores optimization problems for which greedy algorithms provide optimal solutions. Before reading this chapter, you should read about dynamic programming in Chapter 15, particularly Section 15.3.

Greedy algorithms do not always yield optimal solutions, but for many problems they do. We shall first examine, in Section 16.1, a simple but nontrivial problem, the activity-selection problem, for which a greedy algorithm efficiently computes an optimal solution. We shall arrive at the greedy algorithm by first considering a dynamic-programming approach and then showing that we can always make greedy choices to arrive at an optimal solution. Section 16.2 reviews the basic elements of the greedy approach, giving a direct approach for proving greedy algorithms correct. Section 16.3 presents an important application of greedy techniques: designing data-compression (Huffman) codes. In Section 16.4, we investigate some of the theory underlying combinatorial structures called "matroids," for which a greedy algorithm always produces an optimal solution. Finally, Section 16.5 applies matroids to solve a problem of scheduling unit-time tasks with deadlines and penalties.

The greedy method is quite powerful and works well for a wide range of problems. Later chapters will present many algorithms that we can view as applications of the greedy method, including minimum-spanning-tree algorithms (Chapter 23), Dijkstra's algorithm for shortest paths from a single source (Chapter 24), and Chvátal's greedy set-covering heuristic (Chapter 35). Minimum-spanning-tree algorithms furnish a classic example of the greedy method. Although you can read

this chapter and Chapter 23 independently of each other, you might find it useful to read them together.

16.1 An activity-selection problem

Our first example is the problem of scheduling several competing activities that require exclusive use of a common resource, with a goal of selecting a maximum-size set of mutually compatible activities. Suppose we have a set $S = \{a_1, a_2, \ldots, a_n\}$ of n proposed ***activities*** that wish to use a resource, such as a lecture hall, which can serve only one activity at a time. Each activity a_i has a ***start time*** s_i and a ***finish time*** f_i, where $0 \le s_i < f_i < \infty$. If selected, activity a_i takes place during the half-open time interval $[s_i, f_i)$. Activities a_i and a_j are ***compatible*** if the intervals $[s_i, f_i)$ and $[s_j, f_j)$ do not overlap. That is, a_i and a_j are compatible if $s_i \ge f_j$ or $s_j \ge f_i$. In the ***activity-selection problem***, we wish to select a maximum-size subset of mutually compatible activities. We assume that the activities are sorted in monotonically increasing order of finish time:

$$f_1 \le f_2 \le f_3 \le \cdots \le f_{n-1} \le f_n \,. \tag{16.1}$$

(We shall see later the advantage that this assumption provides.) For example, consider the following set S of activities:

i	1	2	3	4	5	6	7	8	9	10	11
s_i	1	3	0	5	3	5	6	8	8	2	12
f_i	4	5	6	7	9	9	10	11	12	14	16

For this example, the subset $\{a_3, a_9, a_{11}\}$ consists of mutually compatible activities. It is not a maximum subset, however, since the subset $\{a_1, a_4, a_8, a_{11}\}$ is larger. In fact, $\{a_1, a_4, a_8, a_{11}\}$ is a largest subset of mutually compatible activities; another largest subset is $\{a_2, a_4, a_9, a_{11}\}$.

We shall solve this problem in several steps. We start by thinking about a dynamic-programming solution, in which we consider several choices when determining which subproblems to use in an optimal solution. We shall then observe that we need to consider only one choice—the greedy choice—and that when we make the greedy choice, only one subproblem remains. Based on these observations, we shall develop a recursive greedy algorithm to solve the activity-scheduling problem. We shall complete the process of developing a greedy solution by converting the recursive algorithm to an iterative one. Although the steps we shall go through in this section are slightly more involved than is typical when developing a greedy algorithm, they illustrate the relationship between greedy algorithms and dynamic programming.

The optimal substructure of the activity-selection problem

We can easily verify that the activity-selection problem exhibits optimal substructure. Let us denote by S_{ij} the set of activities that start after activity a_i finishes and that finish before activity a_j starts. Suppose that we wish to find a maximum set of mutually compatible activities in S_{ij}, and suppose further that such a maximum set is A_{ij}, which includes some activity a_k. By including a_k in an optimal solution, we are left with two subproblems: finding mutually compatible activities in the set S_{ik} (activities that start after activity a_i finishes and that finish before activity a_k starts) and finding mutually compatible activities in the set S_{kj} (activities that start after activity a_k finishes and that finish before activity a_j starts). Let $A_{ik} = A_{ij} \cap S_{ik}$ and $A_{kj} = A_{ij} \cap S_{kj}$, so that A_{ik} contains the activities in A_{ij} that finish before a_k starts and A_{kj} contains the activities in A_{ij} that start after a_k finishes. Thus, we have $A_{ij} = A_{ik} \cup \{a_k\} \cup A_{kj}$, and so the maximum-size set A_{ij} of mutually compatible activities in S_{ij} consists of $|A_{ij}| = |A_{ik}| + |A_{kj}| + 1$ activities.

The usual cut-and-paste argument shows that the optimal solution A_{ij} must also include optimal solutions to the two subproblems for S_{ik} and S_{kj}. If we could find a set A'_{kj} of mutually compatible activities in S_{kj} where $|A'_{kj}| > |A_{kj}|$, then we could use A'_{kj}, rather than A_{kj}, in a solution to the subproblem for S_{ij}. We would have constructed a set of $|A_{ik}| + |A'_{kj}| + 1 > |A_{ik}| + |A_{kj}| + 1 = |A_{ij}|$ mutually compatible activities, which contradicts the assumption that A_{ij} is an optimal solution. A symmetric argument applies to the activities in S_{ik}.

This way of characterizing optimal substructure suggests that we might solve the activity-selection problem by dynamic programming. If we denote the size of an optimal solution for the set S_{ij} by $c[i, j]$, then we would have the recurrence

$$c[i, j] = c[i, k] + c[k, j] + 1 .$$

Of course, if we did not know that an optimal solution for the set S_{ij} includes activity a_k, we would have to examine all activities in S_{ij} to find which one to choose, so that

$$c[i, j] = \begin{cases} 0 & \text{if } S_{ij} = \emptyset , \\ \max\limits_{a_k \in S_{ij}} \{c[i, k] + c[k, j] + 1\} & \text{if } S_{ij} \neq \emptyset . \end{cases} \tag{16.2}$$

We could then develop a recursive algorithm and memoize it, or we could work bottom-up and fill in table entries as we go along. But we would be overlooking another important characteristic of the activity-selection problem that we can use to great advantage.

Making the greedy choice

What if we could choose an activity to add to our optimal solution without having to first solve all the subproblems? That could save us from having to consider all the choices inherent in recurrence (16.2). In fact, for the activity-selection problem, we need consider only one choice: the greedy choice.

What do we mean by the greedy choice for the activity-selection problem? Intuition suggests that we should choose an activity that leaves the resource available for as many other activities as possible. Now, of the activities we end up choosing, one of them must be the first one to finish. Our intuition tells us, therefore, to choose the activity in S with the earliest finish time, since that would leave the resource available for as many of the activities that follow it as possible. (If more than one activity in S has the earliest finish time, then we can choose any such activity.) In other words, since the activities are sorted in monotonically increasing order by finish time, the greedy choice is activity a_1. Choosing the first activity to finish is not the only way to think of making a greedy choice for this problem; Exercise 16.1-3 asks you to explore other possibilities.

If we make the greedy choice, we have only one remaining subproblem to solve: finding activities that start after a_1 finishes. Why don't we have to consider activities that finish before a_1 starts? We have that $s_1 < f_1$, and f_1 is the earliest finish time of any activity, and therefore no activity can have a finish time less than or equal to s_1. Thus, all activities that are compatible with activity a_1 must start after a_1 finishes.

Furthermore, we have already established that the activity-selection problem exhibits optimal substructure. Let $S_k = \{a_i \in S : s_i \geq f_k\}$ be the set of activities that start after activity a_k finishes. If we make the greedy choice of activity a_1, then S_1 remains as the only subproblem to solve.[1] Optimal substructure tells us that if a_1 is in the optimal solution, then an optimal solution to the original problem consists of activity a_1 and all the activities in an optimal solution to the subproblem S_1.

One big question remains: is our intuition correct? Is the greedy choice—in which we choose the first activity to finish—always part of some optimal solution? The following theorem shows that it is.

---

[1] We sometimes refer to the sets S_k as subproblems rather than as just sets of activities. It will always be clear from the context whether we are referring to S_k as a set of activities or as a subproblem whose input is that set.

Theorem 16.1
Consider any nonempty subproblem S_k, and let a_m be an activity in S_k with the earliest finish time. Then a_m is included in some maximum-size subset of mutually compatible activities of S_k.

Proof Let A_k be a maximum-size subset of mutually compatible activities in S_k, and let a_j be the activity in A_k with the earliest finish time. If $a_j = a_m$, we are done, since we have shown that a_m is in some maximum-size subset of mutually compatible activities of S_k. If $a_j \neq a_m$, let the set $A'_k = A_k - \{a_j\} \cup \{a_m\}$ be A_k but substituting a_m for a_j. The activities in A'_k are disjoint, which follows because the activities in A_k are disjoint, a_j is the first activity in A_k to finish, and $f_m \leq f_j$. Since $|A'_k| = |A_k|$, we conclude that A'_k is a maximum-size subset of mutually compatible activities of S_k, and it includes a_m. ■

Thus, we see that although we might be able to solve the activity-selection problem with dynamic programming, we don't need to. (Besides, we have not yet examined whether the activity-selection problem even has overlapping subproblems.) Instead, we can repeatedly choose the activity that finishes first, keep only the activities compatible with this activity, and repeat until no activities remain. Moreover, because we always choose the activity with the earliest finish time, the finish times of the activities we choose must strictly increase. We can consider each activity just once overall, in monotonically increasing order of finish times.

An algorithm to solve the activity-selection problem does not need to work bottom-up, like a table-based dynamic-programming algorithm. Instead, it can work top-down, choosing an activity to put into the optimal solution and then solving the subproblem of choosing activities from those that are compatible with those already chosen. Greedy algorithms typically have this top-down design: make a choice and then solve a subproblem, rather than the bottom-up technique of solving subproblems before making a choice.

A recursive greedy algorithm

Now that we have seen how to bypass the dynamic-programming approach and instead use a top-down, greedy algorithm, we can write a straightforward, recursive procedure to solve the activity-selection problem. The procedure RECURSIVE-ACTIVITY-SELECTOR takes the start and finish times of the activities, represented as arrays s and f,[2] the index k that defines the subproblem S_k it is to solve, and

[2]Because the pseudocode takes s and f as arrays, it indexes into them with square brackets rather than subscripts.

the size n of the original problem. It returns a maximum-size set of mutually compatible activities in S_k. We assume that the n input activities are already ordered by monotonically increasing finish time, according to equation (16.1). If not, we can sort them into this order in $O(n \lg n)$ time, breaking ties arbitrarily. In order to start, we add the fictitious activity a_0 with $f_0 = 0$, so that subproblem S_0 is the entire set of activities S. The initial call, which solves the entire problem, is RECURSIVE-ACTIVITY-SELECTOR$(s, f, 0, n)$.

```
RECURSIVE-ACTIVITY-SELECTOR(s, f, k, n)
1  m = k + 1
2  while m ≤ n and s[m] < f[k]        // find the first activity in S_k to finish
3      m = m + 1
4  if m ≤ n
5      return {a_m} ∪ RECURSIVE-ACTIVITY-SELECTOR(s, f, m, n)
6  else return ∅
```

Figure 16.1 shows the operation of the algorithm. In a given recursive call RECURSIVE-ACTIVITY-SELECTOR(s, f, k, n), the **while** loop of lines 2–3 looks for the first activity in S_k to finish. The loop examines $a_{k+1}, a_{k+2}, \ldots, a_n$, until it finds the first activity a_m that is compatible with a_k; such an activity has $s_m \geq f_k$. If the loop terminates because it finds such an activity, line 5 returns the union of $\{a_m\}$ and the maximum-size subset of S_m returned by the recursive call RECURSIVE-ACTIVITY-SELECTOR(s, f, m, n). Alternatively, the loop may terminate because $m > n$, in which case we have examined all activities in S_k without finding one that is compatible with a_k. In this case, $S_k = \emptyset$, and so the procedure returns $\emptyset$ in line 6.

Assuming that the activities have already been sorted by finish times, the running time of the call RECURSIVE-ACTIVITY-SELECTOR$(s, f, 0, n)$ is $\Theta(n)$, which we can see as follows. Over all recursive calls, each activity is examined exactly once in the **while** loop test of line 2. In particular, activity a_i is examined in the last call made in which $k < i$.

An iterative greedy algorithm

We easily can convert our recursive procedure to an iterative one. The procedure RECURSIVE-ACTIVITY-SELECTOR is almost "tail recursive" (see Problem 7-4): it ends with a recursive call to itself followed by a union operation. It is usually a straightforward task to transform a tail-recursive procedure to an iterative form; in fact, some compilers for certain programming languages perform this task automatically. As written, RECURSIVE-ACTIVITY-SELECTOR works for subproblems S_k, i.e., subproblems that consist of the last activities to finish.

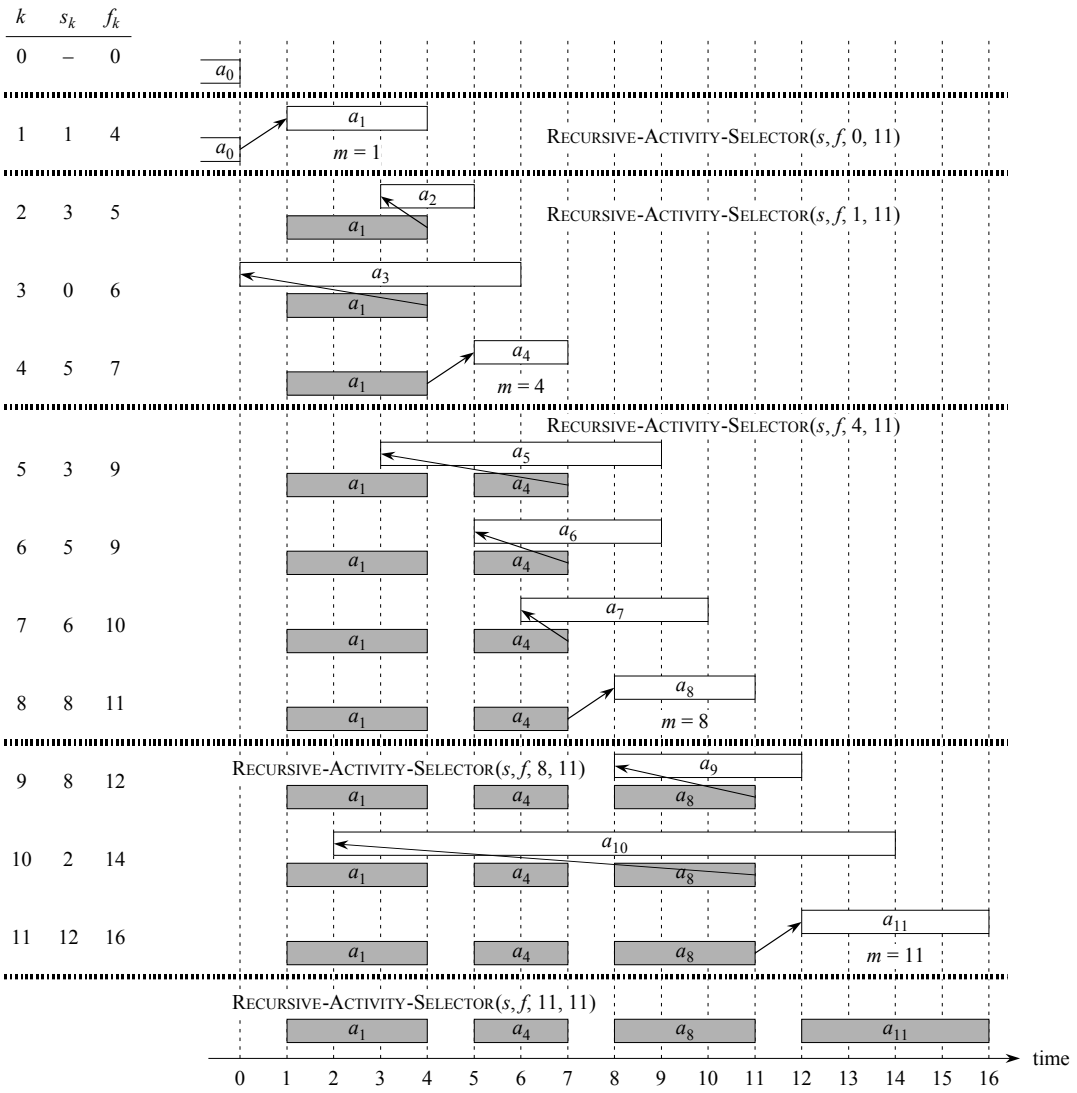


Figure 16.1 The operation of RECURSIVE-ACTIVITY-SELECTOR on the 11 activities given earlier. Activities considered in each recursive call appear between horizontal lines. The fictitious activity a_0 finishes at time 0, and the initial call RECURSIVE-ACTIVITY-SELECTOR$(s, f, 0, 11)$, selects activity a_1. In each recursive call, the activities that have already been selected are shaded, and the activity shown in white is being considered. If the starting time of an activity occurs before the finish time of the most recently added activity (the arrow between them points left), it is rejected. Otherwise (the arrow points directly up or to the right), it is selected. The last recursive call, RECURSIVE-ACTIVITY-SELECTOR$(s, f, 11, 11)$, returns $\emptyset$. The resulting set of selected activities is $\{a_1, a_4, a_8, a_{11}\}$.

The procedure GREEDY-ACTIVITY-SELECTOR is an iterative version of the procedure RECURSIVE-ACTIVITY-SELECTOR. It also assumes that the input activities are ordered by monotonically increasing finish time. It collects selected activities into a set A and returns this set when it is done.

```
GREEDY-ACTIVITY-SELECTOR(s, f)
1  n = s.length
2  A = {a_1}
3  k = 1
4  for m = 2 to n
5      if s[m] ≥ f[k]
6          A = A ∪ {a_m}
7          k = m
8  return A
```

The procedure works as follows. The variable k indexes the most recent addition to A, corresponding to the activity a_k in the recursive version. Since we consider the activities in order of monotonically increasing finish time, f_k is always the maximum finish time of any activity in A. That is,

$$f_k = \max\{f_i : a_i \in A\} \ . \tag{16.3}$$

Lines 2–3 select activity a_1, initialize A to contain just this activity, and initialize k to index this activity. The **for** loop of lines 4–7 finds the earliest activity in S_k to finish. The loop considers each activity a_m in turn and adds a_m to A if it is compatible with all previously selected activities; such an activity is the earliest in S_k to finish. To see whether activity a_m is compatible with every activity currently in A, it suffices by equation (16.3) to check (in line 5) that its start time s_m is not earlier than the finish time f_k of the activity most recently added to A. If activity a_m is compatible, then lines 6–7 add activity a_m to A and set k to m. The set A returned by the call GREEDY-ACTIVITY-SELECTOR(s, f) is precisely the set returned by the call RECURSIVE-ACTIVITY-SELECTOR$(s, f, 0, n)$.

Like the recursive version, GREEDY-ACTIVITY-SELECTOR schedules a set of n activities in $\Theta(n)$ time, assuming that the activities were already sorted initially by their finish times.

Exercises

16.1-1

Give a dynamic-programming algorithm for the activity-selection problem, based on recurrence (16.2). Have your algorithm compute the sizes $c[i, j]$ as defined above and also produce the maximum-size subset of mutually compatible activities.

Assume that the inputs have been sorted as in equation (16.1). Compare the running time of your solution to the running time of GREEDY-ACTIVITY-SELECTOR.

16.1-2

Suppose that instead of always selecting the first activity to finish, we instead select the last activity to start that is compatible with all previously selected activities. Describe how this approach is a greedy algorithm, and prove that it yields an optimal solution.

16.1-3

Not just any greedy approach to the activity-selection problem produces a maximum-size set of mutually compatible activities. Give an example to show that the approach of selecting the activity of least duration from among those that are compatible with previously selected activities does not work. Do the same for the approaches of always selecting the compatible activity that overlaps the fewest other remaining activities and always selecting the compatible remaining activity with the earliest start time.

16.1-4

Suppose that we have a set of activities to schedule among a large number of lecture halls, where any activity can take place in any lecture hall. We wish to schedule all the activities using as few lecture halls as possible. Give an efficient greedy algorithm to determine which activity should use which lecture hall.

(This problem is also known as the ***interval-graph coloring problem***. We can create an interval graph whose vertices are the given activities and whose edges connect incompatible activities. The smallest number of colors required to color every vertex so that no two adjacent vertices have the same color corresponds to finding the fewest lecture halls needed to schedule all of the given activities.)

16.1-5

Consider a modification to the activity-selection problem in which each activity a_i has, in addition to a start and finish time, a value v_i. The objective is no longer to maximize the number of activities scheduled, but instead to maximize the total value of the activities scheduled. That is, we wish to choose a set A of compatible activities such that $\sum_{a_k \in A} v_k$ is maximized. Give a polynomial-time algorithm for this problem.

16.2 Elements of the greedy strategy

A greedy algorithm obtains an optimal solution to a problem by making a sequence of choices. At each decision point, the algorithm makes the choice that seems best at the moment. This heuristic strategy does not always produce an optimal solution, but as we saw in the activity-selection problem, sometimes it does. This section discusses some of the general properties of greedy methods.

The process that we followed in Section 16.1 to develop a greedy algorithm was a bit more involved than is typical. We went through the following steps:

1. Determine the optimal substructure of the problem.
2. Develop a recursive solution. (For the activity-selection problem, we formulated recurrence (16.2), but we bypassed developing a recursive algorithm based on this recurrence.)
3. Show that if we make the greedy choice, then only one subproblem remains.
4. Prove that it is always safe to make the greedy choice. (Steps 3 and 4 can occur in either order.)
5. Develop a recursive algorithm that implements the greedy strategy.
6. Convert the recursive algorithm to an iterative algorithm.

In going through these steps, we saw in great detail the dynamic-programming underpinnings of a greedy algorithm. For example, in the activity-selection problem, we first defined the subproblems S_{ij}, where both i and j varied. We then found that if we always made the greedy choice, we could restrict the subproblems to be of the form S_k.

Alternatively, we could have fashioned our optimal substructure with a greedy choice in mind, so that the choice leaves just one subproblem to solve. In the activity-selection problem, we could have started by dropping the second subscript and defining subproblems of the form S_k. Then, we could have proven that a greedy choice (the first activity a_m to finish in S_k), combined with an optimal solution to the remaining set S_m of compatible activities, yields an optimal solution to S_k. More generally, we design greedy algorithms according to the following sequence of steps:

1. Cast the optimization problem as one in which we make a choice and are left with one subproblem to solve.
2. Prove that there is always an optimal solution to the original problem that makes the greedy choice, so that the greedy choice is always safe.

3. Demonstrate optimal substructure by showing that, having made the greedy choice, what remains is a subproblem with the property that if we combine an optimal solution to the subproblem with the greedy choice we have made, we arrive at an optimal solution to the original problem.

We shall use this more direct process in later sections of this chapter. Nevertheless, beneath every greedy algorithm, there is almost always a more cumbersome dynamic-programming solution.

How can we tell whether a greedy algorithm will solve a particular optimization problem? No way works all the time, but the greedy-choice property and optimal substructure are the two key ingredients. If we can demonstrate that the problem has these properties, then we are well on the way to developing a greedy algorithm for it.

Greedy-choice property

The first key ingredient is the ***greedy-choice property***: we can assemble a globally optimal solution by making locally optimal (greedy) choices. In other words, when we are considering which choice to make, we make the choice that looks best in the current problem, without considering results from subproblems.

Here is where greedy algorithms differ from dynamic programming. In dynamic programming, we make a choice at each step, but the choice usually depends on the solutions to subproblems. Consequently, we typically solve dynamic-programming problems in a bottom-up manner, progressing from smaller subproblems to larger subproblems. (Alternatively, we can solve them top down, but memoizing. Of course, even though the code works top down, we still must solve the subproblems before making a choice.) In a greedy algorithm, we make whatever choice seems best at the moment and then solve the subproblem that remains. The choice made by a greedy algorithm may depend on choices so far, but it cannot depend on any future choices or on the solutions to subproblems. Thus, unlike dynamic programming, which solves the subproblems before making the first choice, a greedy algorithm makes its first choice before solving any subproblems. A dynamic-programming algorithm proceeds bottom up, whereas a greedy strategy usually progresses in a top-down fashion, making one greedy choice after another, reducing each given problem instance to a smaller one.

Of course, we must prove that a greedy choice at each step yields a globally optimal solution. Typically, as in the case of Theorem 16.1, the proof examines a globally optimal solution to some subproblem. It then shows how to modify the solution to substitute the greedy choice for some other choice, resulting in one similar, but smaller, subproblem.

We can usually make the greedy choice more efficiently than when we have to consider a wider set of choices. For example, in the activity-selection problem, as-

suming that we had already sorted the activities in monotonically increasing order of finish times, we needed to examine each activity just once. By preprocessing the input or by using an appropriate data structure (often a priority queue), we often can make greedy choices quickly, thus yielding an efficient algorithm.

Optimal substructure

A problem exhibits ***optimal substructure*** if an optimal solution to the problem contains within it optimal solutions to subproblems. This property is a key ingredient of assessing the applicability of dynamic programming as well as greedy algorithms. As an example of optimal substructure, recall how we demonstrated in Section 16.1 that if an optimal solution to subproblem S_{ij} includes an activity a_k, then it must also contain optimal solutions to the subproblems S_{ik} and S_{kj}. Given this optimal substructure, we argued that if we knew which activity to use as a_k, we could construct an optimal solution to S_{ij} by selecting a_k along with all activities in optimal solutions to the subproblems S_{ik} and S_{kj}. Based on this observation of optimal substructure, we were able to devise the recurrence (16.2) that described the value of an optimal solution.

We usually use a more direct approach regarding optimal substructure when applying it to greedy algorithms. As mentioned above, we have the luxury of assuming that we arrived at a subproblem by having made the greedy choice in the original problem. All we really need to do is argue that an optimal solution to the subproblem, combined with the greedy choice already made, yields an optimal solution to the original problem. This scheme implicitly uses induction on the subproblems to prove that making the greedy choice at every step produces an optimal solution.

