MODULE-2

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3.4 Exhaustive Search

Many important problems require finding an element with a special property in a domain that grows exponentially (or faster) with an instance size. Typically, such problems arise in situations that involve—explicitly or implicitly—combinatorial objects such as permutations, combinations, and subsets of a given set. Many such problems are optimization problems: they ask to find an element that maximizes or minimizes some desired characteristic such as a path length or an assignment cost.

Exhaustive search is simply a brute-force approach to combinatorial problems. It suggests generating each and every element of the problem domain, selecting those of them that satisfy all the constraints, and then finding a desired element (e.g., the one that optimizes some objective function). Note that although the idea of exhaustive search is quite straightforward, its implementation typically requires an algorithm for generating certain combinatorial objects. We delay a discussion of such algorithms until the next chapter and assume here that they exist.

We illustrate exhaustive search by applying it to three important problems: the traveling salesman problem, the knapsack problem, and the assignment problem.

Traveling Salesman Problem

The ***traveling salesman problem (TSP)*** has been intriguing researchers for the last 150 years by its seemingly simple formulation, important applications, and interesting connections to other combinatorial problems. In layman's terms, the problem asks to find the shortest tour through a given set of n cities that visits each city exactly once before returning to the city where it started. The problem can be conveniently modeled by a weighted graph, with the graph's vertices representing the cities and the edge weights specifying the distances. Then the problem can be stated as the problem of finding the shortest ***Hamiltonian circuit*** of the graph. (A Hamiltonian circuit is defined as a cycle that passes through all the vertices of the graph exactly once. It is named after the Irish mathematician Sir William Rowan Hamilton (1805–1865), who became interested in such cycles as an application of his algebraic discoveries.)

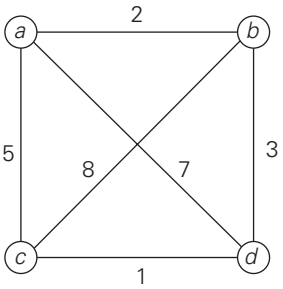
It is easy to see that a Hamiltonian circuit can also be defined as a sequence of $n + 1$ adjacent vertices $v_{i_0}, v_{i_1}, \ldots, v_{i_{n-1}}, v_{i_0}$, where the first vertex of the sequence is the same as the last one and all the other $n - 1$ vertices are distinct. Further, we can assume, with no loss of generality, that all circuits start and end at one particular vertex (they are cycles after all, are they not?). Thus, we can get all the tours by generating all the permutations of $n - 1$ intermediate cities, compute the tour lengths, and find the shortest among them. Figure 3.7 presents a small instance of the problem and its solution by this method.

An inspection of Figure 3.7 reveals three pairs of tours that differ only by their direction. Hence, we could cut the number of vertex permutations by half. We could, for example, choose any two intermediate vertices, say, b and c, and then consider only permutations in which b precedes c. (This trick implicitly defines a tour's direction.)

This improvement cannot brighten the efficiency picture much, however. The total number of permutations needed is still $\frac{1}{2}(n-1)!$, which makes the exhaustive-search approach impractical for all but very small values of n. On the other hand, if you always see your