Greedy versus dynamic programming

Because both the greedy and dynamic-programming strategies exploit optimal substructure, you might be tempted to generate a dynamic-programming solution to a problem when a greedy solution suffices or, conversely, you might mistakenly think that a greedy solution works when in fact a dynamic-programming solution is required. To illustrate the subtleties between the two techniques, let us investigate two variants of a classical optimization problem.

The ***0-1 knapsack problem*** is the following. A thief robbing a store finds n items. The ith item is worth v_i dollars and weighs w_i pounds, where v_i and w_i are integers. The thief wants to take as valuable a load as possible, but he can carry at most W pounds in his knapsack, for some integer W. Which items should he take? (We call this the 0-1 knapsack problem because for each item, the thief must either

take it or leave it behind; he cannot take a fractional amount of an item or take an item more than once.)

In the ***fractional knapsack problem***, the setup is the same, but the thief can take fractions of items, rather than having to make a binary (0-1) choice for each item. You can think of an item in the 0-1 knapsack problem as being like a gold ingot and an item in the fractional knapsack problem as more like gold dust.

Both knapsack problems exhibit the optimal-substructure property. For the 0-1 problem, consider the most valuable load that weighs at most W pounds. If we remove item j from this load, the remaining load must be the most valuable load weighing at most $W - w_j$ that the thief can take from the $n - 1$ original items excluding j. For the comparable fractional problem, consider that if we remove a weight w of one item j from the optimal load, the remaining load must be the most valuable load weighing at most $W - w$ that the thief can take from the $n - 1$ original items plus $w_j - w$ pounds of item j.

Although the problems are similar, we can solve the fractional knapsack problem by a greedy strategy, but we cannot solve the 0-1 problem by such a strategy. To solve the fractional problem, we first compute the value per pound v_i / w_i for each item. Obeying a greedy strategy, the thief begins by taking as much as possible of the item with the greatest value per pound. If the supply of that item is exhausted and he can still carry more, he takes as much as possible of the item with the next greatest value per pound, and so forth, until he reaches his weight limit W. Thus, by sorting the items by value per pound, the greedy algorithm runs in $O(n \lg n)$ time. We leave the proof that the fractional knapsack problem has the greedy-choice property as Exercise 16.2-1.

To see that this greedy strategy does not work for the 0-1 knapsack problem, consider the problem instance illustrated in Figure 16.2(a). This example has 3 items and a knapsack that can hold 50 pounds. Item 1 weighs 10 pounds and is worth 60 dollars. Item 2 weighs 20 pounds and is worth 100 dollars. Item 3 weighs 30 pounds and is worth 120 dollars. Thus, the value per pound of item 1 is 6 dollars per pound, which is greater than the value per pound of either item 2 (5 dollars per pound) or item 3 (4 dollars per pound). The greedy strategy, therefore, would take item 1 first. As you can see from the case analysis in Figure 16.2(b), however, the optimal solution takes items 2 and 3, leaving item 1 behind. The two possible solutions that take item 1 are both suboptimal.

For the comparable fractional problem, however, the greedy strategy, which takes item 1 first, does yield an optimal solution, as shown in Figure 16.2(c). Taking item 1 doesn't work in the 0-1 problem because the thief is unable to fill his knapsack to capacity, and the empty space lowers the effective value per pound of his load. In the 0-1 problem, when we consider whether to include an item in the knapsack, we must compare the solution to the subproblem that includes the item with the solution to the subproblem that excludes the item before we can make the

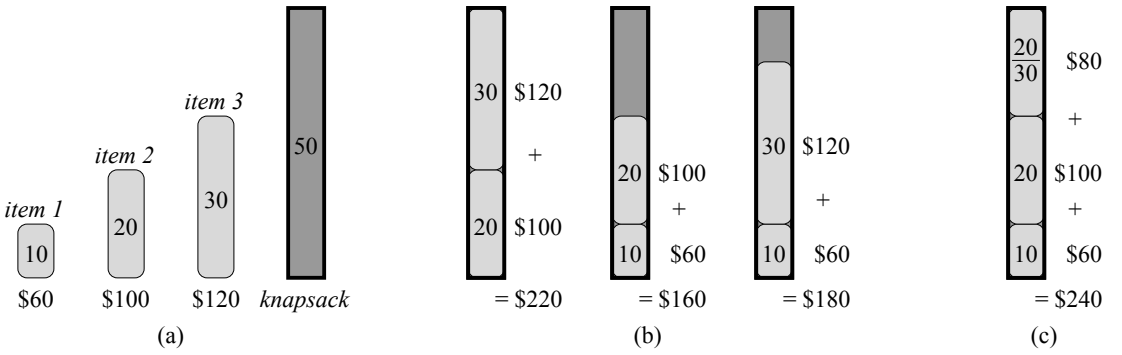


Figure 16.2 An example showing that the greedy strategy does not work for the 0-1 knapsack problem. **(a)** The thief must select a subset of the three items shown whose weight must not exceed 50 pounds. **(b)** The optimal subset includes items 2 and 3. Any solution with item 1 is suboptimal, even though item 1 has the greatest value per pound. **(c)** For the fractional knapsack problem, taking the items in order of greatest value per pound yields an optimal solution.

choice. The problem formulated in this way gives rise to many overlapping subproblems—a hallmark of dynamic programming, and indeed, as Exercise 16.2-2 asks you to show, we can use dynamic programming to solve the 0-1 problem.

Exercises

16.2-1

Prove that the fractional knapsack problem has the greedy-choice property.

16.2-2

Give a dynamic-programming solution to the 0-1 knapsack problem that runs in $O(n\,W)$ time, where n is the number of items and W is the maximum weight of items that the thief can put in his knapsack.

16.2-3

Suppose that in a 0-1 knapsack problem, the order of the items when sorted by increasing weight is the same as their order when sorted by decreasing value. Give an efficient algorithm to find an optimal solution to this variant of the knapsack problem, and argue that your algorithm is correct.

16.2-4

Professor Gekko has always dreamed of inline skating across North Dakota. He plans to cross the state on highway U.S. 2, which runs from Grand Forks, on the eastern border with Minnesota, to Williston, near the western border with Montana.

The professor can carry two liters of water, and he can skate m miles before running out of water. (Because North Dakota is relatively flat, the professor does not have to worry about drinking water at a greater rate on uphill sections than on flat or downhill sections.) The professor will start in Grand Forks with two full liters of water. His official North Dakota state map shows all the places along U.S. 2 at which he can refill his water and the distances between these locations.

The professor's goal is to minimize the number of water stops along his route across the state. Give an efficient method by which he can determine which water stops he should make. Prove that your strategy yields an optimal solution, and give its running time.

16.2-5

Describe an efficient algorithm that, given a set $\{x_1, x_2, \ldots, x_n\}$ of points on the real line, determines the smallest set of unit-length closed intervals that contains all of the given points. Argue that your algorithm is correct.

16.2-6 ⋆

Show how to solve the fractional knapsack problem in $O(n)$ time.

16.2-7

Suppose you are given two sets A and B, each containing n positive integers. You can choose to reorder each set however you like. After reordering, let a_i be the ith element of set A, and let b_i be the ith element of set B. You then receive a payoff of $\prod_{i=1}^{n} a_i^{b_i}$. Give an algorithm that will maximize your payoff. Prove that your algorithm maximizes the payoff, and state its running time.

16.3 Huffman codes

Huffman codes compress data very effectively: savings of 20% to 90% are typical, depending on the characteristics of the data being compressed. We consider the data to be a sequence of characters. Huffman's greedy algorithm uses a table giving how often each character occurs (i.e., its frequency) to build up an optimal way of representing each character as a binary string.

Suppose we have a 100,000-character data file that we wish to store compactly. We observe that the characters in the file occur with the frequencies given by Figure 16.3. That is, only 6 different characters appear, and the character `a` occurs 45,000 times.

We have many options for how to represent such a file of information. Here, we consider the problem of designing a ***binary character code*** (or ***code*** for short)

	a	b	c	d	e	f
Frequency (in thousands)	45	13	12	16	9	5
Fixed-length codeword	000	001	010	011	100	101
Variable-length codeword	0	101	100	111	1101	1100

Figure 16.3 A character-coding problem. A data file of 100,000 characters contains only the characters a–f, with the frequencies indicated. If we assign each character a 3-bit codeword, we can encode the file in 300,000 bits. Using the variable-length code shown, we can encode the file in only 224,000 bits.

in which each character is represented by a unique binary string, which we call a ***codeword***. If we use a ***fixed-length code***, we need 3 bits to represent 6 characters: a = 000, b = 001, ..., f = 101. This method requires 300,000 bits to code the entire file. Can we do better?

A ***variable-length code*** can do considerably better than a fixed-length code, by giving frequent characters short codewords and infrequent characters long codewords. Figure 16.3 shows such a code; here the 1-bit string 0 represents a, and the 4-bit string 1100 represents f. This code requires

$$(45 \cdot 1 + 13 \cdot 3 + 12 \cdot 3 + 16 \cdot 3 + 9 \cdot 4 + 5 \cdot 4) \cdot 1{,}000 = 224{,}000 \text{ bits}$$

to represent the file, a savings of approximately 25%. In fact, this is an optimal character code for this file, as we shall see.

Prefix codes

We consider here only codes in which no codeword is also a prefix of some other codeword. Such codes are called ***prefix codes***.[3] Although we won't prove it here, a prefix code can always achieve the optimal data compression among any character code, and so we suffer no loss of generality by restricting our attention to prefix codes.

Encoding is always simple for any binary character code; we just concatenate the codewords representing each character of the file. For example, with the variable-length prefix code of Figure 16.3, we code the 3-character file abc as $0 \cdot 101 \cdot 100 = 0101100$, where "$\cdot$" denotes concatenation.

Prefix codes are desirable because they simplify decoding. Since no codeword is a prefix of any other, the codeword that begins an encoded file is unambiguous. We can simply identify the initial codeword, translate it back to the original char-

[3] Perhaps "prefix-free codes" would be a better name, but the term "prefix codes" is standard in the literature.

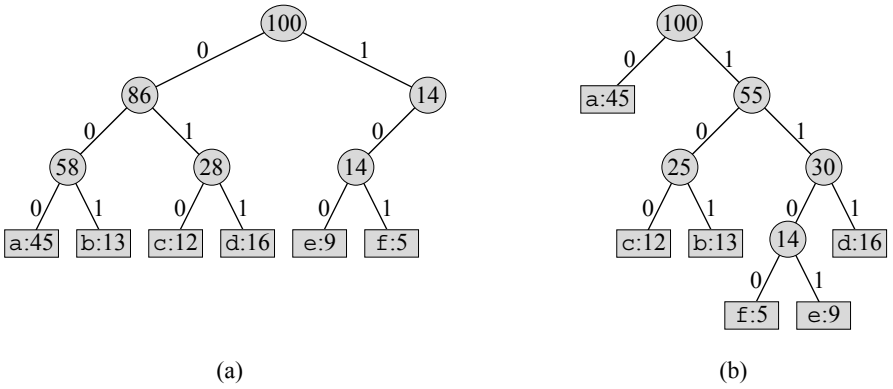


Figure 16.4 Trees corresponding to the coding schemes in Figure 16.3. Each leaf is labeled with a character and its frequency of occurrence. Each internal node is labeled with the sum of the frequencies of the leaves in its subtree. **(a)** The tree corresponding to the fixed-length code a = 000, . . . , f = 101. **(b)** The tree corresponding to the optimal prefix code a = 0, b = 101, . . . , f = 1100.

acter, and repeat the decoding process on the remainder of the encoded file. In our example, the string 001011101 parses uniquely as $0 \cdot 0 \cdot 101 \cdot 1101$, which decodes to aabe.

The decoding process needs a convenient representation for the prefix code so that we can easily pick off the initial codeword. A binary tree whose leaves are the given characters provides one such representation. We interpret the binary codeword for a character as the simple path from the root to that character, where 0 means "go to the left child" and 1 means "go to the right child." Figure 16.4 shows the trees for the two codes of our example. Note that these are not binary search trees, since the leaves need not appear in sorted order and internal nodes do not contain character keys.

An optimal code for a file is always represented by a *full* binary tree, in which every nonleaf node has two children (see Exercise 16.3-2). The fixed-length code in our example is not optimal since its tree, shown in Figure 16.4(a), is not a full binary tree: it contains codewords beginning 10. . . , but none beginning 11. . . . Since we can now restrict our attention to full binary trees, we can say that if C is the alphabet from which the characters are drawn and all character frequencies are positive, then the tree for an optimal prefix code has exactly $|C|$ leaves, one for each letter of the alphabet, and exactly $|C| - 1$ internal nodes (see Exercise B.5-3).

Given a tree T corresponding to a prefix code, we can easily compute the number of bits required to encode a file. For each character c in the alphabet C, let the attribute $c.freq$ denote the frequency of c in the file and let $d_T(c)$ denote the depth

of c's leaf in the tree. Note that $d_T(c)$ is also the length of the codeword for character c. The number of bits required to encode a file is thus

$$B(T) = \sum_{c \in C} c.freq \cdot d_T(c) \,, \tag{16.4}$$

which we define as the ***cost*** of the tree T.

Constructing a Huffman code

Huffman invented a greedy algorithm that constructs an optimal prefix code called a ***Huffman code***. In line with our observations in Section 16.2, its proof of correctness relies on the greedy-choice property and optimal substructure. Rather than demonstrating that these properties hold and then developing pseudocode, we present the pseudocode first. Doing so will help clarify how the algorithm makes greedy choices.

In the pseudocode that follows, we assume that C is a set of n characters and that each character $c \in C$ is an object with an attribute $c.freq$ giving its frequency. The algorithm builds the tree T corresponding to the optimal code in a bottom-up manner. It begins with a set of $|C|$ leaves and performs a sequence of $|C| - 1$ "merging" operations to create the final tree. The algorithm uses a min-priority queue Q, keyed on the *freq* attribute, to identify the two least-frequent objects to merge together. When we merge two objects, the result is a new object whose frequency is the sum of the frequencies of the two objects that were merged.

```
HUFFMAN(C)
1  n = |C|
2  Q = C
3  for i = 1 to n − 1
4       allocate a new node z
5       z.left = x = EXTRACT-MIN(Q)
6       z.right = y = EXTRACT-MIN(Q)
7       z.freq = x.freq + y.freq
8       INSERT(Q, z)
9  return EXTRACT-MIN(Q)      // return the root of the tree
```

For our example, Huffman's algorithm proceeds as shown in Figure 16.5. Since the alphabet contains 6 letters, the initial queue size is $n = 6$, and 5 merge steps build the tree. The final tree represents the optimal prefix code. The codeword for a letter is the sequence of edge labels on the simple path from the root to the letter.

Line 2 initializes the min-priority queue Q with the characters in C. The **for** loop in lines 3–8 repeatedly extracts the two nodes x and y of lowest frequency

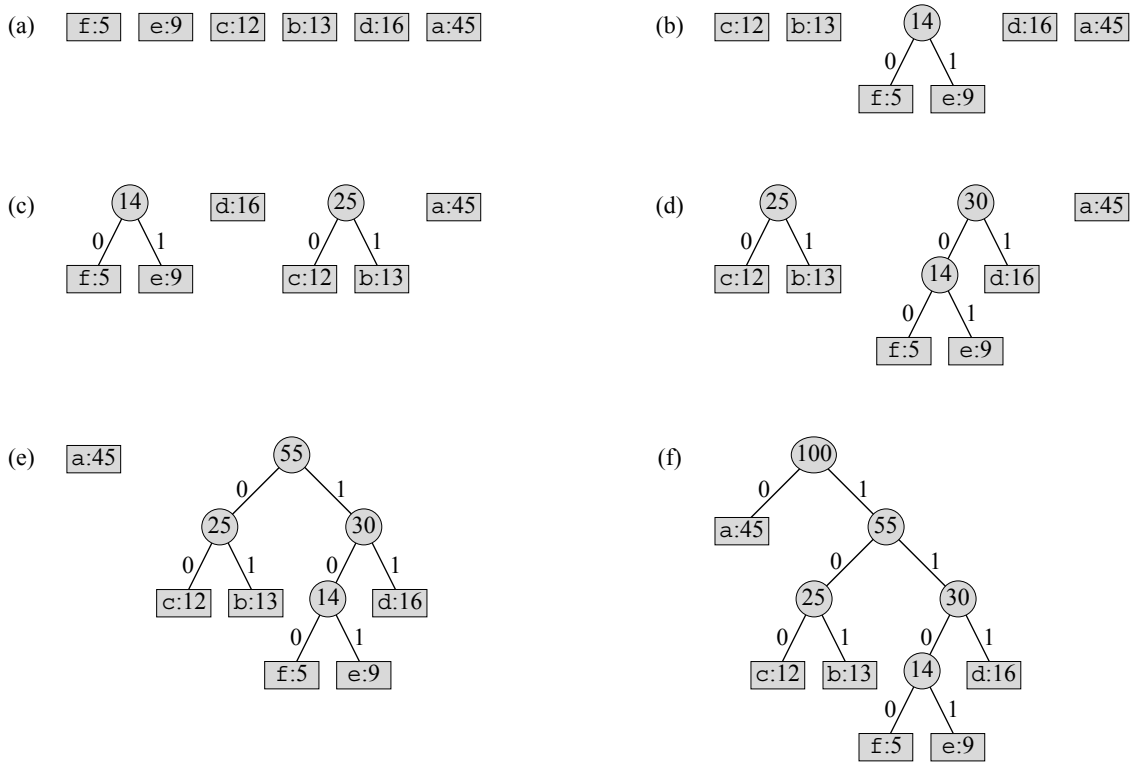


Figure 16.5 The steps of Huffman's algorithm for the frequencies given in Figure 16.3. Each part shows the contents of the queue sorted into increasing order by frequency. At each step, the two trees with lowest frequencies are merged. Leaves are shown as rectangles containing a character and its frequency. Internal nodes are shown as circles containing the sum of the frequencies of their children. An edge connecting an internal node with its children is labeled 0 if it is an edge to a left child and 1 if it is an edge to a right child. The codeword for a letter is the sequence of labels on the edges connecting the root to the leaf for that letter. **(a)** The initial set of $n = 6$ nodes, one for each letter. **(b)–(e)** Intermediate stages. **(f)** The final tree.

from the queue, replacing them in the queue with a new node z representing their merger. The frequency of z is computed as the sum of the frequencies of x and y in line 7. The node z has x as its left child and y as its right child. (This order is arbitrary; switching the left and right child of any node yields a different code of the same cost.) After $n - 1$ mergers, line 9 returns the one node left in the queue, which is the root of the code tree.

Although the algorithm would produce the same result if we were to excise the variables x and y—assigning directly to $z.left$ and $z.right$ in lines 5 and 6, and changing line 7 to $z.freq = z.left.freq + z.right.freq$—we shall use the node

names x and y in the proof of correctness. Therefore, we find it convenient to leave them in.

To analyze the running time of Huffman's algorithm, we assume that Q is implemented as a binary min-heap (see Chapter 6). For a set C of n characters, we can initialize Q in line 2 in $O(n)$ time using the BUILD-MIN-HEAP procedure discussed in Section 6.3. The **for** loop in lines 3–8 executes exactly $n - 1$ times, and since each heap operation requires time $O(\lg n)$, the loop contributes $O(n \lg n)$ to the running time. Thus, the total running time of HUFFMAN on a set of n characters is $O(n \lg n)$. We can reduce the running time to $O(n \lg \lg n)$ by replacing the binary min-heap with a van Emde Boas tree (see Chapter 20).

Correctness of Huffman's algorithm

To prove that the greedy algorithm HUFFMAN is correct, we show that the problem of determining an optimal prefix code exhibits the greedy-choice and optimal-substructure properties. The next lemma shows that the greedy-choice property holds.

Lemma 16.2
Let C be an alphabet in which each character $c \in C$ has frequency $c.freq$. Let x and y be two characters in C having the lowest frequencies. Then there exists an optimal prefix code for C in which the codewords for x and y have the same length and differ only in the last bit.

Proof The idea of the proof is to take the tree T representing an arbitrary optimal prefix code and modify it to make a tree representing another optimal prefix code such that the characters x and y appear as sibling leaves of maximum depth in the new tree. If we can construct such a tree, then the codewords for x and y will have the same length and differ only in the last bit.

Let a and b be two characters that are sibling leaves of maximum depth in T. Without loss of generality, we assume that $a.freq \le b.freq$ and $x.freq \le y.freq$. Since $x.freq$ and $y.freq$ are the two lowest leaf frequencies, in order, and $a.freq$ and $b.freq$ are two arbitrary frequencies, in order, we have $x.freq \le a.freq$ and $y.freq \le b.freq$.

In the remainder of the proof, it is possible that we could have $x.freq = a.freq$ or $y.freq = b.freq$. However, if we had $x.freq = b.freq$, then we would also have $a.freq = b.freq = x.freq = y.freq$ (see Exercise 16.3-1), and the lemma would be trivially true. Thus, we will assume that $x.freq \ne b.freq$, which means that $x \ne b$.

As Figure 16.6 shows, we exchange the positions in T of a and x to produce a tree T', and then we exchange the positions in T' of b and y to produce a tree T''

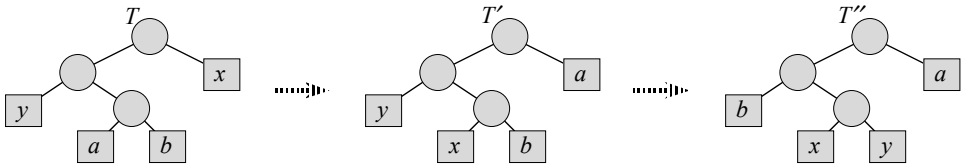


Figure 16.6 An illustration of the key step in the proof of Lemma 16.2. In the optimal tree T, leaves a and b are two siblings of maximum depth. Leaves x and y are the two characters with the lowest frequencies; they appear in arbitrary positions in T. Assuming that $x \neq b$, swapping leaves a and x produces tree T', and then swapping leaves b and y produces tree T''. Since each swap does not increase the cost, the resulting tree T'' is also an optimal tree.

in which x and y are sibling leaves of maximum depth. (Note that if $x = b$ but $y \neq a$, then tree T'' does not have x and y as sibling leaves of maximum depth. Because we assume that $x \neq b$, this situation cannot occur.) By equation (16.4), the difference in cost between T and T' is

$$\begin{aligned}
&B(T) - B(T') \\
&\quad = \sum_{c \in C} c.freq \cdot d_T(c) - \sum_{c \in C} c.freq \cdot d_{T'}(c) \\
&\quad = x.freq \cdot d_T(x) + a.freq \cdot d_T(a) - x.freq \cdot d_{T'}(x) - a.freq \cdot d_{T'}(a) \\
&\quad = x.freq \cdot d_T(x) + a.freq \cdot d_T(a) - x.freq \cdot d_T(a) - a.freq \cdot d_T(x) \\
&\quad = (a.freq - x.freq)(d_T(a) - d_T(x)) \\
&\quad \geq 0 \,,
\end{aligned}$$

because both $a.freq - x.freq$ and $d_T(a) - d_T(x)$ are nonnegative. More specifically, $a.freq - x.freq$ is nonnegative because x is a minimum-frequency leaf, and $d_T(a) - d_T(x)$ is nonnegative because a is a leaf of maximum depth in T. Similarly, exchanging y and b does not increase the cost, and so $B(T') - B(T'')$ is nonnegative. Therefore, $B(T'') \leq B(T)$, and since T is optimal, we have $B(T) \leq B(T'')$, which implies $B(T'') = B(T)$. Thus, T'' is an optimal tree in which x and y appear as sibling leaves of maximum depth, from which the lemma follows. ■

Lemma 16.2 implies that the process of building up an optimal tree by mergers can, without loss of generality, begin with the greedy choice of merging together those two characters of lowest frequency. Why is this a greedy choice? We can view the cost of a single merger as being the sum of the frequencies of the two items being merged. Exercise 16.3-4 shows that the total cost of the tree constructed equals the sum of the costs of its mergers. Of all possible mergers at each step, HUFFMAN chooses the one that incurs the least cost.

The next lemma shows that the problem of constructing optimal prefix codes has the optimal-substructure property.

Lemma 16.3
Let C be a given alphabet with frequency $c.freq$ defined for each character $c \in C$. Let x and y be two characters in C with minimum frequency. Let C' be the alphabet C with the characters x and y removed and a new character z added, so that $C' = C - \{x, y\} \cup \{z\}$. Define $freq$ for C' as for C, except that $z.freq = x.freq + y.freq$. Let T' be any tree representing an optimal prefix code for the alphabet C'. Then the tree T, obtained from T' by replacing the leaf node for z with an internal node having x and y as children, represents an optimal prefix code for the alphabet C.

Proof We first show how to express the cost $B(T)$ of tree T in terms of the cost $B(T')$ of tree T', by considering the component costs in equation (16.4). For each character $c \in C - \{x, y\}$, we have that $d_T(c) = d_{T'}(c)$, and hence $c.freq \cdot d_T(c) = c.freq \cdot d_{T'}(c)$. Since $d_T(x) = d_T(y) = d_{T'}(z) + 1$, we have

$$\begin{aligned} x.freq \cdot d_T(x) + y.freq \cdot d_T(y) &= (x.freq + y.freq)(d_{T'}(z) + 1) \\ &= z.freq \cdot d_{T'}(z) + (x.freq + y.freq) , \end{aligned}$$

from which we conclude that

$$B(T) = B(T') + x.freq + y.freq$$

or, equivalently,

$$B(T') = B(T) - x.freq - y.freq .$$

We now prove the lemma by contradiction. Suppose that T does not represent an optimal prefix code for C. Then there exists an optimal tree T'' such that $B(T'') < B(T)$. Without loss of generality (by Lemma 16.2), T'' has x and y as siblings. Let T''' be the tree T'' with the common parent of x and y replaced by a leaf z with frequency $z.freq = x.freq + y.freq$. Then

$$\begin{aligned} B(T''') &= B(T'') - x.freq - y.freq \\ &< B(T) - x.freq - y.freq \\ &= B(T') , \end{aligned}$$

yielding a contradiction to the assumption that T' represents an optimal prefix code for C'. Thus, T must represent an optimal prefix code for the alphabet C. ■

Theorem 16.4
Procedure HUFFMAN produces an optimal prefix code.

Proof Immediate from Lemmas 16.2 and 16.3. ■

Exercises

16.3-1
Explain why, in the proof of Lemma 16.2, if $x.freq = b.freq$, then we must have $a.freq = b.freq = x.freq = y.freq$.

16.3-2
Prove that a binary tree that is not full cannot correspond to an optimal prefix code.

16.3-3
What is an optimal Huffman code for the following set of frequencies, based on the first 8 Fibonacci numbers?

`a:1 b:1 c:2 d:3 e:5 f:8 g:13 h:21`

Can you generalize your answer to find the optimal code when the frequencies are the first n Fibonacci numbers?

16.3-4
Prove that we can also express the total cost of a tree for a code as the sum, over all internal nodes, of the combined frequencies of the two children of the node.

16.3-5
Prove that if we order the characters in an alphabet so that their frequencies are monotonically decreasing, then there exists an optimal code whose codeword lengths are monotonically increasing.

16.3-6
Suppose we have an optimal prefix code on a set $C = \{0, 1, \ldots, n-1\}$ of characters and we wish to transmit this code using as few bits as possible. Show how to represent any optimal prefix code on C using only $2n - 1 + n\lceil \lg n \rceil$ bits. (*Hint:* Use $2n - 1$ bits to specify the structure of the tree, as discovered by a walk of the tree.)

16.3-7
Generalize Huffman's algorithm to ternary codewords (i.e., codewords using the symbols 0, 1, and 2), and prove that it yields optimal ternary codes.

16.3-8
Suppose that a data file contains a sequence of 8-bit characters such that all 256 characters are about equally common: the maximum character frequency is less than twice the minimum character frequency. Prove that Huffman coding in this case is no more efficient than using an ordinary 8-bit fixed-length code.

16.3-9
Show that no compression scheme can expect to compress a file of randomly chosen 8-bit characters by even a single bit. (*Hint:* Compare the number of possible files with the number of possible encoded files.)

⋆ 16.4 Matroids and greedy methods

In this section, we sketch a beautiful theory about greedy algorithms. This theory describes many situations in which the greedy method yields optimal solutions. It involves combinatorial structures known as "matroids." Although this theory does not cover all cases for which a greedy method applies (for example, it does not cover the activity-selection problem of Section 16.1 or the Huffman-coding problem of Section 16.3), it does cover many cases of practical interest. Furthermore, this theory has been extended to cover many applications; see the notes at the end of this chapter for references.

Matroids

A ***matroid*** is an ordered pair $M = (S, \mathcal{I})$ satisfying the following conditions.

1. S is a finite set.
2. $\mathcal{I}$ is a nonempty family of subsets of S, called the ***independent*** subsets of S, such that if $B \in \mathcal{I}$ and $A \subseteq B$, then $A \in \mathcal{I}$. We say that $\mathcal{I}$ is ***hereditary*** if it satisfies this property. Note that the empty set $\emptyset$ is necessarily a member of $\mathcal{I}$.
3. If $A \in \mathcal{I}$, $B \in \mathcal{I}$, and $|A| < |B|$, then there exists some element $x \in B - A$ such that $A \cup \{x\} \in \mathcal{I}$. We say that M satisfies the ***exchange property***.

The word "matroid" is due to Hassler Whitney. He was studying ***matric matroids***, in which the elements of S are the rows of a given matrix and a set of rows is independent if they are linearly independent in the usual sense. As Exercise 16.4-2 asks you to show, this structure defines a matroid.

As another example of matroids, consider the ***graphic matroid*** $M_G = (S_G, \mathcal{I}_G)$ defined in terms of a given undirected graph $G = (V, E)$ as follows:

- The set S_G is defined to be E, the set of edges of G.
- If A is a subset of E, then $A \in \mathcal{I}_G$ if and only if A is acyclic. That is, a set of edges A is independent if and only if the subgraph $G_A = (V, A)$ forms a forest.

The graphic matroid M_G is closely related to the minimum-spanning-tree problem, which Chapter 23 covers in detail.

Theorem 16.5
If $G = (V, E)$ is an undirected graph, then $M_G = (S_G, \mathcal{I}_G)$ is a matroid.

Proof Clearly, $S_G = E$ is a finite set. Furthermore, $\mathcal{I}_G$ is hereditary, since a subset of a forest is a forest. Putting it another way, removing edges from an acyclic set of edges cannot create cycles.

Thus, it remains to show that M_G satisfies the exchange property. Suppose that $G_A = (V, A)$ and $G_B = (V, B)$ are forests of G and that $|B| > |A|$. That is, A and B are acyclic sets of edges, and B contains more edges than A does.

We claim that a forest $F = (V_F, E_F)$ contains exactly $|V_F| - |E_F|$ trees. To see why, suppose that F consists of t trees, where the ith tree contains v_i vertices and e_i edges. Then, we have

$$\begin{aligned} |E_F| &= \sum_{i=1}^{t} e_i \\ &= \sum_{i=1}^{t} (v_i - 1) \quad \text{(by Theorem B.2)} \\ &= \sum_{i=1}^{t} v_i - t \\ &= |V_F| - t \ , \end{aligned}$$

which implies that $t = |V_F| - |E_F|$. Thus, forest G_A contains $|V| - |A|$ trees, and forest G_B contains $|V| - |B|$ trees.

Since forest G_B has fewer trees than forest G_A does, forest G_B must contain some tree T whose vertices are in two different trees in forest G_A. Moreover, since T is connected, it must contain an edge (u, v) such that vertices u and v are in different trees in forest G_A. Since the edge (u, v) connects vertices in two different trees in forest G_A, we can add the edge (u, v) to forest G_A without creating a cycle. Therefore, M_G satisfies the exchange property, completing the proof that M_G is a matroid. ■

Given a matroid $M = (S, \mathcal{I})$, we call an element $x \notin A$ an ***extension*** of $A \in \mathcal{I}$ if we can add x to A while preserving independence; that is, x is an extension of A if $A \cup \{x\} \in \mathcal{I}$. As an example, consider a graphic matroid M_G. If A is an independent set of edges, then edge e is an extension of A if and only if e is not in A and the addition of e to A does not create a cycle.

If A is an independent subset in a matroid M, we say that A is ***maximal*** if it has no extensions. That is, A is maximal if it is not contained in any larger independent subset of M. The following property is often useful.

Theorem 16.6
All maximal independent subsets in a matroid have the same size.

Proof Suppose to the contrary that A is a maximal independent subset of M and there exists another larger maximal independent subset B of M. Then, the exchange property implies that for some $x \in B - A$, we can extend A to a larger independent set $A \cup \{x\}$, contradicting the assumption that A is maximal. ■

As an illustration of this theorem, consider a graphic matroid M_G for a connected, undirected graph G. Every maximal independent subset of M_G must be a free tree with exactly $|V| - 1$ edges that connects all the vertices of G. Such a tree is called a ***spanning tree*** of G.

We say that a matroid $M = (S, \mathcal{I})$ is ***weighted*** if it is associated with a weight function w that assigns a strictly positive weight $w(x)$ to each element $x \in S$. The weight function w extends to subsets of S by summation:

$$w(A) = \sum_{x \in A} w(x)$$

for any $A \subseteq S$. For example, if we let $w(e)$ denote the weight of an edge e in a graphic matroid M_G, then $w(A)$ is the total weight of the edges in edge set A.

Greedy algorithms on a weighted matroid

Many problems for which a greedy approach provides optimal solutions can be formulated in terms of finding a maximum-weight independent subset in a weighted matroid. That is, we are given a weighted matroid $M = (S, \mathcal{I})$, and we wish to find an independent set $A \in \mathcal{I}$ such that $w(A)$ is maximized. We call such a subset that is independent and has maximum possible weight an ***optimal*** subset of the matroid. Because the weight $w(x)$ of any element $x \in S$ is positive, an optimal subset is always a maximal independent subset—it always helps to make A as large as possible.

For example, in the ***minimum-spanning-tree problem***, we are given a connected undirected graph $G = (V, E)$ and a length function w such that $w(e)$ is the (positive) length of edge e. (We use the term "length" here to refer to the original edge weights for the graph, reserving the term "weight" to refer to the weights in the associated matroid.) We wish to find a subset of the edges that connects all of the vertices together and has minimum total length. To view this as a problem of finding an optimal subset of a matroid, consider the weighted matroid M_G with weight function w', where $w'(e) = w_0 - w(e)$ and w_0 is larger than the maximum length of any edge. In this weighted matroid, all weights are positive and an optimal subset is a spanning tree of minimum total length in the original graph. More specifically, each maximal independent subset A corresponds to a spanning tree

with $|V| - 1$ edges, and since

$$\begin{aligned} w'(A) &= \sum_{e \in A} w'(e) \\ &= \sum_{e \in A} (w_0 - w(e)) \\ &= (|V| - 1)w_0 - \sum_{e \in A} w(e) \\ &= (|V| - 1)w_0 - w(A) \end{aligned}$$

for any maximal independent subset A, an independent subset that maximizes the quantity $w'(A)$ must minimize $w(A)$. Thus, any algorithm that can find an optimal subset A in an arbitrary matroid can solve the minimum-spanning-tree problem.

Chapter 23 gives algorithms for the minimum-spanning-tree problem, but here we give a greedy algorithm that works for any weighted matroid. The algorithm takes as input a weighted matroid $M = (S, \mathcal{I})$ with an associated positive weight function w, and it returns an optimal subset A. In our pseudocode, we denote the components of M by $M.S$ and $M.\mathcal{I}$ and the weight function by w. The algorithm is greedy because it considers in turn each element $x \in S$, in order of monotonically decreasing weight, and immediately adds it to the set A being accumulated if $A \cup \{x\}$ is independent.

```
GREEDY(M, w)
1  A = ∅
2  sort M.S into monotonically decreasing order by weight w
3  for each x ∈ M.S, taken in monotonically decreasing order by weight w(x)
4      if A ∪ {x} ∈ M.I
5          A = A ∪ {x}
6  return A
```

Line 4 checks whether adding each element x to A would maintain A as an independent set. If A would remain independent, then line 5 adds x to A. Otherwise, x is discarded. Since the empty set is independent, and since each iteration of the **for** loop maintains A's independence, the subset A is always independent, by induction. Therefore, GREEDY always returns an independent subset A. We shall see in a moment that A is a subset of maximum possible weight, so that A is an optimal subset.

The running time of GREEDY is easy to analyze. Let n denote $|S|$. The sorting phase of GREEDY takes time $O(n \lg n)$. Line 4 executes exactly n times, once for each element of S. Each execution of line 4 requires a check on whether or not the set $A \cup \{x\}$ is independent. If each such check takes time $O(f(n))$, the entire algorithm runs in time $O(n \lg n + nf(n))$.

We now prove that GREEDY returns an optimal subset.

Lemma 16.7 (Matroids exhibit the greedy-choice property)
Suppose that $M = (S, \mathcal{I})$ is a weighted matroid with weight function w and that S is sorted into monotonically decreasing order by weight. Let x be the first element of S such that $\{x\}$ is independent, if any such x exists. If x exists, then there exists an optimal subset A of S that contains x.

Proof If no such x exists, then the only independent subset is the empty set and the lemma is vacuously true. Otherwise, let B be any nonempty optimal subset. Assume that $x \notin B$; otherwise, letting $A = B$ gives an optimal subset of S that contains x.

No element of B has weight greater than $w(x)$. To see why, observe that $y \in B$ implies that $\{y\}$ is independent, since $B \in \mathcal{I}$ and $\mathcal{I}$ is hereditary. Our choice of x therefore ensures that $w(x) \geq w(y)$ for any $y \in B$.

Construct the set A as follows. Begin with $A = \{x\}$. By the choice of x, set A is independent. Using the exchange property, repeatedly find a new element of B that we can add to A until $|A| = |B|$, while preserving the independence of A. At that point, A and B are the same except that A has x and B has some other element y. That is, $A = B - \{y\} \cup \{x\}$ for some $y \in B$, and so

$$\begin{aligned} w(A) &= w(B) - w(y) + w(x) \\ &\geq w(B) . \end{aligned}$$

Because set B is optimal, set A, which contains x, must also be optimal. ■

We next show that if an element is not an option initially, then it cannot be an option later.

Lemma 16.8
Let $M = (S, \mathcal{I})$ be any matroid. If x is an element of S that is an extension of some independent subset A of S, then x is also an extension of $\emptyset$.

Proof Since x is an extension of A, we have that $A \cup \{x\}$ is independent. Since $\mathcal{I}$ is hereditary, $\{x\}$ must be independent. Thus, x is an extension of $\emptyset$. ■

Corollary 16.9
Let $M = (S, \mathcal{I})$ be any matroid. If x is an element of S such that x is not an extension of $\emptyset$, then x is not an extension of any independent subset A of S.

Proof This corollary is simply the contrapositive of Lemma 16.8. ■

Corollary 16.9 says that any element that cannot be used immediately can never be used. Therefore, GREEDY cannot make an error by passing over any initial elements in S that are not an extension of $\emptyset$, since they can never be used.

Lemma 16.10 (Matroids exhibit the optimal-substructure property)
Let x be the first element of S chosen by GREEDY for the weighted matroid $M = (S, \mathcal{I})$. The remaining problem of finding a maximum-weight independent subset containing x reduces to finding a maximum-weight independent subset of the weighted matroid $M' = (S', \mathcal{I}')$, where

$$\begin{aligned} S' &= \{y \in S : \{x, y\} \in \mathcal{I}\} , \\ \mathcal{I}' &= \{B \subseteq S - \{x\} : B \cup \{x\} \in \mathcal{I}\} , \end{aligned}$$

and the weight function for M' is the weight function for M, restricted to S'. (We call M' the ***contraction*** of M by the element x.)

Proof If A is any maximum-weight independent subset of M containing x, then $A' = A - \{x\}$ is an independent subset of M'. Conversely, any independent subset A' of M' yields an independent subset $A = A' \cup \{x\}$ of M. Since we have in both cases that $w(A) = w(A') + w(x)$, a maximum-weight solution in M containing x yields a maximum-weight solution in M', and vice versa. ■

Theorem 16.11 (Correctness of the greedy algorithm on matroids)
If $M = (S, \mathcal{I})$ is a weighted matroid with weight function w, then GREEDY(M, w) returns an optimal subset.

Proof By Corollary 16.9, any elements that GREEDY passes over initially because they are not extensions of $\emptyset$ can be forgotten about, since they can never be useful. Once GREEDY selects the first element x, Lemma 16.7 implies that the algorithm does not err by adding x to A, since there exists an optimal subset containing x. Finally, Lemma 16.10 implies that the remaining problem is one of finding an optimal subset in the matroid M' that is the contraction of M by x. After the procedure GREEDY sets A to $\{x\}$, we can interpret all of its remaining steps as acting in the matroid $M' = (S', \mathcal{I}')$, because B is independent in M' if and only if $B \cup \{x\}$ is independent in M, for all sets $B \in \mathcal{I}'$. Thus, the subsequent operation of GREEDY will find a maximum-weight independent subset for M', and the overall operation of GREEDY will find a maximum-weight independent subset for M. ■

Exercises

16.4-1
Show that $(S, \mathcal{I}_k)$ is a matroid, where S is any finite set and $\mathcal{I}_k$ is the set of all subsets of S of size at most k, where $k \leq |S|$.

16.4-2 ⋆
Given an $m \times n$ matrix T over some field (such as the reals), show that $(S, \mathcal{I})$ is a matroid, where S is the set of columns of T and $A \in \mathcal{I}$ if and only if the columns in A are linearly independent.

16.4-3 ⋆
Show that if $(S, \mathcal{I})$ is a matroid, then $(S, \mathcal{I}')$ is a matroid, where

$$\mathcal{I}' = \{A' : S - A' \text{ contains some maximal } A \in \mathcal{I}\} .$$

That is, the maximal independent sets of $(S, \mathcal{I}')$ are just the complements of the maximal independent sets of $(S, \mathcal{I})$.

16.4-4 ⋆
Let S be a finite set and let $S_1, S_2, \ldots, S_k$ be a partition of S into nonempty disjoint subsets. Define the structure $(S, \mathcal{I})$ by the condition that $\mathcal{I} = \{A : |A \cap S_i| \leq 1$ for $i = 1, 2, \ldots, k\}$. Show that $(S, \mathcal{I})$ is a matroid. That is, the set of all sets A that contain at most one member of each subset in the partition determines the independent sets of a matroid.

16.4-5
Show how to transform the weight function of a weighted matroid problem, where the desired optimal solution is a *minimum-weight* maximal independent subset, to make it a standard weighted-matroid problem. Argue carefully that your transformation is correct.

⋆ 16.5 A task-scheduling problem as a matroid

An interesting problem that we can solve using matroids is the problem of optimally scheduling unit-time tasks on a single processor, where each task has a deadline, along with a penalty paid if the task misses its deadline. The problem looks complicated, but we can solve it in a surprisingly simple manner by casting it as a matroid and using a greedy algorithm.

A ***unit-time task*** is a job, such as a program to be run on a computer, that requires exactly one unit of time to complete. Given a finite set S of unit-time tasks, a

schedule for S is a permutation of S specifying the order in which to perform these tasks. The first task in the schedule begins at time 0 and finishes at time 1, the second task begins at time 1 and finishes at time 2, and so on.

The problem of ***scheduling unit-time tasks with deadlines and penalties for a single processor*** has the following inputs:

- a set $S = \{a_1, a_2, \ldots, a_n\}$ of n unit-time tasks;
- a set of n integer ***deadlines*** $d_1, d_2, \ldots, d_n$, such that each d_i satisfies $1 \le d_i \le n$ and task a_i is supposed to finish by time d_i; and
- a set of n nonnegative weights or ***penalties*** $w_1, w_2, \ldots, w_n$, such that we incur a penalty of w_i if task a_i is not finished by time d_i, and we incur no penalty if a task finishes by its deadline.

We wish to find a schedule for S that minimizes the total penalty incurred for missed deadlines.

Consider a given schedule. We say that a task is ***late*** in this schedule if it finishes after its deadline. Otherwise, the task is ***early*** in the schedule. We can always transform an arbitrary schedule into ***early-first form***, in which the early tasks precede the late tasks. To see why, note that if some early task a_i follows some late task a_j, then we can switch the positions of a_i and a_j, and a_i will still be early and a_j will still be late.

Furthermore, we claim that we can always transform an arbitrary schedule into ***canonical form***, in which the early tasks precede the late tasks and we schedule the early tasks in order of monotonically increasing deadlines. To do so, we put the schedule into early-first form. Then, as long as there exist two early tasks a_i and a_j finishing at respective times k and $k + 1$ in the schedule such that $d_j < d_i$, we swap the positions of a_i and a_j. Since a_j is early before the swap, $k + 1 \le d_j$. Therefore, $k + 1 < d_i$, and so a_i is still early after the swap. Because task a_j is moved earlier in the schedule, it remains early after the swap.

The search for an optimal schedule thus reduces to finding a set A of tasks that we assign to be early in the optimal schedule. Having determined A, we can create the actual schedule by listing the elements of A in order of monotonically increasing deadlines, then listing the late tasks (i.e., $S - A$) in any order, producing a canonical ordering of the optimal schedule.

We say that a set A of tasks is ***independent*** if there exists a schedule for these tasks such that no tasks are late. Clearly, the set of early tasks for a schedule forms an independent set of tasks. Let $\mathcal{I}$ denote the set of all independent sets of tasks.

Consider the problem of determining whether a given set A of tasks is independent. For $t = 0, 1, 2, \ldots, n$, let $N_t(A)$ denote the number of tasks in A whose deadline is t or earlier. Note that $N_0(A) = 0$ for any set A.

Lemma 16.12
For any set of tasks A, the following statements are equivalent.

1. The set A is independent.
2. For $t = 0, 1, 2, \ldots, n$, we have $N_t(A) \leq t$.
3. If the tasks in A are scheduled in order of monotonically increasing deadlines, then no task is late.

Proof To show that (1) implies (2), we prove the contrapositive: if $N_t(A) > t$ for some t, then there is no way to make a schedule with no late tasks for set A, because more than t tasks must finish before time t. Therefore, (1) implies (2). If (2) holds, then (3) must follow: there is no way to "get stuck" when scheduling the tasks in order of monotonically increasing deadlines, since (2) implies that the ith largest deadline is at least i. Finally, (3) trivially implies (1). ■

Using property 2 of Lemma 16.12, we can easily compute whether or not a given set of tasks is independent (see Exercise 16.5-2).

The problem of minimizing the sum of the penalties of the late tasks is the same as the problem of maximizing the sum of the penalties of the early tasks. The following theorem thus ensures that we can use the greedy algorithm to find an independent set A of tasks with the maximum total penalty.

Theorem 16.13
If S is a set of unit-time tasks with deadlines, and $\mathcal{I}$ is the set of all independent sets of tasks, then the corresponding system $(S, \mathcal{I})$ is a matroid.

Proof Every subset of an independent set of tasks is certainly independent. To prove the exchange property, suppose that B and A are independent sets of tasks and that $|B| > |A|$. Let k be the largest t such that $N_t(B) \leq N_t(A)$. (Such a value of t exists, since $N_0(A) = N_0(B) = 0$.) Since $N_n(B) = |B|$ and $N_n(A) = |A|$, but $|B| > |A|$, we must have that $k < n$ and that $N_j(B) > N_j(A)$ for all j in the range $k + 1 \leq j \leq n$. Therefore, B contains more tasks with deadline $k + 1$ than A does. Let a_i be a task in $B - A$ with deadline $k + 1$. Let $A' = A \cup \{a_i\}$.

We now show that A' must be independent by using property 2 of Lemma 16.12. For $0 \leq t \leq k$, we have $N_t(A') = N_t(A) \leq t$, since A is independent. For $k < t \leq n$, we have $N_t(A') \leq N_t(B) \leq t$, since B is independent. Therefore, A' is independent, completing our proof that $(S, \mathcal{I})$ is a matroid. ■

By Theorem 16.11, we can use a greedy algorithm to find a maximum-weight independent set of tasks A. We can then create an optimal schedule having the tasks in A as its early tasks. This method is an efficient algorithm for scheduling

	Task						
a_i	1	2	3	4	5	6	7
d_i	4	2	4	3	1	4	6
w_i	70	60	50	40	30	20	10

Figure 16.7 An instance of the problem of scheduling unit-time tasks with deadlines and penalties for a single processor.

unit-time tasks with deadlines and penalties for a single processor. The running time is $O(n^2)$ using GREEDY, since each of the $O(n)$ independence checks made by that algorithm takes time $O(n)$ (see Exercise 16.5-2). Problem 16-4 gives a faster implementation.

Figure 16.7 demonstrates an example of the problem of scheduling unit-time tasks with deadlines and penalties for a single processor. In this example, the greedy algorithm selects, in order, tasks a_1, a_2, a_3, and a_4, then rejects a_5 (because $N_4(\{a_1, a_2, a_3, a_4, a_5\}) = 5$) and a_6 (because $N_4(\{a_1, a_2, a_3, a_4, a_6\}) = 5$), and finally accepts a_7. The final optimal schedule is

$$\langle a_2, a_4, a_1, a_3, a_7, a_5, a_6 \rangle ,$$

which has a total penalty incurred of $w_5 + w_6 = 50$.

Exercises

16.5-1
Solve the instance of the scheduling problem given in Figure 16.7, but with each penalty w_i replaced by $80 - w_i$.

16.5-2
Show how to use property 2 of Lemma 16.12 to determine in time $O(|A|)$ whether or not a given set A of tasks is independent.

Problems

16-1 Coin changing

Consider the problem of making change for n cents using the fewest number of coins. Assume that each coin's value is an integer.

a. Describe a greedy algorithm to make change consisting of quarters, dimes, nickels, and pennies. Prove that your algorithm yields an optimal solution.

b. Suppose that the available coins are in the denominations that are powers of c, i.e., the denominations are $c^0, c^1, \ldots, c^k$ for some integers $c > 1$ and $k \geq 1$. Show that the greedy algorithm always yields an optimal solution.

c. Give a set of coin denominations for which the greedy algorithm does not yield an optimal solution. Your set should include a penny so that there is a solution for every value of n.

d. Give an $O(nk)$-time algorithm that makes change for any set of k different coin denominations, assuming that one of the coins is a penny.

16-2 Scheduling to minimize average completion time

Suppose you are given a set $S = \{a_1, a_2, \ldots, a_n\}$ of tasks, where task a_i requires p_i units of processing time to complete, once it has started. You have one computer on which to run these tasks, and the computer can run only one task at a time. Let c_i be the ***completion time*** of task a_i, that is, the time at which task a_i completes processing. Your goal is to minimize the average completion time, that is, to minimize $(1/n)\sum_{i=1}^{n} c_i$. For example, suppose there are two tasks, a_1 and a_2, with $p_1 = 3$ and $p_2 = 5$, and consider the schedule in which a_2 runs first, followed by a_1. Then $c_2 = 5$, $c_1 = 8$, and the average completion time is $(5 + 8)/2 = 6.5$. If task a_1 runs first, however, then $c_1 = 3$, $c_2 = 8$, and the average completion time is $(3 + 8)/2 = 5.5$.

a. Give an algorithm that schedules the tasks so as to minimize the average completion time. Each task must run non-preemptively, that is, once task a_i starts, it must run continuously for p_i units of time. Prove that your algorithm minimizes the average completion time, and state the running time of your algorithm.

b. Suppose now that the tasks are not all available at once. That is, each task cannot start until its ***release time*** r_i. Suppose also that we allow ***preemption***, so that a task can be suspended and restarted at a later time. For example, a task a_i with processing time $p_i = 6$ and release time $r_i = 1$ might start running at time 1 and be preempted at time 4. It might then resume at time 10 but be preempted at time 11, and it might finally resume at time 13 and complete at time 15. Task a_i has run for a total of 6 time units, but its running time has been divided into three pieces. In this scenario, a_i's completion time is 15. Give an algorithm that schedules the tasks so as to minimize the average completion time in this new scenario. Prove that your algorithm minimizes the average completion time, and state the running time of your algorithm.

16-3 Acyclic subgraphs

a. The ***incidence matrix*** for an undirected graph $G = (V, E)$ is a $|V| \times |E|$ matrix M such that $M_{ve} = 1$ if edge e is incident on vertex v, and $M_{ve} = 0$ otherwise. Argue that a set of columns of M is linearly independent over the field of integers modulo 2 if and only if the corresponding set of edges is acyclic.

b. Suppose that we associate a nonnegative weight $w(e)$ with each edge in an undirected graph $G = (V, E)$. Give an efficient algorithm to find an acyclic subset of E of maximum total weight.

c. Let $G(V, E)$ be an arbitrary directed graph, and let $(E, \mathcal{I})$ be defined so that $A \in \mathcal{I}$ if and only if A does not contain any directed cycles. Give an example of a directed graph G such that the associated system $(E, \mathcal{I})$ is not a matroid. Specify which defining condition for a matroid fails to hold.

d. The ***incidence matrix*** for a directed graph $G = (V, E)$ with no self-loops is a $|V| \times |E|$ matrix M such that $M_{ve} = -1$ if edge e leaves vertex v, $M_{ve} = 1$ if edge e enters vertex v, and $M_{ve} = 0$ otherwise. Argue that if a set of columns of M is linearly independent, then the corresponding set of edges does not contain a directed cycle.

e. Exercise 16.4-2 tells us that the set of linearly independent sets of columns of any matrix M forms a matroid. Explain carefully why the results of parts (c) and (e) are not contradictory. How can there fail to be a perfect correspondence between the notion of a set of edges being acyclic and the notion of the associated set of columns of the incidence matrix being linearly independent?

16-4 Scheduling variations

Consider the following algorithm for the problem from Section 16.5 of scheduling unit-time tasks with deadlines and penalties. Let all n time slots be initially empty, where time slot i is the unit-length slot of time that finishes at time i. We consider the tasks in order of monotonically decreasing penalty. When considering task a_j, if there exists a time slot at or before a_j's deadline d_j that is still empty, assign a_j to the latest such slot, filling it. If there is no such slot, assign task a_j to the latest of the as yet unfilled slots.

a. Argue that this algorithm always gives an optimal answer.

b. Use the fast disjoint-set forest presented in Section 21.3 to implement the algorithm efficiently. Assume that the set of input tasks has already been sorted into monotonically decreasing order by penalty. Analyze the running time of your implementation.

16-5 Off-line caching

Modern computers use a cache to store a small amount of data in a fast memory. Even though a program may access large amounts of data, by storing a small subset of the main memory in the ***cache***—a small but faster memory—overall access time can greatly decrease. When a computer program executes, it makes a sequence $\langle r_1, r_2, \ldots, r_n \rangle$ of n memory requests, where each request is for a particular data element. For example, a program that accesses 4 distinct elements $\{a, b, c, d\}$ might make the sequence of requests $\langle d, b, d, b, d, a, c, d, b, a, c, b \rangle$. Let k be the size of the cache. When the cache contains k elements and the program requests the $(k + 1)$st element, the system must decide, for this and each subsequent request, which k elements to keep in the cache. More precisely, for each request r_i, the cache-management algorithm checks whether element r_i is already in the cache. If it is, then we have a ***cache hit***; otherwise, we have a ***cache miss***. Upon a cache miss, the system retrieves r_i from the main memory, and the cache-management algorithm must decide whether to keep r_i in the cache. If it decides to keep r_i and the cache already holds k elements, then it must evict one element to make room for r_i. The cache-management algorithm evicts data with the goal of minimizing the number of cache misses over the entire sequence of requests.

Typically, caching is an on-line problem. That is, we have to make decisions about which data to keep in the cache without knowing the future requests. Here, however, we consider the off-line version of this problem, in which we are given in advance the entire sequence of n requests and the cache size k, and we wish to minimize the total number of cache misses.

We can solve this off-line problem by a greedy strategy called ***furthest-in-future***, which chooses to evict the item in the cache whose next access in the request sequence comes furthest in the future.

a. Write pseudocode for a cache manager that uses the furthest-in-future strategy. The input should be a sequence $\langle r_1, r_2, \ldots, r_n \rangle$ of requests and a cache size k, and the output should be a sequence of decisions about which data element (if any) to evict upon each request. What is the running time of your algorithm?

b. Show that the off-line caching problem exhibits optimal substructure.

c. Prove that furthest-in-future produces the minimum possible number of cache misses.

Chapter notes

Much more material on greedy algorithms and matroids can be found in Lawler [224] and Papadimitriou and Steiglitz [271].

The greedy algorithm first appeared in the combinatorial optimization literature in a 1971 article by Edmonds [101], though the theory of matroids dates back to a 1935 article by Whitney [355].

Our proof of the correctness of the greedy algorithm for the activity-selection problem is based on that of Gavril [131]. The task-scheduling problem is studied in Lawler [224]; Horowitz, Sahni, and Rajasekaran [181]; and Brassard and Bratley [54].

Huffman codes were invented in 1952 [185]; Lelewer and Hirschberg [231] surveys data-compression techniques known as of 1987.

An extension of matroid theory to greedoid theory was pioneered by Korte and Lovász [216, 217, 218, 219], who greatly generalize the theory presented here.

17 Amortized Analysis

In an ***amortized analysis***, we average the time required to perform a sequence of data-structure operations over all the operations performed. With amortized analysis, we can show that the average cost of an operation is small, if we average over a sequence of operations, even though a single operation within the sequence might be expensive. Amortized analysis differs from average-case analysis in that probability is not involved; an amortized analysis guarantees the *average performance of each operation in the worst case*.

The first three sections of this chapter cover the three most common techniques used in amortized analysis. Section 17.1 starts with aggregate analysis, in which we determine an upper bound $T(n)$ on the total cost of a sequence of n operations. The average cost per operation is then $T(n)/n$. We take the average cost as the amortized cost of each operation, so that all operations have the same amortized cost.

Section 17.2 covers the accounting method, in which we determine an amortized cost of each operation. When there is more than one type of operation, each type of operation may have a different amortized cost. The accounting method overcharges some operations early in the sequence, storing the overcharge as "prepaid credit" on specific objects in the data structure. Later in the sequence, the credit pays for operations that are charged less than they actually cost.

Section 17.3 discusses the potential method, which is like the accounting method in that we determine the amortized cost of each operation and may overcharge operations early on to compensate for undercharges later. The potential method maintains the credit as the "potential energy" of the data structure as a whole instead of associating the credit with individual objects within the data structure.

We shall use two examples to examine these three methods. One is a stack with the additional operation MULTIPOP, which pops several objects at once. The other is a binary counter that counts up from 0 by means of the single operation INCREMENT.

While reading this chapter, bear in mind that the charges assigned during an amortized analysis are for analysis purposes only. They need not—and should not—appear in the code. If, for example, we assign a credit to an object x when using the accounting method, we have no need to assign an appropriate amount to some attribute, such as $x.credit$, in the code.

When we perform an amortized analysis, we often gain insight into a particular data structure, and this insight can help us optimize the design. In Section 17.4, for example, we shall use the potential method to analyze a dynamically expanding and contracting table.

17.1 Aggregate analysis

In ***aggregate analysis***, we show that for all n, a sequence of n operations takes *worst-case* time $T(n)$ in total. In the worst case, the average cost, or ***amortized cost***, per operation is therefore $T(n)/n$. Note that this amortized cost applies to each operation, even when there are several types of operations in the sequence. The other two methods we shall study in this chapter, the accounting method and the potential method, may assign different amortized costs to different types of operations.

Stack operations

In our first example of aggregate analysis, we analyze stacks that have been augmented with a new operation. Section 10.1 presented the two fundamental stack operations, each of which takes $O(1)$ time:

PUSH(S, x) pushes object x onto stack S.

POP(S) pops the top of stack S and returns the popped object. Calling POP on an empty stack generates an error.

Since each of these operations runs in $O(1)$ time, let us consider the cost of each to be 1. The total cost of a sequence of n PUSH and POP operations is therefore n, and the actual running time for n operations is therefore $\Theta(n)$.

Now we add the stack operation MULTIPOP(S, k), which removes the k top objects of stack S, popping the entire stack if the stack contains fewer than k objects. Of course, we assume that k is positive; otherwise the MULTIPOP operation leaves the stack unchanged. In the following pseudocode, the operation STACK-EMPTY returns TRUE if there are no objects currently on the stack, and FALSE otherwise.

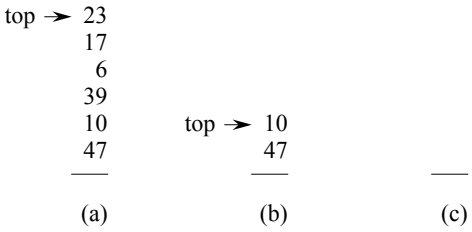


Figure 17.1 The action of MULTIPOP on a stack S, shown initially in **(a)**. The top 4 objects are popped by MULTIPOP$(S, 4)$, whose result is shown in **(b)**. The next operation is MULTIPOP$(S, 7)$, which empties the stack—shown in **(c)**—since there were fewer than 7 objects remaining.

```
MULTIPOP(S, k)
1  while not STACK-EMPTY(S) and k > 0
2      POP(S)
3      k = k − 1
```

Figure 17.1 shows an example of MULTIPOP.

What is the running time of MULTIPOP(S, k) on a stack of s objects? The actual running time is linear in the number of POP operations actually executed, and thus we can analyze MULTIPOP in terms of the abstract costs of 1 each for PUSH and POP. The number of iterations of the **while** loop is the number $\min(s, k)$ of objects popped off the stack. Each iteration of the loop makes one call to POP in line 2. Thus, the total cost of MULTIPOP is $\min(s, k)$, and the actual running time is a linear function of this cost.

Let us analyze a sequence of n PUSH, POP, and MULTIPOP operations on an initially empty stack. The worst-case cost of a MULTIPOP operation in the sequence is $O(n)$, since the stack size is at most n. The worst-case time of any stack operation is therefore $O(n)$, and hence a sequence of n operations costs $O(n^2)$, since we may have $O(n)$ MULTIPOP operations costing $O(n)$ each. Although this analysis is correct, the $O(n^2)$ result, which we obtained by considering the worst-case cost of each operation individually, is not tight.

Using aggregate analysis, we can obtain a better upper bound that considers the entire sequence of n operations. In fact, although a single MULTIPOP operation can be expensive, any sequence of n PUSH, POP, and MULTIPOP operations on an initially empty stack can cost at most $O(n)$. Why? We can pop each object from the stack at most once for each time we have pushed it onto the stack. Therefore, the number of times that POP can be called on a nonempty stack, including calls within MULTIPOP, is at most the number of PUSH operations, which is at most n. For any value of n, any sequence of n PUSH, POP, and MULTIPOP operations takes a total of $O(n)$ time. The average cost of an operation is $O(n)/n = O(1)$. In aggregate

analysis, we assign the amortized cost of each operation to be the average cost. In this example, therefore, all three stack operations have an amortized cost of $O(1)$.

We emphasize again that although we have just shown that the average cost, and hence the running time, of a stack operation is $O(1)$, we did not use probabilistic reasoning. We actually showed a *worst-case* bound of $O(n)$ on a sequence of n operations. Dividing this total cost by n yielded the average cost per operation, or the amortized cost.

Incrementing a binary counter

As another example of aggregate analysis, consider the problem of implementing a k-bit binary counter that counts upward from 0. We use an array $A[0..k-1]$ of bits, where $A.length = k$, as the counter. A binary number x that is stored in the counter has its lowest-order bit in $A[0]$ and its highest-order bit in $A[k-1]$, so that $x = \sum_{i=0}^{k-1} A[i] \cdot 2^i$. Initially, $x = 0$, and thus $A[i] = 0$ for $i = 0, 1, \ldots, k-1$. To add 1 (modulo 2^k) to the value in the counter, we use the following procedure.

```
INCREMENT(A)
1  i = 0
2  while i < A.length and A[i] == 1
3       A[i] = 0
4       i = i + 1
5  if i < A.length
6       A[i] = 1
```

Figure 17.2 shows what happens to a binary counter as we increment it 16 times, starting with the initial value 0 and ending with the value 16. At the start of each iteration of the **while** loop in lines 2–4, we wish to add a 1 into position i. If $A[i] = 1$, then adding 1 flips the bit to 0 in position i and yields a carry of 1, to be added into position $i + 1$ on the next iteration of the loop. Otherwise, the loop ends, and then, if $i < k$, we know that $A[i] = 0$, so that line 6 adds a 1 into position i, flipping the 0 to a 1. The cost of each INCREMENT operation is linear in the number of bits flipped.

As with the stack example, a cursory analysis yields a bound that is correct but not tight. A single execution of INCREMENT takes time $\Theta(k)$ in the worst case, in which array A contains all 1s. Thus, a sequence of n INCREMENT operations on an initially zero counter takes time $O(nk)$ in the worst case.

We can tighten our analysis to yield a worst-case cost of $O(n)$ for a sequence of n INCREMENT operations by observing that not all bits flip each time INCREMENT is called. As Figure 17.2 shows, $A[0]$ does flip each time INCREMENT is called. The next bit up, $A[1]$, flips only every other time: a sequence of n INCREMENT

Counter value	A[7]	A[6]	A[5]	A[4]	A[3]	A[2]	A[1]	A[0]	Total cost
0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	1	1
2	0	0	0	0	0	0	1	0	3
3	0	0	0	0	0	0	1	1	4
4	0	0	0	0	0	1	0	0	7
5	0	0	0	0	0	1	0	1	8
6	0	0	0	0	0	1	1	0	10
7	0	0	0	0	0	1	1	1	11
8	0	0	0	0	1	0	0	0	15
9	0	0	0	0	1	0	0	1	16
10	0	0	0	0	1	0	1	0	18
11	0	0	0	0	1	0	1	1	19
12	0	0	0	0	1	1	0	0	22
13	0	0	0	0	1	1	0	1	23
14	0	0	0	0	1	1	1	0	25
15	0	0	0	0	1	1	1	1	26
16	0	0	0	1	0	0	0	0	31

Figure 17.2 An 8-bit binary counter as its value goes from 0 to 16 by a sequence of 16 INCREMENT operations. Bits that flip to achieve the next value are shaded. The running cost for flipping bits is shown at the right. Notice that the total cost is always less than twice the total number of INCREMENT operations.

operations on an initially zero counter causes $A[1]$ to flip $\lfloor n/2 \rfloor$ times. Similarly, bit $A[2]$ flips only every fourth time, or $\lfloor n/4 \rfloor$ times in a sequence of n INCREMENT operations. In general, for $i = 0, 1, \ldots, k-1$, bit $A[i]$ flips $\lfloor n/2^i \rfloor$ times in a sequence of n INCREMENT operations on an initially zero counter. For $i \geq k$, bit $A[i]$ does not exist, and so it cannot flip. The total number of flips in the sequence is thus

$$\begin{aligned} \sum_{i=0}^{k-1} \left\lfloor \frac{n}{2^i} \right\rfloor &< n \sum_{i=0}^{\infty} \frac{1}{2^i} \\ &= 2n \,, \end{aligned}$$

by equation (A.6). The worst-case time for a sequence of n INCREMENT operations on an initially zero counter is therefore $O(n)$. The average cost of each operation, and therefore the amortized cost per operation, is $O(n)/n = O(1)$.

Exercises

17.1-1
If the set of stack operations included a MULTIPUSH operation, which pushes k items onto the stack, would the $O(1)$ bound on the amortized cost of stack operations continue to hold?

17.1-2
Show that if a DECREMENT operation were included in the k-bit counter example, n operations could cost as much as $\Theta(nk)$ time.

17.1-3
Suppose we perform a sequence of n operations on a data structure in which the ith operation costs i if i is an exact power of 2, and 1 otherwise. Use aggregate analysis to determine the amortized cost per operation.

17.2 The accounting method

In the ***accounting method*** of amortized analysis, we assign differing charges to different operations, with some operations charged more or less than they actually cost. We call the amount we charge an operation its ***amortized cost***. When an operation's amortized cost exceeds its actual cost, we assign the difference to specific objects in the data structure as ***credit***. Credit can help pay for later operations whose amortized cost is less than their actual cost. Thus, we can view the amortized cost of an operation as being split between its actual cost and credit that is either deposited or used up. Different operations may have different amortized costs. This method differs from aggregate analysis, in which all operations have the same amortized cost.

We must choose the amortized costs of operations carefully. If we want to show that in the worst case the average cost per operation is small by analyzing with amortized costs, we must ensure that the total amortized cost of a sequence of operations provides an upper bound on the total actual cost of the sequence. Moreover, as in aggregate analysis, this relationship must hold for all sequences of operations. If we denote the actual cost of the ith operation by c_i and the amortized cost of the ith operation by $\hat{c}_i$, we require

$$\sum_{i=1}^{n} \hat{c}_i \geq \sum_{i=1}^{n} c_i \tag{17.1}$$

for all sequences of n operations. The total credit stored in the data structure is the difference between the total amortized cost and the total actual cost, or

$\sum_{i=1}^{n} \hat{c}_i - \sum_{i=1}^{n} c_i$. By inequality (17.1), the total credit associated with the data structure must be nonnegative at all times. If we ever were to allow the total credit to become negative (the result of undercharging early operations with the promise of repaying the account later on), then the total amortized costs incurred at that time would be below the total actual costs incurred; for the sequence of operations up to that time, the total amortized cost would not be an upper bound on the total actual cost. Thus, we must take care that the total credit in the data structure never becomes negative.

Stack operations

To illustrate the accounting method of amortized analysis, let us return to the stack example. Recall that the actual costs of the operations were

PUSH	1 ,
POP	1 ,
MULTIPOP	$\min(k, s)$,

where k is the argument supplied to MULTIPOP and s is the stack size when it is called. Let us assign the following amortized costs:

PUSH	2 ,
POP	0 ,
MULTIPOP	0 .

Note that the amortized cost of MULTIPOP is a constant (0), whereas the actual cost is variable. Here, all three amortized costs are constant. In general, the amortized costs of the operations under consideration may differ from each other, and they may even differ asymptotically.

We shall now show that we can pay for any sequence of stack operations by charging the amortized costs. Suppose we use a dollar bill to represent each unit of cost. We start with an empty stack. Recall the analogy of Section 10.1 between the stack data structure and a stack of plates in a cafeteria. When we push a plate on the stack, we use 1 dollar to pay the actual cost of the push and are left with a credit of 1 dollar (out of the 2 dollars charged), which we leave on top of the plate. At any point in time, every plate on the stack has a dollar of credit on it.

The dollar stored on the plate serves as prepayment for the cost of popping it from the stack. When we execute a POP operation, we charge the operation nothing and pay its actual cost using the credit stored in the stack. To pop a plate, we take the dollar of credit off the plate and use it to pay the actual cost of the operation. Thus, by charging the PUSH operation a little bit more, we can charge the POP operation nothing.

Moreover, we can also charge MULTIPOP operations nothing. To pop the first plate, we take the dollar of credit off the plate and use it to pay the actual cost of a POP operation. To pop a second plate, we again have a dollar of credit on the plate to pay for the POP operation, and so on. Thus, we have always charged enough up front to pay for MULTIPOP operations. In other words, since each plate on the stack has 1 dollar of credit on it, and the stack always has a nonnegative number of plates, we have ensured that the amount of credit is always nonnegative. Thus, for *any* sequence of n PUSH, POP, and MULTIPOP operations, the total amortized cost is an upper bound on the total actual cost. Since the total amortized cost is $O(n)$, so is the total actual cost.

Incrementing a binary counter

As another illustration of the accounting method, we analyze the INCREMENT operation on a binary counter that starts at zero. As we observed earlier, the running time of this operation is proportional to the number of bits flipped, which we shall use as our cost for this example. Let us once again use a dollar bill to represent each unit of cost (the flipping of a bit in this example).

For the amortized analysis, let us charge an amortized cost of 2 dollars to set a bit to 1. When a bit is set, we use 1 dollar (out of the 2 dollars charged) to pay for the actual setting of the bit, and we place the other dollar on the bit as credit to be used later when we flip the bit back to 0. At any point in time, every 1 in the counter has a dollar of credit on it, and thus we can charge nothing to reset a bit to 0; we just pay for the reset with the dollar bill on the bit.

Now we can determine the amortized cost of INCREMENT. The cost of resetting the bits within the **while** loop is paid for by the dollars on the bits that are reset. The INCREMENT procedure sets at most one bit, in line 6, and therefore the amortized cost of an INCREMENT operation is at most 2 dollars. The number of 1s in the counter never becomes negative, and thus the amount of credit stays nonnegative at all times. Thus, for n INCREMENT operations, the total amortized cost is $O(n)$, which bounds the total actual cost.

Exercises

17.2-1

Suppose we perform a sequence of stack operations on a stack whose size never exceeds k. After every k operations, we make a copy of the entire stack for backup purposes. Show that the cost of n stack operations, including copying the stack, is $O(n)$ by assigning suitable amortized costs to the various stack operations.

17.2-2
Redo Exercise 17.1-3 using an accounting method of analysis.

17.2-3
Suppose we wish not only to increment a counter but also to reset it to zero (i.e., make all bits in it 0). Counting the time to examine or modify a bit as $\Theta(1)$, show how to implement a counter as an array of bits so that any sequence of n INCREMENT and RESET operations takes time $O(n)$ on an initially zero counter. (*Hint:* Keep a pointer to the high-order 1.)

17.3 The potential method

Instead of representing prepaid work as credit stored with specific objects in the data structure, the ***potential method*** of amortized analysis represents the prepaid work as "potential energy," or just "potential," which can be released to pay for future operations. We associate the potential with the data structure as a whole rather than with specific objects within the data structure.

The potential method works as follows. We will perform n operations, starting with an initial data structure D_0. For each $i = 1, 2, \ldots, n$, we let c_i be the actual cost of the ith operation and D_i be the data structure that results after applying the ith operation to data structure D_{i-1}. A ***potential function*** Φ maps each data structure D_i to a real number $\Phi(D_i)$, which is the ***potential*** associated with data structure D_i. The ***amortized cost*** $\hat{c}_i$ of the ith operation with respect to potential function Φ is defined by

$$\hat{c}_i = c_i + \Phi(D_i) - \Phi(D_{i-1}) \; . \tag{17.2}$$

The amortized cost of each operation is therefore its actual cost plus the change in potential due to the operation. By equation (17.2), the total amortized cost of the n operations is

$$\begin{aligned} \sum_{i=1}^{n} \hat{c}_i &= \sum_{i=1}^{n} (c_i + \Phi(D_i) - \Phi(D_{i-1})) \\ &= \sum_{i=1}^{n} c_i + \Phi(D_n) - \Phi(D_0) \; . \end{aligned} \tag{17.3}$$

The second equality follows from equation (A.9) because the $\Phi(D_i)$ terms telescope.

If we can define a potential function Φ so that $\Phi(D_n) \geq \Phi(D_0)$, then the total amortized cost $\sum_{i=1}^{n} \hat{c}_i$ gives an upper bound on the total actual cost $\sum_{i=1}^{n} c_i$.

In practice, we do not always know how many operations might be performed. Therefore, if we require that $\Phi(D_i) \geq \Phi(D_0)$ for all i, then we guarantee, as in the accounting method, that we pay in advance. We usually just define $\Phi(D_0)$ to be 0 and then show that $\Phi(D_i) \geq 0$ for all i. (See Exercise 17.3-1 for an easy way to handle cases in which $\Phi(D_0) \neq 0$.)

Intuitively, if the potential difference $\Phi(D_i) - \Phi(D_{i-1})$ of the ith operation is positive, then the amortized cost $\hat{c}_i$ represents an overcharge to the ith operation, and the potential of the data structure increases. If the potential difference is negative, then the amortized cost represents an undercharge to the ith operation, and the decrease in the potential pays for the actual cost of the operation.

The amortized costs defined by equations (17.2) and (17.3) depend on the choice of the potential function Φ. Different potential functions may yield different amortized costs yet still be upper bounds on the actual costs. We often find trade-offs that we can make in choosing a potential function; the best potential function to use depends on the desired time bounds.

Stack operations

To illustrate the potential method, we return once again to the example of the stack operations PUSH, POP, and MULTIPOP. We define the potential function Φ on a stack to be the number of objects in the stack. For the empty stack D_0 with which we start, we have $\Phi(D_0) = 0$. Since the number of objects in the stack is never negative, the stack D_i that results after the ith operation has nonnegative potential, and thus

$$\begin{aligned} \Phi(D_i) &\geq 0 \\ &= \Phi(D_0) . \end{aligned}$$

The total amortized cost of n operations with respect to Φ therefore represents an upper bound on the actual cost.

Let us now compute the amortized costs of the various stack operations. If the ith operation on a stack containing s objects is a PUSH operation, then the potential difference is

$$\begin{aligned} \Phi(D_i) - \Phi(D_{i-1}) &= (s+1) - s \\ &= 1 . \end{aligned}$$

By equation (17.2), the amortized cost of this PUSH operation is

$$\begin{aligned} \hat{c}_i &= c_i + \Phi(D_i) - \Phi(D_{i-1}) \\ &= 1 + 1 \\ &= 2 . \end{aligned}$$

Suppose that the ith operation on the stack is MULTIPOP(S, k), which causes $k' = \min(k, s)$ objects to be popped off the stack. The actual cost of the operation is k', and the potential difference is

$$\Phi(D_i) - \Phi(D_{i-1}) = -k' .$$

Thus, the amortized cost of the MULTIPOP operation is

$$\begin{aligned} \hat{c}_i &= c_i + \Phi(D_i) - \Phi(D_{i-1}) \\ &= k' - k' \\ &= 0 . \end{aligned}$$

Similarly, the amortized cost of an ordinary POP operation is 0.

The amortized cost of each of the three operations is $O(1)$, and thus the total amortized cost of a sequence of n operations is $O(n)$. Since we have already argued that $\Phi(D_i) \geq \Phi(D_0)$, the total amortized cost of n operations is an upper bound on the total actual cost. The worst-case cost of n operations is therefore $O(n)$.

Incrementing a binary counter

As another example of the potential method, we again look at incrementing a binary counter. This time, we define the potential of the counter after the ith INCREMENT operation to be b_i, the number of 1s in the counter after the ith operation.

Let us compute the amortized cost of an INCREMENT operation. Suppose that the ith INCREMENT operation resets t_i bits. The actual cost of the operation is therefore at most $t_i + 1$, since in addition to resetting t_i bits, it sets at most one bit to 1. If $b_i = 0$, then the ith operation resets all k bits, and so $b_{i-1} = t_i = k$. If $b_i > 0$, then $b_i = b_{i-1} - t_i + 1$. In either case, $b_i \leq b_{i-1} - t_i + 1$, and the potential difference is

$$\begin{aligned} \Phi(D_i) - \Phi(D_{i-1}) &\leq (b_{i-1} - t_i + 1) - b_{i-1} \\ &= 1 - t_i . \end{aligned}$$

The amortized cost is therefore

$$\begin{aligned} \hat{c}_i &= c_i + \Phi(D_i) - \Phi(D_{i-1}) \\ &\leq (t_i + 1) + (1 - t_i) \\ &= 2 . \end{aligned}$$

If the counter starts at zero, then $\Phi(D_0) = 0$. Since $\Phi(D_i) \geq 0$ for all i, the total amortized cost of a sequence of n INCREMENT operations is an upper bound on the total actual cost, and so the worst-case cost of n INCREMENT operations is $O(n)$.

The potential method gives us an easy way to analyze the counter even when it does not start at zero. The counter starts with b_0 1s, and after n INCREMENT

operations it has b_n 1s, where $0 \le b_0, b_n \le k$. (Recall that k is the number of bits in the counter.) We can rewrite equation (17.3) as

$$\sum_{i=1}^{n} c_i = \sum_{i=1}^{n} \hat{c}_i - \Phi(D_n) + \Phi(D_0) \; . \tag{17.4}$$

We have $\hat{c}_i \le 2$ for all $1 \le i \le n$. Since $\Phi(D_0) = b_0$ and $\Phi(D_n) = b_n$, the total actual cost of n INCREMENT operations is

$$\begin{aligned} \sum_{i=1}^{n} c_i &\le \sum_{i=1}^{n} 2 - b_n + b_0 \\ &= 2n - b_n + b_0 \; . \end{aligned}$$

Note in particular that since $b_0 \le k$, as long as $k = O(n)$, the total actual cost is $O(n)$. In other words, if we execute at least $n = \Omega(k)$ INCREMENT operations, the total actual cost is $O(n)$, no matter what initial value the counter contains.

Exercises

17.3-1

Suppose we have a potential function Φ such that $\Phi(D_i) \ge \Phi(D_0)$ for all i, but $\Phi(D_0) \ne 0$. Show that there exists a potential function Φ' such that $\Phi'(D_0) = 0$, $\Phi'(D_i) \ge 0$ for all $i \ge 1$, and the amortized costs using Φ' are the same as the amortized costs using Φ.

17.3-2

Redo Exercise 17.1-3 using a potential method of analysis.

17.3-3

Consider an ordinary binary min-heap data structure with n elements supporting the instructions INSERT and EXTRACT-MIN in $O(\lg n)$ worst-case time. Give a potential function Φ such that the amortized cost of INSERT is $O(\lg n)$ and the amortized cost of EXTRACT-MIN is $O(1)$, and show that it works.

17.3-4

What is the total cost of executing n of the stack operations PUSH, POP, and MULTIPOP, assuming that the stack begins with s_0 objects and finishes with s_n objects?

17.3-5

Suppose that a counter begins at a number with b 1s in its binary representation, rather than at 0. Show that the cost of performing n INCREMENT operations is $O(n)$ if $n = \Omega(b)$. (Do not assume that b is constant.)

17.3-6
Show how to implement a queue with two ordinary stacks (Exercise 10.1-6) so that the amortized cost of each ENQUEUE and each DEQUEUE operation is $O(1)$.

17.3-7
Design a data structure to support the following two operations for a dynamic multiset S of integers, which allows duplicate values:

INSERT(S, x) inserts x into S.

DELETE-LARGER-HALF(S) deletes the largest $\lceil |S| / 2 \rceil$ elements from S.

Explain how to implement this data structure so that any sequence of m INSERT and DELETE-LARGER-HALF operations runs in $O(m)$ time. Your implementation should also include a way to output the elements of S in $O(|S|)$ time.

17.4 Dynamic tables

We do not always know in advance how many objects some applications will store in a table. We might allocate space for a table, only to find out later that it is not enough. We must then reallocate the table with a larger size and copy all objects stored in the original table over into the new, larger table. Similarly, if many objects have been deleted from the table, it may be worthwhile to reallocate the table with a smaller size. In this section, we study this problem of dynamically expanding and contracting a table. Using amortized analysis, we shall show that the amortized cost of insertion and deletion is only $O(1)$, even though the actual cost of an operation is large when it triggers an expansion or a contraction. Moreover, we shall see how to guarantee that the unused space in a dynamic table never exceeds a constant fraction of the total space.

We assume that the dynamic table supports the operations TABLE-INSERT and TABLE-DELETE. TABLE-INSERT inserts into the table an item that occupies a single ***slot***, that is, a space for one item. Likewise, TABLE-DELETE removes an item from the table, thereby freeing a slot. The details of the data-structuring method used to organize the table are unimportant; we might use a stack (Section 10.1), a heap (Chapter 6), or a hash table (Chapter 11). We might also use an array or collection of arrays to implement object storage, as we did in Section 10.3.

We shall find it convenient to use a concept introduced in our analysis of hashing (Chapter 11). We define the ***load factor*** $\alpha(T)$ of a nonempty table T to be the number of items stored in the table divided by the size (number of slots) of the table. We assign an empty table (one with no items) size 0, and we define its load factor to be 1. If the load factor of a dynamic table is bounded below by a constant,

the unused space in the table is never more than a constant fraction of the total amount of space.

We start by analyzing a dynamic table in which we only insert items. We then consider the more general case in which we both insert and delete items.

17.4.1 Table expansion

Let us assume that storage for a table is allocated as an array of slots. A table fills up when all slots have been used or, equivalently, when its load factor is 1.[1] In some software environments, upon attempting to insert an item into a full table, the only alternative is to abort with an error. We shall assume, however, that our software environment, like many modern ones, provides a memory-management system that can allocate and free blocks of storage on request. Thus, upon inserting an item into a full table, we can ***expand*** the table by allocating a new table with more slots than the old table had. Because we always need the table to reside in contiguous memory, we must allocate a new array for the larger table and then copy items from the old table into the new table.

A common heuristic allocates a new table with twice as many slots as the old one. If the only table operations are insertions, then the load factor of the table is always at least $1/2$, and thus the amount of wasted space never exceeds half the total space in the table.

In the following pseudocode, we assume that T is an object representing the table. The attribute $T.table$ contains a pointer to the block of storage representing the table, $T.num$ contains the number of items in the table, and $T.size$ gives the total number of slots in the table. Initially, the table is empty: $T.num = T.size = 0$.

```
TABLE-INSERT(T, x)
 1  if T.size == 0
 2      allocate T.table with 1 slot
 3      T.size = 1
 4  if T.num == T.size
 5      allocate new-table with 2 · T.size slots
 6      insert all items in T.table into new-table
 7      free T.table
 8      T.table = new-table
 9      T.size = 2 · T.size
10  insert x into T.table
11  T.num = T.num + 1
```

[1] In some situations, such as an open-address hash table, we may wish to consider a table to be full if its load factor equals some constant strictly less than 1. (See Exercise 17.4-1.)

Notice that we have two "insertion" procedures here: the TABLE-INSERT procedure itself and the ***elementary insertion*** into a table in lines 6 and 10. We can analyze the running time of TABLE-INSERT in terms of the number of elementary insertions by assigning a cost of 1 to each elementary insertion. We assume that the actual running time of TABLE-INSERT is linear in the time to insert individual items, so that the overhead for allocating an initial table in line 2 is constant and the overhead for allocating and freeing storage in lines 5 and 7 is dominated by the cost of transferring items in line 6. We call the event in which lines 5–9 are executed an ***expansion***.

Let us analyze a sequence of n TABLE-INSERT operations on an initially empty table. What is the cost c_i of the ith operation? If the current table has room for the new item (or if this is the first operation), then $c_i = 1$, since we need only perform the one elementary insertion in line 10. If the current table is full, however, and an expansion occurs, then $c_i = i$: the cost is 1 for the elementary insertion in line 10 plus $i - 1$ for the items that we must copy from the old table to the new table in line 6. If we perform n operations, the worst-case cost of an operation is $O(n)$, which leads to an upper bound of $O(n^2)$ on the total running time for n operations.

This bound is not tight, because we rarely expand the table in the course of n TABLE-INSERT operations. Specifically, the ith operation causes an expansion only when $i - 1$ is an exact power of 2. The amortized cost of an operation is in fact $O(1)$, as we can show using aggregate analysis. The cost of the ith operation is

$$c_i = \begin{cases} i & \text{if } i-1 \text{ is an exact power of 2 ,} \\ 1 & \text{otherwise .} \end{cases}$$

The total cost of n TABLE-INSERT operations is therefore

$$\begin{aligned} \sum_{i=1}^{n} c_i &\le n + \sum_{j=0}^{\lfloor \lg n \rfloor} 2^j \\ &< n + 2n \\ &= 3n \ , \end{aligned}$$

because at most n operations cost 1 and the costs of the remaining operations form a geometric series. Since the total cost of n TABLE-INSERT operations is bounded by $3n$, the amortized cost of a single operation is at most 3.

By using the accounting method, we can gain some feeling for why the amortized cost of a TABLE-INSERT operation should be 3. Intuitively, each item pays for 3 elementary insertions: inserting itself into the current table, moving itself when the table expands, and moving another item that has already been moved once when the table expands. For example, suppose that the size of the table is m immediately after an expansion. Then the table holds $m/2$ items, and it contains

no credit. We charge 3 dollars for each insertion. The elementary insertion that occurs immediately costs 1 dollar. We place another dollar as credit on the item inserted. We place the third dollar as credit on one of the $m/2$ items already in the table. The table will not fill again until we have inserted another $m/2 - 1$ items, and thus, by the time the table contains m items and is full, we will have placed a dollar on each item to pay to reinsert it during the expansion.

We can use the potential method to analyze a sequence of n TABLE-INSERT operations, and we shall use it in Section 17.4.2 to design a TABLE-DELETE operation that has an $O(1)$ amortized cost as well. We start by defining a potential function Φ that is 0 immediately after an expansion but builds to the table size by the time the table is full, so that we can pay for the next expansion by the potential. The function

$$\Phi(T) = 2 \cdot T.num - T.size \tag{17.5}$$

is one possibility. Immediately after an expansion, we have $T.num = T.size/2$, and thus $\Phi(T) = 0$, as desired. Immediately before an expansion, we have $T.num = T.size$, and thus $\Phi(T) = T.num$, as desired. The initial value of the potential is 0, and since the table is always at least half full, $T.num \geq T.size/2$, which implies that $\Phi(T)$ is always nonnegative. Thus, the sum of the amortized costs of n TABLE-INSERT operations gives an upper bound on the sum of the actual costs.

To analyze the amortized cost of the ith TABLE-INSERT operation, we let num_i denote the number of items stored in the table after the ith operation, $size_i$ denote the total size of the table after the ith operation, and Φ_i denote the potential after the ith operation. Initially, we have $num_0 = 0$, $size_0 = 0$, and $\Phi_0 = 0$.

If the ith TABLE-INSERT operation does not trigger an expansion, then we have $size_i = size_{i-1}$ and the amortized cost of the operation is

$$\begin{aligned}
\widehat{c}_i &= c_i + \Phi_i - \Phi_{i-1} \\
&= 1 + (2 \cdot num_i - size_i) - (2 \cdot num_{i-1} - size_{i-1}) \\
&= 1 + (2 \cdot num_i - size_i) - (2(num_i - 1) - size_i) \\
&= 3 .
\end{aligned}$$

If the ith operation does trigger an expansion, then we have $size_i = 2 \cdot size_{i-1}$ and $size_{i-1} = num_{i-1} = num_i - 1$, which implies that $size_i = 2 \cdot (num_i - 1)$. Thus, the amortized cost of the operation is

$$\begin{aligned}
\widehat{c}_i &= c_i + \Phi_i - \Phi_{i-1} \\
&= num_i + (2 \cdot num_i - size_i) - (2 \cdot num_{i-1} - size_{i-1}) \\
&= num_i + (2 \cdot num_i - 2 \cdot (num_i - 1)) - (2(num_i - 1) - (num_i - 1)) \\
&= num_i + 2 - (num_i - 1) \\
&= 3 .
\end{aligned}$$

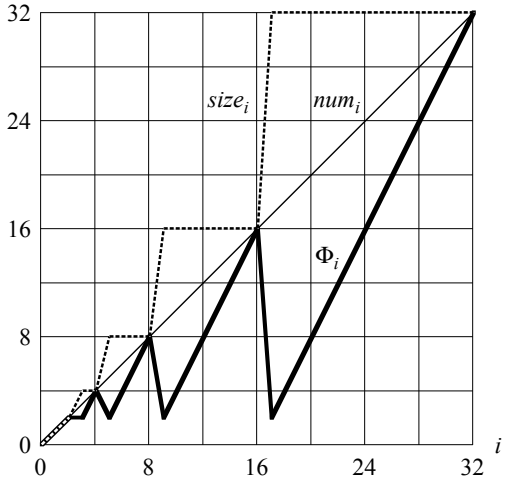


Figure 17.3 The effect of a sequence of n TABLE-INSERT operations on the number num_i of items in the table, the number $size_i$ of slots in the table, and the potential $\Phi_i = 2 \cdot num_i - size_i$, each being measured after the ith operation. The thin line shows num_i, the dashed line shows $size_i$, and the thick line shows Φ_i. Notice that immediately before an expansion, the potential has built up to the number of items in the table, and therefore it can pay for moving all the items to the new table. Afterwards, the potential drops to 0, but it is immediately increased by 2 upon inserting the item that caused the expansion.

Figure 17.3 plots the values of num_i, $size_i$, and Φ_i against i. Notice how the potential builds to pay for expanding the table.

17.4.2 Table expansion and contraction

To implement a TABLE-DELETE operation, it is simple enough to remove the specified item from the table. In order to limit the amount of wasted space, however, we might wish to ***contract*** the table when the load factor becomes too small. Table contraction is analogous to table expansion: when the number of items in the table drops too low, we allocate a new, smaller table and then copy the items from the old table into the new one. We can then free the storage for the old table by returning it to the memory-management system. Ideally, we would like to preserve two properties:

- the load factor of the dynamic table is bounded below by a positive constant, and
- the amortized cost of a table operation is bounded above by a constant.

We assume that we measure the cost in terms of elementary insertions and deletions.

You might think that we should double the table size upon inserting an item into a full table and halve the size when a deleting an item would cause the table to become less than half full. This strategy would guarantee that the load factor of the table never drops below $1/2$, but unfortunately, it can cause the amortized cost of an operation to be quite large. Consider the following scenario. We perform n operations on a table T, where n is an exact power of 2. The first $n/2$ operations are insertions, which by our previous analysis cost a total of $\Theta(n)$. At the end of this sequence of insertions, $T.num = T.size = n/2$. For the second $n/2$ operations, we perform the following sequence:

insert, delete, delete, insert, insert, delete, delete, insert, insert, ...

The first insertion causes the table to expand to size n. The two following deletions cause the table to contract back to size $n/2$. Two further insertions cause another expansion, and so forth. The cost of each expansion and contraction is $\Theta(n)$, and there are $\Theta(n)$ of them. Thus, the total cost of the n operations is $\Theta(n^2)$, making the amortized cost of an operation $\Theta(n)$.

The downside of this strategy is obvious: after expanding the table, we do not delete enough items to pay for a contraction. Likewise, after contracting the table, we do not insert enough items to pay for an expansion.

We can improve upon this strategy by allowing the load factor of the table to drop below $1/2$. Specifically, we continue to double the table size upon inserting an item into a full table, but we halve the table size when deleting an item causes the table to become less than $1/4$ full, rather than $1/2$ full as before. The load factor of the table is therefore bounded below by the constant $1/4$.

Intuitively, we would consider a load factor of $1/2$ to be ideal, and the table's potential would then be 0. As the load factor deviates from $1/2$, the potential increases so that by the time we expand or contract the table, the table has garnered sufficient potential to pay for copying all the items into the newly allocated table. Thus, we will need a potential function that has grown to $T.num$ by the time that the load factor has either increased to 1 or decreased to $1/4$. After either expanding or contracting the table, the load factor goes back to $1/2$ and the table's potential reduces back to 0.

We omit the code for TABLE-DELETE, since it is analogous to TABLE-INSERT. For our analysis, we shall assume that whenever the number of items in the table drops to 0, we free the storage for the table. That is, if $T.num = 0$, then $T.size = 0$.

We can now use the potential method to analyze the cost of a sequence of n TABLE-INSERT and TABLE-DELETE operations. We start by defining a potential function Φ that is 0 immediately after an expansion or contraction and builds as the load factor increases to 1 or decreases to $1/4$. Let us denote the load fac-

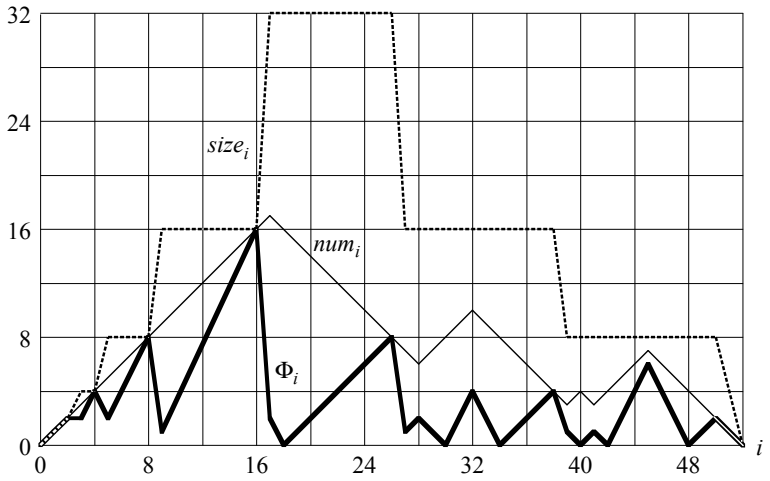


Figure 17.4 The effect of a sequence of n TABLE-INSERT and TABLE-DELETE operations on the number num_i of items in the table, the number $size_i$ of slots in the table, and the potential

$$\Phi_i = \begin{cases} 2 \cdot num_i - size_i & \text{if } \alpha_i \geq 1/2 , \\ size_i/2 - num_i & \text{if } \alpha_i < 1/2 , \end{cases}$$

each measured after the ith operation. The thin line shows num_i, the dashed line shows $size_i$, and the thick line shows Φ_i. Notice that immediately before an expansion, the potential has built up to the number of items in the table, and therefore it can pay for moving all the items to the new table. Likewise, immediately before a contraction, the potential has built up to the number of items in the table.

tor of a nonempty table T by $\alpha(T) = T.num/T.size$. Since for an empty table, $T.num = T.size = 0$ and $\alpha(T) = 1$, we always have $T.num = \alpha(T) \cdot T.size$, whether the table is empty or not. We shall use as our potential function

$$\Phi(T) = \begin{cases} 2 \cdot T.num - T.size & \text{if } \alpha(T) \geq 1/2 , \\ T.size/2 - T.num & \text{if } \alpha(T) < 1/2 . \end{cases} \tag{17.6}$$

Observe that the potential of an empty table is 0 and that the potential is never negative. Thus, the total amortized cost of a sequence of operations with respect to Φ provides an upper bound on the actual cost of the sequence.

Before proceeding with a precise analysis, we pause to observe some properties of the potential function, as illustrated in Figure 17.4. Notice that when the load factor is $1/2$, the potential is 0. When the load factor is 1, we have $T.size = T.num$, which implies $\Phi(T) = T.num$, and thus the potential can pay for an expansion if an item is inserted. When the load factor is $1/4$, we have $T.size = 4 \cdot T.num$, which

implies $\Phi(T) = T.num$, and thus the potential can pay for a contraction if an item is deleted.

To analyze a sequence of n TABLE-INSERT and TABLE-DELETE operations, we let c_i denote the actual cost of the ith operation, $\widehat{c}_i$ denote its amortized cost with respect to Φ, num_i denote the number of items stored in the table after the ith operation, $size_i$ denote the total size of the table after the ith operation, α_i denote the load factor of the table after the ith operation, and Φ_i denote the potential after the ith operation. Initially, $num_0 = 0$, $size_0 = 0$, $\alpha_0 = 1$, and $\Phi_0 = 0$.

We start with the case in which the ith operation is TABLE-INSERT. The analysis is identical to that for table expansion in Section 17.4.1 if $\alpha_{i-1} \geq 1/2$. Whether the table expands or not, the amortized cost $\widehat{c}_i$ of the operation is at most 3. If $\alpha_{i-1} < 1/2$, the table cannot expand as a result of the operation, since the table expands only when $\alpha_{i-1} = 1$. If $\alpha_i < 1/2$ as well, then the amortized cost of the ith operation is

$$\begin{aligned}
\widehat{c}_i &= c_i + \Phi_i - \Phi_{i-1} \\
&= 1 + (size_i/2 - num_i) - (size_{i-1}/2 - num_{i-1}) \\
&= 1 + (size_i/2 - num_i) - (size_i/2 - (num_i - 1)) \\
&= 0 .
\end{aligned}$$

If $\alpha_{i-1} < 1/2$ but $\alpha_i \geq 1/2$, then

$$\begin{aligned}
\widehat{c}_i &= c_i + \Phi_i - \Phi_{i-1} \\
&= 1 + (2 \cdot num_i - size_i) - (size_{i-1}/2 - num_{i-1}) \\
&= 1 + (2(num_{i-1} + 1) - size_{i-1}) - (size_{i-1}/2 - num_{i-1}) \\
&= 3 \cdot num_{i-1} - \frac{3}{2} size_{i-1} + 3 \\
&= 3\alpha_{i-1} size_{i-1} - \frac{3}{2} size_{i-1} + 3 \\
&< \frac{3}{2} size_{i-1} - \frac{3}{2} size_{i-1} + 3 \\
&= 3 .
\end{aligned}$$

Thus, the amortized cost of a TABLE-INSERT operation is at most 3.

We now turn to the case in which the ith operation is TABLE-DELETE. In this case, $num_i = num_{i-1} - 1$. If $\alpha_{i-1} < 1/2$, then we must consider whether the operation causes the table to contract. If it does not, then $size_i = size_{i-1}$ and the amortized cost of the operation is

$$\begin{aligned}
\widehat{c}_i &= c_i + \Phi_i - \Phi_{i-1} \\
&= 1 + (size_i/2 - num_i) - (size_{i-1}/2 - num_{i-1}) \\
&= 1 + (size_i/2 - num_i) - (size_i/2 - (num_i + 1)) \\
&= 2 .
\end{aligned}$$

If $\alpha_{i-1} < 1/2$ and the ith operation does trigger a contraction, then the actual cost of the operation is $c_i = num_i + 1$, since we delete one item and move num_i items. We have $size_i/2 = size_{i-1}/4 = num_{i-1} = num_i + 1$, and the amortized cost of the operation is

$$\begin{aligned}
\widehat{c}_i &= c_i + \Phi_i - \Phi_{i-1} \\
&= (num_i + 1) + (size_i/2 - num_i) - (size_{i-1}/2 - num_{i-1}) \\
&= (num_i + 1) + ((num_i + 1) - num_i) - ((2 \cdot num_i + 2) - (num_i + 1)) \\
&= 1 \, .
\end{aligned}$$

When the ith operation is a TABLE-DELETE and $\alpha_{i-1} \geq 1/2$, the amortized cost is also bounded above by a constant. We leave the analysis as Exercise 17.4-2.

In summary, since the amortized cost of each operation is bounded above by a constant, the actual time for any sequence of n operations on a dynamic table is $O(n)$.

Exercises

17.4-1

Suppose that we wish to implement a dynamic, open-address hash table. Why might we consider the table to be full when its load factor reaches some value α that is strictly less than 1? Describe briefly how to make insertion into a dynamic, open-address hash table run in such a way that the expected value of the amortized cost per insertion is $O(1)$. Why is the expected value of the actual cost per insertion not necessarily $O(1)$ for all insertions?

17.4-2

Show that if $\alpha_{i-1} \geq 1/2$ and the ith operation on a dynamic table is TABLE-DELETE, then the amortized cost of the operation with respect to the potential function (17.6) is bounded above by a constant.

17.4-3

Suppose that instead of contracting a table by halving its size when its load factor drops below $1/4$, we contract it by multiplying its size by $2/3$ when its load factor drops below $1/3$. Using the potential function

$$\Phi(T) = |2 \cdot T.num - T.size| \, ,$$

show that the amortized cost of a TABLE-DELETE that uses this strategy is bounded above by a constant.

Problems

17-1 Bit-reversed binary counter

Chapter 30 examines an important algorithm called the fast Fourier transform, or FFT. The first step of the FFT algorithm performs a ***bit-reversal permutation*** on an input array $A[0..n-1]$ whose length is $n = 2^k$ for some nonnegative integer k. This permutation swaps elements whose indices have binary representations that are the reverse of each other.

We can express each index a as a k-bit sequence $\langle a_{k-1}, a_{k-2}, \ldots, a_0 \rangle$, where $a = \sum_{i=0}^{k-1} a_i \, 2^i$. We define

$$\mathrm{rev}_k(\langle a_{k-1}, a_{k-2}, \ldots, a_0 \rangle) = \langle a_0, a_1, \ldots, a_{k-1} \rangle \; ;$$

thus,

$$\mathrm{rev}_k(a) = \sum_{i=0}^{k-1} a_{k-i-1} 2^i \; .$$

For example, if $n = 16$ (or, equivalently, $k = 4$), then $\mathrm{rev}_k(3) = 12$, since the 4-bit representation of 3 is 0011, which when reversed gives 1100, the 4-bit representation of 12.

a. Given a function rev_k that runs in $\Theta(k)$ time, write an algorithm to perform the bit-reversal permutation on an array of length $n = 2^k$ in $O(nk)$ time.

We can use an algorithm based on an amortized analysis to improve the running time of the bit-reversal permutation. We maintain a "bit-reversed counter" and a procedure BIT-REVERSED-INCREMENT that, when given a bit-reversed-counter value a, produces $\mathrm{rev}_k(\mathrm{rev}_k(a) + 1)$. If $k = 4$, for example, and the bit-reversed counter starts at 0, then successive calls to BIT-REVERSED-INCREMENT produce the sequence

$$0000, 1000, 0100, 1100, 0010, 1010, \ldots = 0, 8, 4, 12, 2, 10, \ldots \; .$$

b. Assume that the words in your computer store k-bit values and that in unit time, your computer can manipulate the binary values with operations such as shifting left or right by arbitrary amounts, bitwise-AND, bitwise-OR, etc. Describe an implementation of the BIT-REVERSED-INCREMENT procedure that allows the bit-reversal permutation on an n-element array to be performed in a total of $O(n)$ time.

c. Suppose that you can shift a word left or right by only one bit in unit time. Is it still possible to implement an $O(n)$-time bit-reversal permutation?

17-2 Making binary search dynamic

Binary search of a sorted array takes logarithmic search time, but the time to insert a new element is linear in the size of the array. We can improve the time for insertion by keeping several sorted arrays.

Specifically, suppose that we wish to support SEARCH and INSERT on a set of n elements. Let $k = \lceil \lg(n+1) \rceil$, and let the binary representation of n be $\langle n_{k-1}, n_{k-2}, \ldots, n_0 \rangle$. We have k sorted arrays $A_0, A_1, \ldots, A_{k-1}$, where for $i = 0, 1, \ldots, k-1$, the length of array A_i is 2^i. Each array is either full or empty, depending on whether $n_i = 1$ or $n_i = 0$, respectively. The total number of elements held in all k arrays is therefore $\sum_{i=0}^{k-1} n_i \, 2^i = n$. Although each individual array is sorted, elements in different arrays bear no particular relationship to each other.

a. Describe how to perform the SEARCH operation for this data structure. Analyze its worst-case running time.

b. Describe how to perform the INSERT operation. Analyze its worst-case and amortized running times.

c. Discuss how to implement DELETE.

17-3 Amortized weight-balanced trees

Consider an ordinary binary search tree augmented by adding to each node x the attribute $x.size$ giving the number of keys stored in the subtree rooted at x. Let α be a constant in the range $1/2 \le \alpha < 1$. We say that a given node x is ***α-balanced*** if $x.left.size \le \alpha \cdot x.size$ and $x.right.size \le \alpha \cdot x.size$. The tree as a whole is ***α-balanced*** if every node in the tree is α-balanced. The following amortized approach to maintaining weight-balanced trees was suggested by G. Varghese.

a. A $1/2$-balanced tree is, in a sense, as balanced as it can be. Given a node x in an arbitrary binary search tree, show how to rebuild the subtree rooted at x so that it becomes $1/2$-balanced. Your algorithm should run in time $\Theta(x.size)$, and it can use $O(x.size)$ auxiliary storage.

b. Show that performing a search in an n-node α-balanced binary search tree takes $O(\lg n)$ worst-case time.

For the remainder of this problem, assume that the constant α is strictly greater than $1/2$. Suppose that we implement INSERT and DELETE as usual for an n-node binary search tree, except that after every such operation, if any node in the tree is no longer α-balanced, then we "rebuild" the subtree rooted at the highest such node in the tree so that it becomes $1/2$-balanced.

We shall analyze this rebuilding scheme using the potential method. For a node x in a binary search tree T, we define

$$\Delta(x) = |x.left.size - x.right.size| ,$$

and we define the potential of T as

$$\Phi(T) = c \sum_{x \in T : \Delta(x) \geq 2} \Delta(x) ,$$

where c is a sufficiently large constant that depends on α.

c. Argue that any binary search tree has nonnegative potential and that a $1/2$-balanced tree has potential 0.

d. Suppose that m units of potential can pay for rebuilding an m-node subtree. How large must c be in terms of α in order for it to take $O(1)$ amortized time to rebuild a subtree that is not α-balanced?

e. Show that inserting a node into or deleting a node from an n-node α-balanced tree costs $O(\lg n)$ amortized time.

17-4 The cost of restructuring red-black trees

There are four basic operations on red-black trees that perform ***structural modifications***: node insertions, node deletions, rotations, and color changes. We have seen that RB-INSERT and RB-DELETE use only $O(1)$ rotations, node insertions, and node deletions to maintain the red-black properties, but they may make many more color changes.

a. Describe a legal red-black tree with n nodes such that calling RB-INSERT to add the $(n + 1)$st node causes $\Omega(\lg n)$ color changes. Then describe a legal red-black tree with n nodes for which calling RB-DELETE on a particular node causes $\Omega(\lg n)$ color changes.

Although the worst-case number of color changes per operation can be logarithmic, we shall prove that any sequence of m RB-INSERT and RB-DELETE operations on an initially empty red-black tree causes $O(m)$ structural modifications in the worst case. Note that we count each color change as a structural modification.

b. Some of the cases handled by the main loop of the code of both RB-INSERT-FIXUP and RB-DELETE-FIXUP are ***terminating***: once encountered, they cause the loop to terminate after a constant number of additional operations. For each of the cases of RB-INSERT-FIXUP and RB-DELETE-FIXUP, specify which are terminating and which are not. (*Hint:* Look at Figures 13.5, 13.6, and 13.7.)

We shall first analyze the structural modifications when only insertions are performed. Let T be a red-black tree, and define $\Phi(T)$ to be the number of red nodes in T. Assume that 1 unit of potential can pay for the structural modifications performed by any of the three cases of RB-INSERT-FIXUP.

c. Let T' be the result of applying Case 1 of RB-INSERT-FIXUP to T. Argue that $\Phi(T') = \Phi(T) - 1$.

d. When we insert a node into a red-black tree using RB-INSERT, we can break the operation into three parts. List the structural modifications and potential changes resulting from lines 1–16 of RB-INSERT, from nonterminating cases of RB-INSERT-FIXUP, and from terminating cases of RB-INSERT-FIXUP.

e. Using part (d), argue that the amortized number of structural modifications performed by any call of RB-INSERT is $O(1)$.

We now wish to prove that there are $O(m)$ structural modifications when there are both insertions and deletions. Let us define, for each node x,

$$w(x) = \begin{cases} 0 & \text{if } x \text{ is red ,} \\ 1 & \text{if } x \text{ is black and has no red children ,} \\ 0 & \text{if } x \text{ is black and has one red child ,} \\ 2 & \text{if } x \text{ is black and has two red children .} \end{cases}$$

Now we redefine the potential of a red-black tree T as

$$\Phi(T) = \sum_{x \in T} w(x) ,$$

and let T' be the tree that results from applying any nonterminating case of RB-INSERT-FIXUP or RB-DELETE-FIXUP to T.

f. Show that $\Phi(T') \le \Phi(T) - 1$ for all nonterminating cases of RB-INSERT-FIXUP. Argue that the amortized number of structural modifications performed by any call of RB-INSERT-FIXUP is $O(1)$.

g. Show that $\Phi(T') \le \Phi(T) - 1$ for all nonterminating cases of RB-DELETE-FIXUP. Argue that the amortized number of structural modifications performed by any call of RB-DELETE-FIXUP is $O(1)$.

h. Complete the proof that in the worst case, any sequence of m RB-INSERT and RB-DELETE operations performs $O(m)$ structural modifications.

17-5 Competitive analysis of self-organizing lists with move-to-front

A ***self-organizing list*** is a linked list of n elements, in which each element has a unique key. When we search for an element in the list, we are given a key, and we want to find an element with that key.

A self-organizing list has two important properties:

1. To find an element in the list, given its key, we must traverse the list from the beginning until we encounter the element with the given key. If that element is the kth element from the start of the list, then the cost to find the element is k.
2. We may reorder the list elements after any operation, according to a given rule with a given cost. We may choose any heuristic we like to decide how to reorder the list.

Assume that we start with a given list of n elements, and we are given an access sequence $\sigma = \langle \sigma_1, \sigma_2, \ldots, \sigma_m \rangle$ of keys to find, in order. The cost of the sequence is the sum of the costs of the individual accesses in the sequence.

Out of the various possible ways to reorder the list after an operation, this problem focuses on transposing adjacent list elements—switching their positions in the list—with a unit cost for each transpose operation. You will show, by means of a potential function, that a particular heuristic for reordering the list, move-to-front, entails a total cost no worse than 4 times that of any other heuristic for maintaining the list order—even if the other heuristic knows the access sequence in advance! We call this type of analysis a ***competitive analysis***.

For a heuristic H and a given initial ordering of the list, denote the access cost of sequence σ by $C_H(\sigma)$. Let m be the number of accesses in σ.

a. Argue that if heuristic H does not know the access sequence in advance, then the worst-case cost for H on an access sequence σ is $C_H(\sigma) = \Omega(mn)$.

With the ***move-to-front*** heuristic, immediately after searching for an element x, we move x to the first position on the list (i.e., the front of the list).

Let $\text{rank}_L(x)$ denote the rank of element x in list L, that is, the position of x in list L. For example, if x is the fourth element in L, then $\text{rank}_L(x) = 4$. Let c_i denote the cost of access σ_i using the move-to-front heuristic, which includes the cost of finding the element in the list and the cost of moving it to the front of the list by a series of transpositions of adjacent list elements.

b. Show that if σ_i accesses element x in list L using the move-to-front heuristic, then $c_i = 2 \cdot \text{rank}_L(x) - 1$.

Now we compare move-to-front with any other heuristic H that processes an access sequence according to the two properties above. Heuristic H may transpose

elements in the list in any way it wants, and it might even know the entire access sequence in advance.

Let L_i be the list after access σ_i using move-to-front, and let L_i^* be the list after access σ_i using heuristic H. We denote the cost of access σ_i by c_i for move-to-front and by c_i^* for heuristic H. Suppose that heuristic H performs t_i^* transpositions during access σ_i.

c. In part (b), you showed that $c_i = 2 \cdot \text{rank}_{L_{i-1}}(x) - 1$. Now show that $c_i^* = \text{rank}_{L_{i-1}^*}(x) + t_i^*$.

We define an ***inversion*** in list L_i as a pair of elements y and z such that y precedes z in L_i and z precedes y in list L_i^*. Suppose that list L_i has q_i inversions after processing the access sequence $\langle \sigma_1, \sigma_2, \ldots, \sigma_i \rangle$. Then, we define a potential function Φ that maps L_i to a real number by $\Phi(L_i) = 2q_i$. For example, if L_i has the elements $\langle e, c, a, d, b \rangle$ and L_i^* has the elements $\langle c, a, b, d, e \rangle$, then L_i has 5 inversions $((e,c),(e,a),(e,d),(e,b),(d,b))$, and so $\Phi(L_i) = 10$. Observe that $\Phi(L_i) \geq 0$ for all i and that, if move-to-front and heuristic H start with the same list L_0, then $\Phi(L_0) = 0$.

d. Argue that a transposition either increases the potential by 2 or decreases the potential by 2.

Suppose that access σ_i finds the element x. To understand how the potential changes due to σ_i, let us partition the elements other than x into four sets, depending on where they are in the lists just before the ith access:

- Set A consists of elements that precede x in both L_{i-1} and L_{i-1}^*.
- Set B consists of elements that precede x in L_{i-1} and follow x in L_{i-1}^*.
- Set C consists of elements that follow x in L_{i-1} and precede x in L_{i-1}^*.
- Set D consists of elements that follow x in both L_{i-1} and L_{i-1}^*.

e. Argue that $\text{rank}_{L_{i-1}}(x) = |A| + |B| + 1$ and $\text{rank}_{L_{i-1}^*}(x) = |A| + |C| + 1$.

f. Show that access σ_i causes a change in potential of

$$\Phi(L_i) - \Phi(L_{i-1}) \leq 2(|A| - |B| + t_i^*) ,$$

where, as before, heuristic H performs t_i^* transpositions during access σ_i.

Define the amortized cost $\widehat{c}_i$ of access σ_i by $\widehat{c}_i = c_i + \Phi(L_i) - \Phi(L_{i-1})$.

g. Show that the amortized cost $\widehat{c}_i$ of access σ_i is bounded from above by $4c_i^*$.

h. Conclude that the cost $C_{\text{MTF}}(\sigma)$ of access sequence σ with move-to-front is at most 4 times the cost $C_H(\sigma)$ of σ with any other heuristic H, assuming that both heuristics start with the same list.

Chapter notes

Aho, Hopcroft, and Ullman [5] used aggregate analysis to determine the running time of operations on a disjoint-set forest; we shall analyze this data structure using the potential method in Chapter 21. Tarjan [331] surveys the accounting and potential methods of amortized analysis and presents several applications. He attributes the accounting method to several authors, including M. R. Brown, R. E. Tarjan, S. Huddleston, and K. Mehlhorn. He attributes the potential method to D. D. Sleator. The term "amortized" is due to D. D. Sleator and R. E. Tarjan.

Potential functions are also useful for proving lower bounds for certain types of problems. For each configuration of the problem, we define a potential function that maps the configuration to a real number. Then we determine the potential Φ_{init} of the initial configuration, the potential Φ_{final} of the final configuration, and the maximum change in potential $\Delta\Phi_{\max}$ due to any step. The number of steps must therefore be at least $|\Phi_{\text{final}} - \Phi_{\text{init}}| / |\Delta\Phi_{\max}|$. Examples of potential functions to prove lower bounds in I/O complexity appear in works by Cormen, Sundquist, and Wisniewski [79]; Floyd [107]; and Aggarwal and Vitter [3]. Krumme, Cybenko, and Venkataraman [221] applied potential functions to prove lower bounds on ***gossiping***: communicating a unique item from each vertex in a graph to every other vertex.

The move-to-front heuristic from Problem 17-5 works quite well in practice. Moreover, if we recognize that when we find an element, we can splice it out of its position in the list and relocate it to the front of the list in constant time, we can show that the cost of move-to-front is at most twice the cost of any other heuristic including, again, one that knows the entire access sequence in advance.

Selected Solutions

by Thomas H. Cormen

to Accompany

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Selected Solutions for Chapter 2: Getting Started

Solution to Exercise 2.2-2

```
SELECTION-SORT(A, n)
 for i = 1 to n − 1
     smallest = i
     for j = i + 1 to n
         if A[j] < A[smallest]
             smallest = j
     exchange A[i] with A[smallest]
```

The algorithm maintains the loop invariant that at the start of each iteration of the outer **for** loop, the subarray $A[1 : i - 1]$ consists of the $i - 1$ smallest elements in the array $A[1 : n]$, and this subarray is in sorted order. After the first $n - 1$ elements, the subarray $A[1 : n - 1]$ contains the smallest $n - 1$ elements, sorted, and therefore element $A[n]$ must be the largest element.

The running time of the algorithm is $\Theta(n^2)$ for all cases.

Solution to Exercise 2.2-4

Modify the algorithm so that it first checks the input array to see whether it is already sorted, taking $\Theta(n)$ time for an n-element array. If the array is already sorted, then the algorithm is done. Otherwise, sort the array as usual. The best-case running time is generally not a good measure of an algorithm's efficiency.

Solution to Exercise 2.3-6

Procedure BINARY-SEARCH takes a sorted array A, a value x, and a range $[low : high]$ of the array, in which we search for the value x. The procedure compares x to the array entry at the midpoint of the range and decides to eliminate half the range from further consideration. We give both iterative and recursive versions, each of which returns either an index i such that $A[i] = x$, or NIL if no entry of

$A[low : high]$ contains the value x. The initial call to either version should have the parameters $A, x, 1, n$.

```
ITERATIVE-BINARY-SEARCH(A, x, low, high)
  while low ≤ high
      mid = ⌊(low + high)/2⌋
      if x == A[mid]
          return mid
      elseif x > A[mid]
          low = mid + 1
      else high = mid − 1
  return NIL
```

```
RECURSIVE-BINARY-SEARCH(A, x, low, high)
  if low > high
      return NIL
  mid = ⌊(low + high)/2⌋
  if x == A[mid]
      return mid
  elseif x > A[mid]
      return RECURSIVE-BINARY-SEARCH(A, x, mid + 1, high)
  else return RECURSIVE-BINARY-SEARCH(A, x, low, mid − 1)
```

Both procedures terminate the search unsuccessfully when the range is empty (i.e., $low > high$) and terminate it successfully if the value x has been found. Based on the comparison of x to the middle element in the searched range, the search continues with the range halved. The recurrence for these procedures is therefore $T(n) = T(n/2) + \Theta(1)$, whose solution is $T(n) = \Theta(\lg n)$.

Solution to Problem 2-4

a. The inversions are $(1, 5), (2, 5), (3, 4), (3, 5), (4, 5)$. (Remember that inversions are specified by indices rather than by the values in the array.)

b. The array with elements drawn from $\{1, 2, \ldots, n\}$ with the most inversions is $\langle n, n-1, n-2, \ldots, 2, 1\rangle$. For all $1 \le i < j \le n$, there is an inversion (i, j). The number of such inversions is $\binom{n}{2} = n(n-1)/2$.

c. Suppose that the array A starts out with an inversion (k, i). Then $k < i$ and $A[k] > A[i]$. At the time that the outer **for** loop of lines 1–8 sets $key = A[i]$, the value that started in $A[k]$ is still somewhere to the left of $A[i]$. That is, it's in $A[j]$, where $1 \le j < i$, and so the inversion has become (j, i). Some iteration of the **while** loop of lines 5–7 moves $A[j]$ one position to the right. Line 8 will eventually drop *key* to the left of this element, thus eliminating the inversion. Because line 5 moves only elements that are greater than *key*, it moves only elements that correspond to inversions. In other words, each iteration of the **while** loop of lines 5–7 corresponds to the elimination of one inversion.

d. We follow the hint and modify merge sort to count the number of inversions in $\Theta(n \lg n)$ time.

To start, let us define a ***merge-inversion*** as a situation within the execution of merge sort in which the MERGE procedure, after copying $A[p:q]$ to L and $A[q+1:r]$ to R, has values x in L and y in R such that $x > y$. Consider an inversion (i, j), and let $x = A[i]$ and $y = A[j]$, so that $i < j$ and $x > y$. We claim that if we were to run merge sort, there would be exactly one merge-inversion involving x and y. To see why, observe that the only way in which array elements change their positions is within the MERGE procedure. Moreover, since MERGE keeps elements within L in the same relative order to each other, and correspondingly for R, the only way in which two elements can change their ordering relative to each other is for the greater one to appear in L and the lesser one to appear in R. Thus, there is at least one merge-inversion involving x and y. To see that there is exactly one such merge-inversion, observe that after any call of MERGE that involves both x and y, they are in the same sorted subarray and will therefore both appear in L or both appear in R in any given call thereafter. Thus, we have proven the claim.

We have shown that every inversion implies one merge-inversion. In fact, the correspondence between inversions and merge-inversions is one-to-one. Suppose we have a merge-inversion involving values x and y, where x originally was $A[i]$ and y was originally $A[j]$. Since we have a merge-inversion, $x > y$. And since x is in L and y is in R, x must be within a subarray preceding the subarray containing y. Therefore x started out in a position i preceding y's original position j, and so (i, j) is an inversion.

Having shown a one-to-one correspondence between inversions and merge-inversions, it suffices for us to count merge-inversions.

Consider a merge-inversion involving y in R. Let z be the smallest value in L that is greater than y. At some point during the merging process, z and y will be the "exposed" values in L and R, i.e., we will have $z = L[i]$ and $y = R[j]$ in line 13 of MERGE. At that time, there will be merge-inversions involving y and $L[i], L[i+1], L[i+2], \ldots, L[n_L - 1]$, and these $n_L - i$ merge-inversions will be the only ones involving y. Therefore, we need to detect the first time that z and y become exposed during the MERGE procedure and add the value of $n_L - i$ at that time to the total count of merge-inversions.

The following pseudocode, modeled on merge sort, works as we have just described. It also sorts the array A.

```
MERGE-INVERSIONS(A, p, q, r)
  n_L = q − p + 1
  n_R = r − q
  let L[0 : n_L − 1] and R[0 : n_R − 1] be new arrays
  for i = 0 to n_L − 1
      L[i] = A[p + i − 1]
  for j = 0 to n_R − 1
      R[j] = A[q + j]
  i = 0
  j = 0
  k = p
  inversions = 0
  while i < n_L and j < n_R
      if L[i] ≤ R[j]
          inversions = inversions + n_L − i
          A[k] = L[i]
          i = i + 1
      else A[k] = R[j]
          j = j + 1
      k = k + 1
  while i < n_L
      A[k] = L[i]
      i = i + 1
      k = k + 1
  while j < n_R
      A[k] = R[j]
      j = j + 1
      k = k + 1
  return inversions
```

```
COUNT-INVERSIONS(A, p, r)
  inversions = 0
  if p < r
      q = ⌊(p + r)/2⌋
      inversions = inversions + COUNT-INVERSIONS(A, p, q)
      inversions = inversions + COUNT-INVERSIONS(A, q + 1, r)
      inversions = inversions + MERGE-INVERSIONS(A, p, q, r)
  return inversions
```

The initial call is COUNT-INVERSIONS$(A, 1, n)$.

In MERGE-INVERSIONS, whenever $R[j]$ is exposed and a value greater than $R[j]$ becomes exposed in the L array, we increase *inversions* by the number of remaining elements in L. Then because $R[j+1]$ becomes exposed, $R[j]$ can never be exposed again.

Since we have added only a constant amount of additional work to each procedure call and to each iteration of the last **for** loop of the merging procedure, the total running time of the above pseudocode is the same as for merge sort: $\Theta(n \lg n)$.

Selected Solutions for Chapter 3: Characterizing Running Times

Solution to Exercise 3.2-2

Since O-notation provides only an upper bound, and not a tight bound, the statement is saying that the running of time of algorithm A is at least a function whose rate of growth is at most n^2.

Solution to Exercise 3.2-3

$2^{n+1} = O(2^n)$, but $2^{2n} \neq O(2^n)$.

To show that $2^{n+1} = O(2^n)$, we must find constants $c, n_0 > 0$ such that

$0 \leq 2^{n+1} \leq c \cdot 2^n$ for all $n \geq n_0$.

Since $2^{n+1} = 2 \cdot 2^n$ for all n, we can satisfy the definition with $c = 2$ and $n_0 = 1$.

To show that $2^{2n} \neq O(2^n)$, assume there exist constants $c, n_0 > 0$ such that

$0 \leq 2^{2n} \leq c \cdot 2^n$ for all $n \geq n_0$.

Then $2^{2n} = 2^n \cdot 2^n \leq c \cdot 2^n \Rightarrow 2^n \leq c$. But no constant is greater than all 2^n, and so the assumption leads to a contradiction.

Solution to Exercise 3.3-5

$\lceil \lg n \rceil !$ is not polynomially bounded, but $\lceil \lg \lg n \rceil !$ is.

Proving that a function $f(n)$ is polynomially bounded is equivalent to proving that $\lg f(n) = O(\lg n)$ for the following reasons.

- If $f(n)$ is polynomially bounded, then there exist positive constants c, k, and n_0 such that $0 \leq f(n) \leq cn^k$ for all $n \geq n_0$. Without loss of generality, assume that $c \geq 1$, since if $c < 1$, then $f(n) \leq cn^k$ implies that $f(n) \leq n^k$. Assume also that $n_0 \geq 2$, so that $n \geq n_0$ implies that $\lg c \leq (\lg c)(\lg n)$. Then, we have
$$\begin{aligned} \lg f(n) &\leq \lg c + k \lg n \\ &\leq (\lg c + k) \lg n \ , \end{aligned}$$
which, since c and k are constants, means that $\lg f(n) = O(\lg n)$.

- Now suppose that $\lg f(n) = O(\lg n)$. Then there exist positive constants c and n_0 such that $0 \le \lg f(n) \le c \lg n$ for all $n \ge n_0$. Then, we have

  $$0 \le f(n) = 2^{\lg f(n)} \le 2^{c \lg n} = (2^{\lg n})^c = n^c$$

  for all $n \ge n_0$, so that $f(n)$ is polynomially bounded.

In the following proofs, we will make use of the following two facts:

1. $\lg(n!) = \Theta(n \lg n)$ (by equation (3.28)).
2. $\lceil \lg n \rceil = \Theta(\lg n)$, because
   - $\lceil \lg n \rceil \ge \lg n$, and
   - $\lceil \lg n \rceil < \lg n + 1 \le 2 \lg n$ for all $n \ge 2$.

We have

$$\begin{aligned}
\lg(\lceil \lg n \rceil !) &= \Theta(\lceil \lg n \rceil \lg \lceil \lg n \rceil) \\
&= \Theta((\lg n)(\lg \lg n)) \\
&= \omega(\lg n) \, .
\end{aligned}$$

Therefore, $\lg(\lceil \lg n \rceil !)$ is not $O(\lg n)$, and so $\lceil \lg n \rceil !$ is not polynomially bounded.

We also have

$$\begin{aligned}
\lg(\lceil \lg \lg n \rceil !) &= \Theta(\lceil \lg \lg n \rceil \lg \lceil \lg \lg n \rceil) \\
&= \Theta((\lg \lg n)(\lg \lg \lg n)) \\
&= o((\lg \lg n)^2) \\
&= o(\lg^2(\lg n)) \\
&= o(\lg n) \, .
\end{aligned}$$

The last step above follows from the property that any polylogarithmic function grows more slowly than any positive polynomial function, i.e., that for constants $a, b > 0$, we have $\lg^b n = o(n^a)$. Substitute $\lg n$ for n, 2 for b, and 1 for a, giving $\lg^2(\lg n) = o(\lg n)$.

Therefore, $\lg(\lceil \lg \lg n \rceil !) = O(\lg n)$, and so $\lceil \lg \lg n \rceil !$ is polynomially bounded.

Selected Solutions for Chapter 4: Divide-and-Conquer

Solution to Exercise 4.2-3

If you can multiply 3×3 matrices using k multiplications, then you can multiply $n \times n$ matrices by recursively multiplying $n/3 \times n/3$ matrices, in time $T(n) = kT(n/3) + \Theta(n^2)$.

Using the master method to solve this recurrence, consider the ratio of $n^{\log_3 k}$ and n^2:

- If $\log_3 k = 2$, case 2 applies and $T(n) = \Theta(n^2 \lg n)$. In this case, $k = 9$ and $T(n) = o(n^{\lg 7})$.
- If $\log_3 k < 2$, case 3 applies and $T(n) = \Theta(n^2)$. In this case, $k < 9$ and $T(n) = o(n^{\lg 7})$.
- If $\log_3 k > 2$, case 1 applies and $T(n) = \Theta(n^{\log_3 k})$. In this case, $k > 9$. $T(n) = o(n^{\lg 7})$ when $\log_3 k < \lg 7$, i.e., when $k < 3^{\lg 7} \approx 21.85$. The largest such integer k is 21.

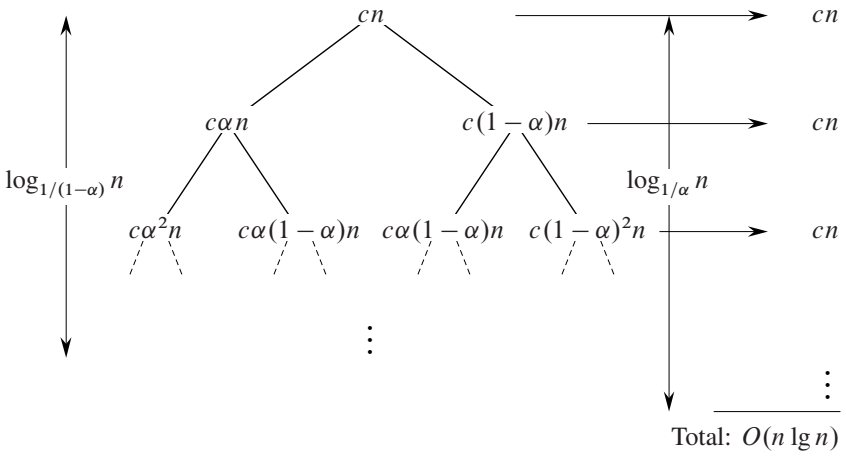
Thus, $k = 21$ and the running time is $\Theta(n^{\log_3 k}) = \Theta(n^{\log_3 21}) = O(n^{2.80})$ (since $\log_3 21 \approx 2.77$).

Solution to Exercise 4.4-4

$T(n) = T(\alpha n) + T((1-\alpha)n) + cn$

We saw the solution to the recurrence $T(n) = T(n/3) + T(2n/3) + cn$ in the text. This recurrence can be similarly solved.

Without loss of generality, let $\alpha \geq 1-\alpha$, so that $0 < 1-\alpha \leq 1/2$ and $1/2 \leq \alpha < 1$.



The recursion tree is full for $\log_{1/(1-\alpha)} n$ levels, each contributing cn, so we guess $\Omega(n \log_{1/(1-\alpha)} n) = \Omega(n \lg n)$. It has $\log_{1/\alpha} n$ levels, each contributing $\le cn$, so we guess $O(n \log_{1/\alpha} n) = O(n \lg n)$.

Now we show that $T(n) = \Theta(n \lg n)$ by substitution. To prove the upper bound, we need to show that $T(n) \le dn \lg n$ for a suitable constant $d > 0$:

$$\begin{aligned}
T(n) &= T(\alpha n) + T((1-\alpha)n) + cn \\
&\le d\alpha n \lg(\alpha n) + d(1-\alpha)n \lg((1-\alpha)n) + cn \\
&= d\alpha n \lg\alpha + d\alpha n \lg n + d(1-\alpha)n \lg(1-\alpha) + d(1-\alpha)n \lg n + cn \\
&= dn \lg n + dn(\alpha \lg\alpha + (1-\alpha)\lg(1-\alpha)) + cn \\
&\le dn \lg n \ ,
\end{aligned}$$

if $dn(\alpha \lg\alpha + (1-\alpha)\lg(1-\alpha)) + cn \le 0$. This condition is equivalent to

$$d(\alpha \lg\alpha + (1-\alpha)\lg(1-\alpha)) \le -c \ .$$

Since $1/2 \le \alpha < 1$ and $0 < 1-\alpha \le 1/2$, we have that $\lg\alpha < 0$ and $\lg(1-\alpha) < 0$. Thus, $\alpha \lg\alpha + (1-\alpha)\lg(1-\alpha) < 0$, so that when we multiply both sides of the inequality by this factor, we need to reverse the inequality:

$$d \ge \frac{-c}{\alpha \lg\alpha + (1-\alpha)\lg(1-\alpha)}$$

or

$$d \ge \frac{c}{-\alpha \lg\alpha + -(1-\alpha)\lg(1-\alpha)} \ .$$

The fraction on the right-hand side is a positive constant, and so it suffices to pick any value of d that is greater than or equal to this fraction.

To prove the lower bound, we need to show that $T(n) \ge dn \lg n$ for a suitable constant $d > 0$. We can use the same proof as for the upper bound, substituting $\ge$ for $\le$, and we get the requirement that

$$0 < d \le \frac{c}{-\alpha \lg\alpha - (1-\alpha)\lg(1-\alpha)} \ .$$

Therefore, $T(n) = \Theta(n \lg n)$.

Selected Solutions for Chapter 6: Heapsort

Solution to Exercise 6.1-1

Since a heap is an almost-complete binary tree (complete at all levels except possibly the lowest), it has at most $2^{h+1} - 1$ elements (if it is complete) and at least $2^h - 1 + 1 = 2^h$ elements (if the lowest level has just 1 element and the other levels are complete).

Solution to Exercise 6.1-2

Given an n-element heap of height h, we know from Exercise 6.1-1 that

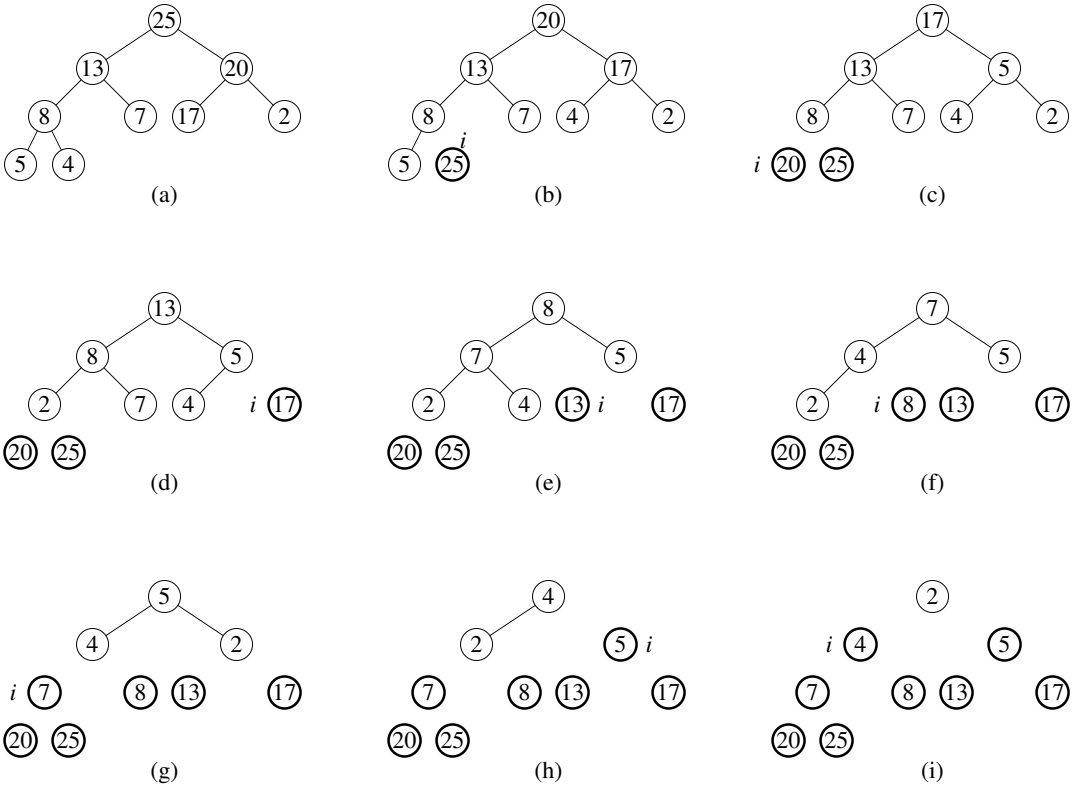
$$2^h \le n \le 2^{h+1} - 1 < 2^{h+1} .$$

Thus, $h \le \lg n < h + 1$. Since h is an integer, $h = \lfloor \lg n \rfloor$ (by definition of $\lfloor\ \rfloor$).

Solution to Exercise 6.2-7

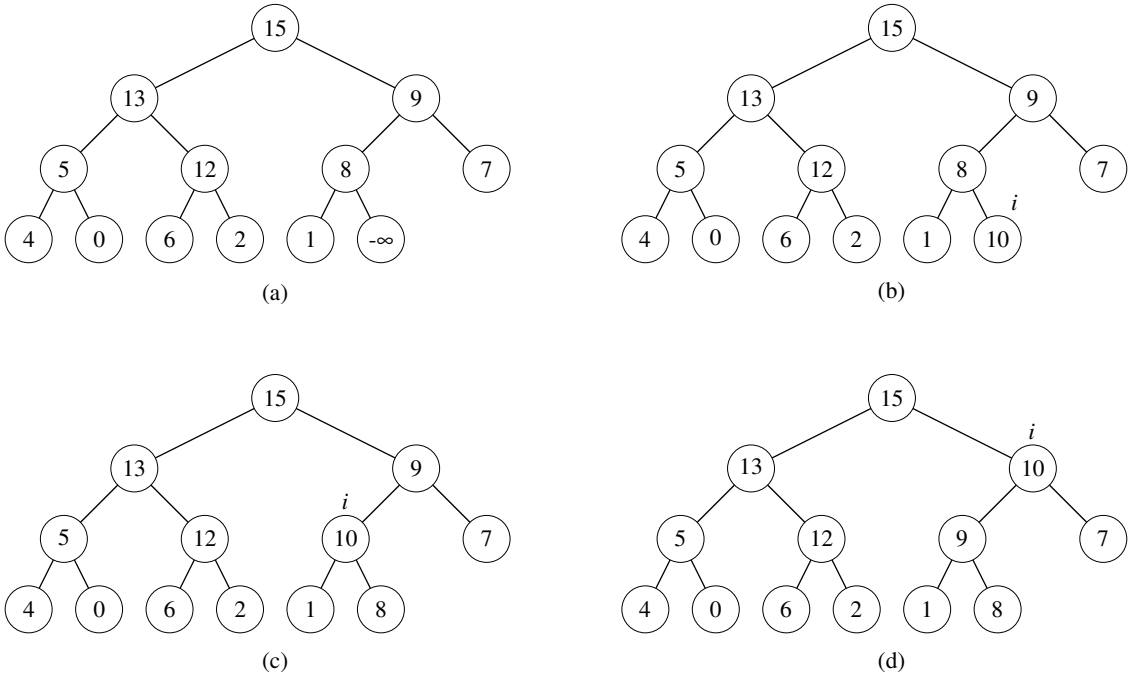
If you put a value at the root that is less than every value in the left and right subtrees, then MAX-HEAPIFY will be called recursively until a leaf is reached. To make the recursive calls traverse the longest path to a leaf, choose values that make MAX-HEAPIFY always recurse on the left child. It follows the left branch when the left child is greater than or equal to the right child, so putting 0 at the root and 1 at all the other nodes, for example, will accomplish that. With such values, MAX-HEAPIFY will be called h times (where h is the heap height, which is the number of edges in the longest path from the root to a leaf), so its running time will be $\Theta(h)$ (since each call does $\Theta(1)$ work), which is $\Theta(\lg n)$. Since we have a case in which MAX-HEAPIFY's running time is $\Theta(\lg n)$, its worst-case running time is $\Omega(\lg n)$.

Solution to Exercise 6.4-1



A	2	4	5	7	8	13	17	20	25

Solution to Exercise 6.5-2

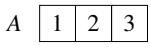


The running time is $O(\lg n)$ plus the overhead for mapping priority queue objects to array indices.

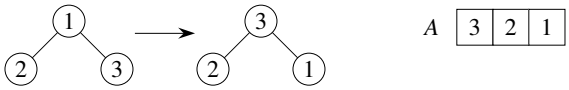
Solution to Problem 6-1

a. The procedures BUILD-MAX-HEAP and BUILD-MAX-HEAP′ do not always create the same heap when run on the same input array. Consider the following counterexample.

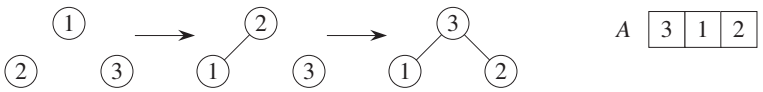
Input array A:



BUILD-MAX-HEAP(A):



BUILD-MAX-HEAP′(A):



b. An upper bound of $O(n \lg n)$ time follows immediately from there being $n - 1$ calls to MAX-HEAP-INSERT, each taking $O(\lg n)$ time. For a lower bound of $\Omega(n \lg n)$, consider the case in which the input array is given in strictly increasing order. Each call to MAX-HEAP-INSERT causes HEAP-INCREASE-KEY to go all the way up to the root. Since the depth of node i is $\lfloor \lg i \rfloor$, the total time is

$$\begin{aligned}
\sum_{i=1}^{n} \Theta(\lfloor \lg i \rfloor) &\geq \sum_{i=\lceil n/2 \rceil}^{n} \Theta(\lfloor \lg \lceil n/2 \rceil \rfloor) \\
&\geq \sum_{i=\lceil n/2 \rceil}^{n} \Theta(\lfloor \lg(n/2) \rfloor) \\
&= \sum_{i=\lceil n/2 \rceil}^{n} \Theta(\lfloor \lg n - 1 \rfloor) \\
&\geq (n/2) \cdot \Theta(\lg n) \\
&= \Omega(n \lg n) \; .
\end{aligned}$$

In the worst case, therefore, BUILD-MAX-HEAP′ requires $\Theta(n \lg n)$ time to build an n-element heap.

Selected Solutions for Chapter 7: Quicksort

Solution to Exercise 7.2-3

Suppose that PARTITION is called on a subarray $A[p:r]$ whose elements are distinct and in decreasing order. PARTITION chooses the smallest element, in $A[r]$, as the pivot. Every test in line 4 comes up false, so that no elements are exchanged during the execution of the **for** loop. Before PARTITION returns, line 6 finds that $i = p - 1$, and so it swaps the elements in $A[p]$ and $A[r]$. PARTITION returns p as the position of the pivot. The subarray containing elements less than or equal to the pivot is empty. The subarray containing elements greater than the pivot, $A[p+1:r]$, has all but the pivot and is in decreasing order except that the maximum element of this subarray is in $A[r]$.

When QUICKSORT calls PARTITION on $A[p:q-1]$, nothing changes, as this subarray is empty. When QUICKSORT calls PARTITION on $A[q+1:r]$, now the pivot is the greatest element in the subarray. Although every test in line 4 comes up true, the indices i and j are always equal in line 6, so that just as in the case where the pivot is the smallest element, no elements are exchanged during the execution of the **for** loop. Before PARTITION returns, line 6 finds that $i = r-1$, so that the swap in line 6 leaves the pivot in $A[r]$. PARTITION returns r as the position of the pivot. Now the subarray containing elements less than or equal to the pivot has all but the pivot and is in decreasing order, and the subarray containing elements greater than the pivot is empty. The next call to PARTITION, therefore, is on a subarray that is in decreasing order, so that it goes back to the first case above.

Therefore, each recursive call is on a subarray only one element smaller, giving a recurrence for the running time of $T(n) = T(n-1) + \Theta(n)$, whose solution is $\Theta(n^2)$.

Solution to Exercise 7.2-5

The minimum depth follows a path that always takes the smaller part of the partition—i.e., that multiplies the number of elements by α. One level of recursion reduces the number of elements from n to αn, and i levels of recursion reduce the number of elements to $\alpha^i n$. At a leaf, there is just one remaining element, and so at a minimum-depth leaf of depth m, we have $\alpha^m n = 1$. Thus, $\alpha^m = 1/n$. Taking

logarithms, we get $m \lg \alpha = -\lg n$, or $m = -\lg n / \lg \alpha$. (This quantity is positive because $0 < \alpha < 1$ implies that $\lg \alpha < 0$.)

Similarly, the maximum-depth path corresponds to always taking the larger part of the partition, i.e., keeping a fraction β of the elements each time. The maximum depth M is reached when there is one element left, that is, when $\beta^M n = 1$. Thus, $M = -\lg n / \lg \beta$. (Again, this quantity is positive because $0 < \beta < 1$ implies that $\lg \beta < 0$.)

All these equations are approximate because we are ignoring floors and ceilings.

Selected Solutions for Chapter 8: Sorting in Linear Time

Solution to Exercise 8.1-3

If the sort runs in linear time for m input permutations, then the height h of the portion of the decision tree consisting of the m corresponding leaves and their ancestors is linear.

Use the same argument as in the proof of Theorem 8.1 to show that this is impossible for $m = n!/2$, $n!/n$, or $n!/2^n$.

We have $2^h \geq m$, which gives us $h \geq \lg m$. For all the possible values of m given here, $\lg m = \Omega(n \lg n)$, hence $h = \Omega(n \lg n)$.

In particular, using equation (3.25):

$$\lg \frac{n!}{2} = \lg n! - 1 \geq n \lg n - n \lg e - 1 ,$$

$$\lg \frac{n!}{n} = \lg n! - \lg n \geq n \lg n - n \lg e - \lg n ,$$

$$\lg \frac{n!}{2^n} = \lg n! - n \geq n \lg n - n \lg e - n .$$

Solution to Exercise 8.2-3

The following solution also answers Exercise 8.2-2.

Notice that the correctness argument in the text does not depend on the order in which A is processed. The algorithm is correct whether A is processed front to back or back to front.

But the modified algorithm is not stable. As before, in the final **for** loop an element equal to one taken from A earlier is placed before the earlier one (i.e., at a lower index position) in the output arrray B. The original algorithm was stable because an element taken from A later started out with a lower index than one taken earlier. But in the modified algorithm, an element taken from A later started out with a higher index than one taken earlier.

In particular, the algorithm still places the elements with value k in positions $C[k-1]+1$ through $C[k]$, but in the reverse order of their appearance in A.

Rewrite of COUNTING-SORT that writes elements with the same value into the output array in order of increasing index and is stable:

```
COUNTING-SORT(A, n, k)
  let B[1:n], C[0:k], and L[0:k] be new arrays
  for i = 0 to k
      C[i] = 0
  for j = 1 to n
      C[A[j]] = C[A[j]] + 1
  // C[i] now contains the number of elements equal to i.
  L[0] = 1
  for i = 1 to k
      L[i] = L[i − 1] + C[i − 1]
  // L[i] now contains the index of the first element of A with value i
  for j = 1 to n
      B[L[A[j]]] = A[j]
      L[A[j]] = L[A[j]] + 1
  return B
```

Solution to Exercise 8.3-3

Basis: If $d = 1$, there's only one digit, so sorting on that digit sorts the array.

Inductive step: Assuming that radix sort works for $d - 1$ digits, we'll show that it works for d digits.

Radix sort sorts separately on each digit, starting from digit 1. Thus, radix sort of d digits, which sorts on digits $1, \ldots, d$ is equivalent to radix sort of the low-order $d - 1$ digits followed by a sort on digit d. By our induction hypothesis, the sort of the low-order $d - 1$ digits works, so just before the sort on digit d, the elements are in order according to their low-order $d - 1$ digits.

The sort on digit d will order the elements by their dth digit. Consider two elements, a and b, with dth digits a_d and b_d respectively.

- If $a_d < b_d$, the sort will put a before b, which is correct, since $a < b$ regardless of the low-order digits.
- If $a_d > b_d$, the sort will put a after b, which is correct, since $a > b$ regardless of the low-order digits.
- If $a_d = b_d$, the sort will leave a and b in the same order they were in, because it is stable. But that order is already correct, since the correct order of a and b is determined by the low-order $d - 1$ digits when their dth digits are equal, and the elements are already sorted by their low-order $d - 1$ digits.

If the intermediate sort were not stable, it might rearrange elements whose dth digits were equal—elements that *were* in the right order after the sort on their lower-order digits.

Solution to Exercise 8.3-5

Treat the numbers as 3-digit numbers in radix n. Each digit ranges from 0 to $n - 1$. Sort these 3-digit numbers with radix sort.

There are 3 calls to counting sort, each taking $\Theta(n + n) = \Theta(n)$ time, so that the total time is $\Theta(n)$.

Solution to Problem 8-1

a. For a comparison algorithm A to sort, no two input permutations can reach the same leaf of the decision tree, so that there must be at least $n!$ leaves reached in T_A, one for each possible input permutation. Since A is a deterministic algorithm, it must always reach the same leaf when given a particular permutation as input, so at most $n!$ leaves are reached (one for each permutation). Therefore exactly $n!$ leaves are reached, one for each input permutation.

These $n!$ leaves will each have probability $1/n!$, since each of the $n!$ possible permutations is the input with the probability $1/n!$. Any remaining leaves will have probability 0, since they are not reached for any input.

Without loss of generality, we can assume for the rest of this problem that paths leading only to 0-probability leaves aren't in the tree, since they cannot affect the running time of the sort. That is, we can assume that T_A consists of only the $n!$ leaves labeled $1/n!$ and their ancestors.

b. If $k > 1$, then the root of T is not a leaf. All of T's leaves must be leaves in LT and RT. Since every leaf at depth h in LT or RT has depth $h + 1$ in T, $D(T)$ must be the sum of $D(LT)$, $D(RT)$, and k, the total number of leaves. To prove this last assertion, let $d_T(x) =$ depth of node x in tree T. Then,

$$\begin{aligned}
D(T) &= \sum_{x \in \text{ leaves}(T)} d_T(x) \\
&= \sum_{x \in \text{ leaves}(LT)} d_T(x) + \sum_{x \in \text{ leaves}(RT)} d_T(x) \\
&= \sum_{x \in \text{ leaves}(LT)} (d_{LT}(x) + 1) + \sum_{x \in \text{ leaves}(RT)} (d_{RT}(x) + 1) \\
&= \sum_{x \in \text{ leaves}(LT)} d_{LT}(x) + \sum_{x \in \text{ leaves}(RT)} d_{RT}(x) + \sum_{x \in \text{ leaves}(T)} 1 \\
&= D(LT) + D(RT) + k \ .
\end{aligned}$$

c. To show that $d(k) = \min\{d(i) + d(k - i) + k : 1 \le i \le k - 1\}$, we will show separately that $d(k) \le \min\{d(i) + d(k - i) + k : 1 \le i \le k - 1\}$ and $d(k) \ge \min\{d(i) + d(k - i) + k : 1 \le i \le k - 1\}$.

- We show that $d(k) \le \min\{d(i) + d(k - i) + k : 1 \le i \le k - 1\}$ by showing that $d(k) \le d(i)+d(k-i)+k$ for $i = 1, 2, \ldots, k-1$. By Exercise B.5-4, there are full binary trees with i leaves for any i from 1 to $k - 1$. Therefore, we can create decision trees LT with i leaves and RT with $k-i$ leaves such that $D(LT) = d(i)$ and $D(RT) = d(k - i)$. Construct T such that LT and RT are the left and right subtrees of T's root, respectively. Then

  $d(k)$

  $\le D(T)$ (by definition of d as minimum $D(T)$ value)

$= D(LT) + D(RT) + k$ (by part (b))
$= d(i) + d(k-i) + k$ (by choice of LT and RT) .

- We show that $d(k) \geq \min\{d(i) + d(k-i) + k : 1 \leq i \leq k-1\}$ by showing that $d(k) \geq d(i) + d(k-i) + k$, for some i in $\{1, 2, \ldots, k-1\}$. Take the tree T with k leaves such that $D(T) = d(k)$, let LT and RT be T's left and right subtree, respectively, and let i be the number of leaves in LT. Then $k-i$ is the number of leaves in RT and

  $d(k)$
  $= D(T)$ (by choice of T)
  $= D(LT) + D(RT) + k$ (by part (b))
  $\geq d(i) + d(k-i) + k$ (by definition of d as minimum $D(T)$ value) .

  Neither i nor $k-i$ can be 0 (and hence $1 \leq i \leq k-1$), since if one of these were 0, either LT or RT would contain all k leaves of T. The root of T would have only one child, so that T would not be a full binary tree and hence not a decision tree.

d. Let $f_k(i) = i \lg i + (k-i)\lg(k-i)$. To find the value of i that minimizes f_k, find the i for which the derivative of f_k with respect to i is 0:

$$\begin{aligned} f_k'(i) &= \frac{d}{di}\left(\frac{i\ln i + (k-i)\ln(k-i)}{\ln 2}\right) \\ &= \frac{\ln i + 1 - \ln(k-i) - 1}{\ln 2} \\ &= \frac{\ln i - \ln(k-i)}{\ln 2} \end{aligned}$$

is 0 at $i = k/2$. To verify that this is indeed a minimum (not a maximum), check that the second derivative of f_k is positive at $i = k/2$:

$$\begin{aligned} f_k''(i) &= \frac{d}{di}\left(\frac{\ln i - \ln(k-i)}{\ln 2}\right) \\ &= \frac{1}{\ln 2}\left(\frac{1}{i} + \frac{1}{k-i}\right) . \\ f_k''(k/2) &= \frac{1}{\ln 2}\left(\frac{2}{k} + \frac{2}{k}\right) \\ &= \frac{1}{\ln 2}\cdot\frac{4}{k} \\ &> 0 \qquad (\text{since } k > 1) . \end{aligned}$$

Now we use substitution to prove $d(k) = \Omega(kb\lg k)$. The base case of the induction is satisfied because $d(1) \geq 0 = c \cdot 1 \cdot \lg 1$ for any constant c. For the inductive step, assume that $d(i) \geq ci\lg i$ for $1 \leq i \leq k-1$, where c is some constant to be determined:

$$\begin{aligned} d(k) &= \min\{d(i) + d(k-i) + k : 1 \leq i \leq k-1\} \\ &\geq \min\{c(i\lg i + (k-i)\lg(k-i)) + k : 1 \leq i \leq k-1\} \\ &= c\left(\frac{k}{2}\lg\frac{k}{2} + \left(k - \frac{k}{2}\right)\lg\left(k - \frac{k}{2}\right)\right) + k \end{aligned}$$

$$
\begin{aligned}
&= ck \lg\left(\frac{k}{2}\right) + k \\
&= c(k \lg k - k) + k \\
&= ck \lg k + (k - ck) \\
&\geq ck \lg k \qquad \text{if } c \leq 1 \ ,
\end{aligned}
$$

and so $d(k) = \Omega(k \lg k)$.

e. Using the result of part (d) and the fact that T_A (as modified in our solution to part (a)) has $n!$ leaves, we can conclude that

$$D(T_A) \geq d(n!) = \Omega(n! \lg(n!)) \ .$$

$D(T_A)$ is the sum of the decision-tree path lengths for sorting all input permutations, and the path lengths are proportional to the run time. Since the $n!$ permutations have equal probability $1/n!$, the expected time to sort n random elements (one input permutation) is the total time for all permutations divided by $n!$:

$$\frac{\Omega(n! \lg(n!))}{n!} = \Omega(\lg(n!)) = \Omega(n \lg n) \ .$$

f. We will show how to modify a randomized decision tree (algorithm) to define a deterministic decision tree (algorithm) that is at least as good as the randomized one in terms of the average number of comparisons.

At each randomized node, pick the child with the smallest subtree (the subtree with the smallest average number of comparisons on a path to a leaf). Delete all the other children of the randomized node and splice out the randomized node itself.

The deterministic algorithm corresponding to this modified tree still works, because the randomized algorithm worked no matter which path was taken from each randomized node.

The average number of comparisons for the modified algorithm is no larger than the average number for the original randomized tree, since we discarded the higher-average subtrees in each case. In particular, each time we splice out a randomized node, we leave the overall average less than or equal to what it was, because

- the same set of input permutations reaches the modified subtree as before, but those inputs are handled in less than or equal to average time than before, and
- the rest of the tree is unmodified.

The randomized algorithm thus takes at least as much time on average as the corresponding deterministic one. (We've shown that the average-case running time for a deterministic comparison sort is $\Omega(n \lg n)$, hence the expected time for a randomized comparison sort is also $\Omega(n \lg n)$.)

Selected Solutions for Chapter 9: Medians and Order Statistics

Solution to Exercise 9.3-1

For groups of 7, the algorithm still works in linear time. The number g of groups is at most $n/7$. There are at least $4(\lfloor g/2 \rfloor + 1) \geq 2g$ elements greater than or equal to the pivot, and at least $4\lceil g/2 \rceil \geq 2g$ elements less than or equal to the pivot. That leaves at most $7g - 2g = 5g \leq 5n/7$ elements in the recursive call. The recurrence becomes $T(n) \leq T(n/7) + T(5n/7) + O(n)$, which you can show by substitution has the solution $T(n) = O(n)$.

In fact, any odd group size ≥ 5 works in linear time.

Solution to Exercise 9.3-3

A modification to quicksort that allows it to run in $O(n \lg n)$ time in the worst case uses the deterministic PARTITION-AROUND procedure that takes an element to partition around as an input parameter.

SELECT takes an array A, the bounds p and r of the subarray in A, and the rank i of an order statistic, and in time linear in the size of the subarray $A[p:r]$ it returns the ith smallest element in $A[p:r]$.

```
BEST-CASE-QUICKSORT(A, p, r)
  if p < r
      i = ⌊(r − p + 1)/2⌋
      x = SELECT(A, p, r, i)
      q = PARTITION-AROUND(A, p, r, x)
      BEST-CASE-QUICKSORT(A, p, q − 1)
      BEST-CASE-QUICKSORT(A, q + 1, r)
```

For an n-element array, the largest subarray that BEST-CASE-QUICKSORT recurses on has $n/2$ elements. This situation occurs when $n = r - p + 1$ is even; then the subarray $A[q+1:r]$ has $n/2$ elements, and the subarray $A[p:q-1]$ has $n/2 - 1$ elements.

Because BEST-CASE-QUICKSORT always recurses on subarrays that are at most half the size of the original array, the recurrence for the worst-case running time is $T(n) \leq 2T(n/2) + \Theta(n) = O(n \lg n)$.

Solution to Exercise 9.3-6

Let the procedure MEDIAN take as parameters an array A and subarray indices p and r and return the value of the median element of $A[p:r]$ in $O(n)$ time in the worst case.

Given MEDIAN, here is a linear-time algorithm SELECT$'$ for finding the ith smallest element in $A[p:r]$. This algorithm uses the deterministic PARTITION-AROUND procedure that takes an element to partition around as an input parameter.

```
SELECT'(A, p, r, i)
  if p == r
      return A[p]
  x = MEDIAN(A, p, r)
  q = PARTITION-AROUND(A, p, r, x)
  k = q − p + 1
  if i == k
      return A[q]
  elseif i < k
      return SELECT'(A, p, q − 1, i)
  else return SELECT'(A, q + 1, r, i − k)
```

Because x is the median of $A[p:r]$, each subarray $A[p:q-1]$ and $A[q+1:r]$ has at most half the number of elements of $A[p:r]$. The recurrence for the worst-case running time of SELECT$'$ is $T(n) \le T(n/2) + O(n) = O(n)$.

Solution to Problem 9-1

Assume that the numbers start out in an array.

a. Sort the numbers using merge sort or heapsort, which take $\Theta(n \lg n)$ worst-case time. (Don't use quicksort or insertion sort, which can take $\Theta(n^2)$ time.) Put the i largest elements (directly accessible in the sorted array) into the output array, taking $\Theta(i)$ time.

Total worst-case running time: $\Theta(n \lg n + i) = \Theta(n \lg n)$ (because $i \le n$).

b. Implement the priority queue as a heap. Build the heap using BUILD-HEAP, which takes $\Theta(n)$ time, then call HEAP-EXTRACT-MAX i times to get the i largest elements, in $\Theta(i \lg n)$ worst-case time, and store them in reverse order of extraction in the output array. The worst-case extraction time is $\Theta(i \lg n)$ because

- i extractions from a heap with $O(n)$ elements takes $i \cdot O(\lg n) = O(i \lg n)$ time, and
- half of the i extractions are from a heap with $\ge n/2$ elements, so those $i/2$ extractions take $(i/2)\Omega(\lg(n/2)) = \Omega(i \lg n)$ time in the worst case.

Total worst-case running time: $\Theta(n + i \lg n)$.

c. Use the SELECT algorithm of Section 9.3 to find the ith largest number in $\Theta(n)$ time. Partition around that number in $\Theta(n)$ time. Sort the i largest numbers in $\Theta(i \lg i)$ worst-case time (with merge sort or heapsort).

Total worst-case running time: $\Theta(n + i \lg i)$.

Note that method (c) is always asymptotically at least as good as the other two methods, and that method (b) is asymptotically at least as good as (a).

Selected Solutions for Chapter 15: Greedy Algorithms

Solution to Exercise 15.1-4

Let S be the set of n activities.

The "obvious" solution of using GREEDY-ACTIVITY-SELECTOR to find a maximum-size set S_1 of compatible activities from S for the first lecture hall, then using it again to find a maximum-size set S_2 of compatible activities from $S - S_1$ for the second hall, (and so on until all the activities are assigned), requires $\Theta(n^2)$ time in the worst case. Moreover, it can produce a result that uses more lecture halls than necessary. Consider activities with the intervals $\{[1, 4), [2, 5), [6, 7), [4, 8)\}$. GREEDY-ACTIVITY-SELECTOR would choose the activities with intervals $[1, 4)$ and $[6, 7)$ for the first lecture hall, and then each of the activities with intervals $[2, 5)$ and $[4, 8)$ would have to go into its own hall, for a total of three halls used. An optimal solution would put the activities with intervals $[1, 4)$ and $[4, 8)$ into one hall and the activities with intervals $[2, 5)$ and $[6, 7)$ into another hall, for only two halls used.

There is a correct algorithm, however, whose asymptotic time is just the time needed to sort the activities by time—$O(n \lg n)$ time for arbitrary times, or possibly as fast as $O(n)$ if the times are small integers.

The general idea is to go through the activities in order of start time, assigning each to any hall that is available at that time. To do this, move through the set of events consisting of activities starting and activities finishing, in order of event time. Maintain two lists of lecture halls: Halls that are busy at the current event-time t (because they have been assigned an activity i that started at $s_i \le t$ but won't finish until $f_i > t$) and halls that are free at time t. (As in the activity-selection problem in Section 15.1, we are assuming that activity time intervals are half open—i.e., that if $s_i \ge f_j$, then activities i and j are compatible.) When t is the start time of some activity, assign that activity to a free hall and move the hall from the free list to the busy list. When t is the finish time of some activity, move the activity's hall from the busy list to the free list. (The activity is certainly in some hall, because the event times are processed in order and the activity must have started before its finish time t, hence must have been assigned to a hall.)

To avoid using more halls than necessary, always pick a hall that has already had an activity assigned to it, if possible, before picking a never-used hall. (This can be done by always working at the front of the free-halls list—putting freed halls onto

the front of the list and taking halls from the front of the list—so that a new hall doesn't come to the front and get chosen if there are previously-used halls.)

This guarantees that the algorithm uses as few lecture halls as possible: The algorithm will terminate with a schedule requiring $m \leq n$ lecture halls. Let activity i be the first activity scheduled in lecture hall m. The reason that i was put in the mth lecture hall is that the first $m-1$ lecture halls were busy at time s_i. So at this time there are m activities occurring simultaneously. Therefore any schedule must use at least m lecture halls, so the schedule returned by the algorithm is optimal.

Run time:

- Sort the $2n$ activity-starts/activity-ends events. (In the sorted order, an activity-ending event should precede an activity-starting event that is at the same time.) $O(n \lg n)$ time for arbitrary times, possibly $O(n)$ if the times are restricted (e.g., to small integers).
- Process the events in $O(n)$ time: Scan the $2n$ events, doing $O(1)$ work for each (moving a hall from one list to the other and possibly associating an activity with it).

Total: $O(n + \text{time to sort})$

Solution to Exercise 15.2-2

The solution is based on the optimal-substructure observation in the text: Let i be the highest-numbered item in an optimal solution S for W pounds and items $1, \ldots, n$. Then $S' = S - \{i\}$ must be an optimal solution for $W - w_i$ pounds and items $1, \ldots, i-1$, and the value of the solution S is v_i plus the value of the subproblem solution S'.

We can express this relationship in the following formula: Define $c[i, w]$ to be the value of the solution for items $1, \ldots, i$ and maximum weight w. Then

$$c[i, w] = \begin{cases} 0 & \text{if } i = 0 \text{ or } w = 0\,, \\ c[i-1, w] & \text{if } w_i > w\,, \\ \max\{v_i + c[i-1, w-w_i], c[i-1, w]\} & \text{if } i > 0 \text{ and } w \geq w_i\,. \end{cases}$$

The last case says that the value of a solution for i items either includes item i, in which case it is v_i plus a subproblem solution for $i-1$ items and the weight excluding w_i, or doesn't include item i, in which case it is a subproblem solution for $i-1$ items and the same weight. That is, if the thief picks item i, then v_i value is added, and the thief can choose from items $1, \ldots, i-1$ up to the weight limit $w - w_i$, gaining $c[i-1, w-w_i]$ additional value. On the other hand, if the thief decides not to take item i, then choices remain from items $1, \ldots, i-1$ up to the weight limit w, giving $c[i-1, w]$ value. The better of these two choices should be made.

The algorithm takes as inputs the maximum weight W, the number n of items, and the two sequences $v = \langle v_1, v_2, \ldots, v_n \rangle$ and $w = \langle w_1, w_2, \ldots, w_n \rangle$. It stores the $c[i, j]$ values in a table $c[0\,..\,n, 0\,..\,W]$ whose entries are computed in row-major

order. (That is, the first row of c is filled in from left to right, then the second row, and so on.) At the end of the computation, $c[n, W]$ contains the maximum value the thief can take.

```
DYNAMIC-0-1-KNAPSACK(v, w, n, W)
  let c[0:n, 0:W] be a new array
  for w = 0 to W
      c[0, w] = 0
  for i = 1 to n
      c[i, 0] = 0
      for w = 1 to W
          if w_i ≤ w and v_i + c[i − 1, w − w_i] > c[i − 1, w]
              c[i, w] = v_i + c[i − 1, w − w_i]
          else c[i, w] = c[i − 1, w]
```

We can use the c table to deduce the set of items to take by starting at $c[n, W]$ and tracing where the optimal values came from. If $c[i, w] = c[i-1, w]$, then item i is not part of the solution, and we continue tracing with $c[i-1, w]$. Otherwise item i is part of the solution, and we continue tracing with $c[i-1, w-w_i]$.

The above algorithm takes $\Theta(nW)$ time total:

- $\Theta(nW)$ to fill in the c table: $(n+1)\cdot(W+1)$ entries, each requiring $\Theta(1)$ time to compute.
- $O(n)$ time to trace the solution (since it starts in row n of the table and moves up one row at each step).

Solution to Exercise 15.2-7

Sort A and B into monotonically decreasing order.

Here's a proof that this method yields an optimal solution. Consider any indices i and j such that $i < j$, and consider the terms ${a_i}^{b_i}$ and ${a_j}^{b_j}$. We want to show that it is no worse to include these terms in the payoff than to include ${a_i}^{b_j}$ and ${a_j}^{b_i}$, i.e., that ${a_i}^{b_i}{a_j}^{b_j} \geq {a_i}^{b_j}{a_j}^{b_i}$. Since A and B are sorted into monotonically decreasing order and $i < j$, we have $a_i \geq a_j$ and $b_i \geq b_j$. Since a_i and a_j are positive and $b_i - b_j$ is nonnegative, we have ${a_i}^{b_i - b_j} \geq {a_j}^{b_i - b_j}$. Multiplying both sides by ${a_i}^{b_j}{a_j}^{b_j}$ yields ${a_i}^{b_i}{a_j}^{b_j} \geq {a_i}^{b_j}{a_j}^{b_i}$.

Since the order of multiplication doesn't matter, sorting A and B into monotonically increasing order works as well.

Selected Solutions for Chapter 16: Amortized Analysis

Solution to Exercise 16.1-3

Let c_i = cost of ith operation.

$$c_i = \begin{cases} i & \text{if } i \text{ is an exact power of 2 ,} \\ 1 & \text{otherwise .} \end{cases}$$

Operation	Cost
1	1
2	2
3	1
4	4
5	1
6	1
7	1
8	8
9	1
10	1
⋮	⋮

n operations cost

$$\sum_{i=1}^{n} c_i \le n + \sum_{j=0}^{\lg n} 2^j = n + (2n - 1) < 3n .$$

(Note: Ignoring floor in upper bound of $\sum 2^j$.)

$$\text{Average cost of operation} = \frac{\text{Total cost}}{\text{\# operations}} < 3 .$$

By aggregate analysis, the amortized cost per operation $= O(1)$.

Solution to Exercise 16.2-2

Let c_i = cost of ith operation.

$$c_i = \begin{cases} i & \text{if } i \text{ is an exact power of 2 ,} \\ 1 & \text{otherwise .} \end{cases}$$

Charge each operation \$3 (amortized cost $\widehat{c}_i$).

- If i is not an exact power of 2, pay \$1, and store \$2 as credit.
- If i is an exact power of 2, pay \$$i$, using stored credit.

Operation	Amortized cost	Actual cost	Credit remaining
1	3	1	2
2	3	2	3
3	3	1	5
4	3	4	4
5	3	1	6
6	3	1	8
7	3	1	10
8	3	8	5
9	3	1	7
10	3	1	9
⋮	⋮	⋮	⋮

Since the amortized cost is \$3 per operation, $\sum_{i=1}^{n} \widehat{c}_i = 3n$.

We know from Exercise 16.1-3 that $\sum_{i=1}^{n} c_i < 3n$.

Then we have $\sum_{i=1}^{n} \widehat{c}_i \geq \sum_{i=1}^{n} c_i \Rightarrow$ credit = amortized cost − actual cost ≥ 0.

Since the amortized cost of each operation is $O(1)$, and the amount of credit never goes negative, the total cost of n operations is $O(n)$.

Solution to Exercise 16.2-3

We introduce a new field $A.max$ to hold the index of the high-order 1 in A. Initially, $A.max$ is set to -1, since the low-order bit of A is at index 0 and there are initially no 1s in A. The value of $A.max$ is updated as appropriate when the counter is incremented or reset, and this value limits how much of A must be looked at to reset it. By controlling the cost of RESET in this way, we can limit it to an amount that can be covered by credit from earlier INCREMENT operations.

```
INCREMENT(A, k)
  i = 0
  while i < k and A[i] == 1
      A[i] = 0
      i = i + 1
  if i < k
      A[i] = 1
      // Additions to book's INCREMENT start here.
      A.max = max{A.max, i}
  else A.max = −1

RESET(A)
  for i = 0 to A.max
      A[i] = 0
  A.max = −1
```

As for the counter in the book, we assume that it costs \$1 to flip a bit. In addition, we assume it costs \$1 to update $A.max$.

Setting and resetting of bits by INCREMENT will work exactly as for the original counter in the book: \$1 pays to set one bit to 1, \$1 is placed on the bit that is set to 1 as credit, and the credit on each 1 bit pays to reset the bit during incrementing.

In addition, \$1 pays for updating *max*, and if *max* increases, place an additional \$1 of credit on the new high-order 1. (If *max* doesn't increase, we can just waste that \$1—it won't be needed.) Since RESET manipulates bits at positions only up to $A.max$, and since each bit up to there must have become the high-order 1 at some time before the high-order 1 got up to $A.max$, every bit seen by RESET has \$1 of credit on it. So the zeroing of bits of A by RESET can be completely paid for by the credit stored on the bits. We just need \$1 to pay for resetting *max*.

Thus charging \$4 for each INCREMENT and \$1 for each RESET is sufficient, so that the sequence of n INCREMENT and RESET operations takes $O(n)$ time.

Selected Solutions for Chapter 17: Augmenting Data Structures

Solution to Exercise 17.1-7

Let $A[1:n]$ be the array of n distinct numbers.

One way to count the inversions is to add up, for each element, the number of larger elements that precede it in the array:

$$\#\text{ of inversions} = \sum_{j=1}^{n} |Inv(j)| \ ,$$

where $Inv(j) = \{i : i < j \text{ and } A[i] > A[j]\}$.

Note that $|Inv(j)|$ is related to $A[j]$'s rank in the subarray $A[1:j]$ because the elements in $Inv(j)$ are the reason that $A[j]$ is not positioned according to its rank. Let $r(j)$ be the rank of $A[j]$ in $A[1:j]$. Then $j = r(j) + |Inv(j)|$, so that we can compute

$$|Inv(j)| = j - r(j)$$

by inserting $A[1], \ldots, A[n]$ into an order-statistic tree and using OS-RANK to find the rank of each $A[j]$ in the tree immediately after it is inserted into the tree. (This OS-RANK value is $r(j)$.)

Insertion and OS-RANK each take $O(\lg n)$ time, and so the total time for n elements is $O(n \lg n)$.

Solution to Exercise 17.2-2

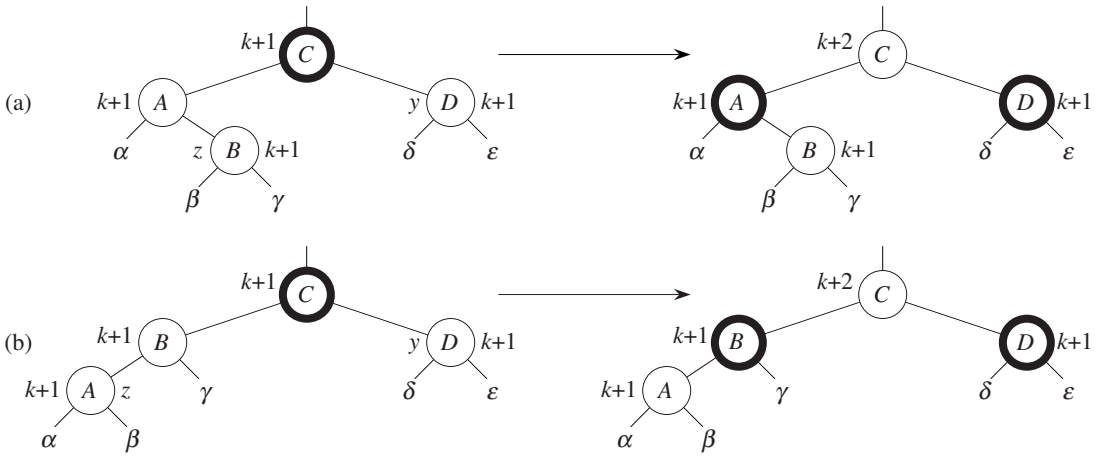
Yes, it is possible to maintain black-heights as attributes in the nodes of a red-black tree without affecting the asymptotic performance of the red-black tree operations. We appeal to Theorem 17.1, because the black-height of a node can be computed from the information at the node and its two children. Actually, the black-height can be computed from just one child's information: the black-height of a node is the black-height of a red child, or the black height of a black child plus one. The second child does not need to be checked because of property 5 of red-black trees.

The RB-INSERT-FIXUP and RB-DELETE-FIXUP procedures change node colors, and each color change can potentially cause $O(\lg n)$ black-height changes. We'll

show that the color changes of the fixup procedures cause only local black-height changes and thus are constant-time operations. Assume that the black-height of each node x is kept in the attribute $x.bh$.

For RB-INSERT-FIXUP, there are three cases to examine.

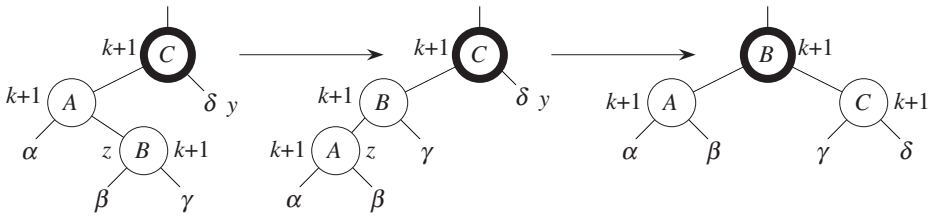
Case 1: z's uncle is red.



- Before color changes, suppose that all subtrees $\alpha, \beta, \gamma, \delta, \epsilon$ have the same black-height k with a black root, so that nodes A, B, C, and D have black-heights of $k + 1$.
- After color changes, the only node whose black-height changed is node C. To fix that, add $z.p.p.bh = z.p.p.bh+1$ after lines 7 and 21 in RB-INSERT-FIXUP.
- Since the number of black nodes between $z.p.p$ and z remains the same, nodes above $z.p.p$ are not affected by the color change.

Case 2: z's uncle y is black, and z is a right child.

Case 3: z''s uncle y is black, and z is a left child.



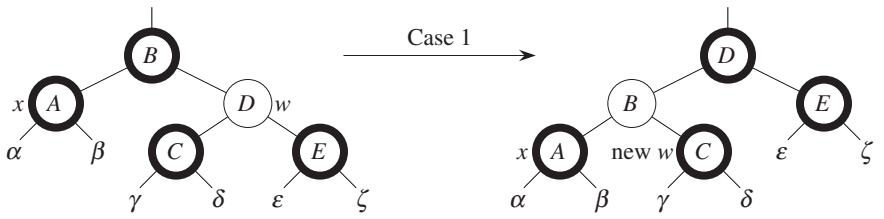
Case 2 Case 3

- With subtrees $\alpha, \beta, \gamma, \delta, \epsilon$ of black-height k, even with color changes and rotations, the black-heights of nodes A, B, and C remain the same $(k + 1)$.

Thus, RB-INSERT-FIXUP maintains its original $O(\lg n)$ time.

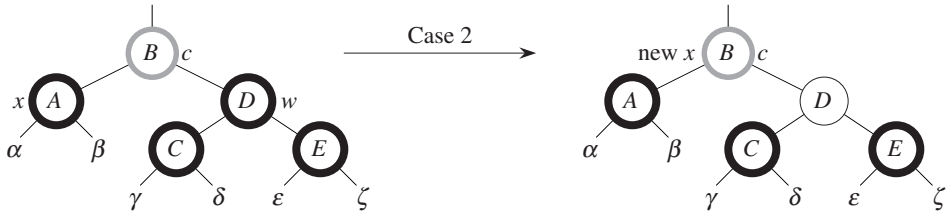
For RB-DELETE-FIXUP, there are four cases to examine.

Case 1: x's sibling w is red.



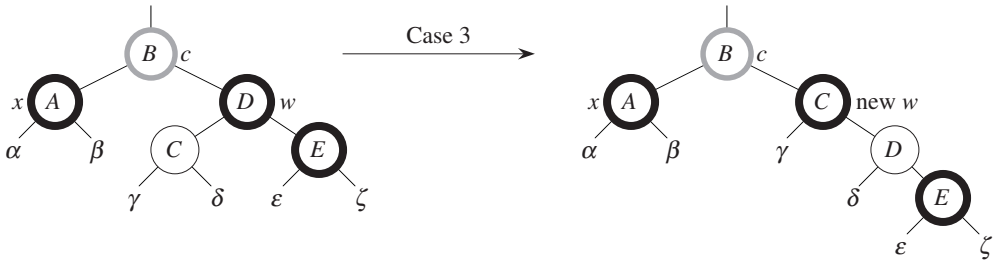
- Even though case 1 changes colors of nodes and does a rotation, black-heights are not changed.
- Case 1 changes the structure of the tree, but waits for cases 2, 3, and 4 to deal with the "extra black" on x.

Case 2: x's sibling w is black, and both of w's children are black.



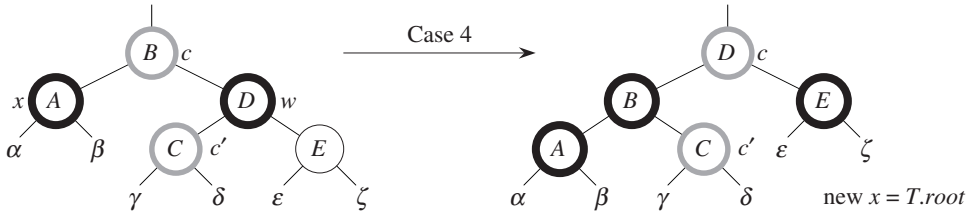
- w is colored red, and x's "extra" black is moved up to $x.p$.
- Add $x.p.bh = x.bh$ after lines 10 and 31 in RB-DELETE-FIXUP.
- This is a constant-time update. Then, keep looping to deal with the extra black on $x.p$.

Case 3: x's sibling w is black, w's left child is red, and w's right child is black.



- Regardless of the color changes and rotation of this case, the black-heights don't change.
- Case 3 just sets up the structure of the tree, so it can fall correctly into case 4.

Case 4: x's sibling w is black, and w's right child is red.



- Nodes A, C, and E keep the same subtrees, so their black-heights don't change.
- Add these two constant-time assignments in RB-DELETE-FIXUP after lines 21 and 42:

  $x.p.bh = x.bh + 1$
  $x.p.p.bh = x.p.bh + 1$

- The extra black is taken care of, and the loop terminates.

Thus, RB-DELETE-FIXUP maintains its original $O(\lg n)$ time.

Therefore, we conclude that black-heights of nodes can be maintained as attributes in red-black trees without affecting the asymptotic performance of red-black tree operations.

For the second part of the question, no, we cannot maintain node depths without affecting the asymptotic performance of red-black tree operations. The depth of a node depends on the depth of its parent. When the depth of a node changes, the depths of all nodes below it in the tree must be updated. Updating the root node causes $n - 1$ other nodes to be updated, which would mean that operations on the tree that change node depths might not run in $O(n \lg n)$ time.

Solution to Exercise 17.3-6

General idea: Move a sweep line from left to right, while maintaining the set of rectangles currently intersected by the line in an interval tree. The interval tree will organize all rectangles whose x interval includes the current position of the sweep line, and it will be based on the y intervals of the rectangles, so that any overlapping y intervals in the interval tree correspond to overlapping rectangles.

Details:

1. Sort the rectangles by their x-coordinates. (Actually, each rectangle must appear twice in the sorted list—once for its left x-coordinate and once for its right x-coordinate.)
2. Scan the sorted list (from lowest to highest x-coordinate).

   - When an x-coordinate of a left edge is found, check whether the rectangle's y-coordinate interval overlaps an interval in the tree, and insert the rectangle (keyed on its y-coordinate interval) into the tree.
   - When an x-coordinate of a right edge is found, delete the rectangle from the interval tree.

   The interval tree always contains the set of "open" rectangles intersected by the sweep line. If an overlap is ever found in the interval tree, there are overlapping rectangles.

Time: $O(n \lg n)$

- $O(n \lg n)$ to sort the rectangles (use merge sort or heap sort).
- $O(n \lg n)$ for interval-tree operations (insert, delete, and check for overlap).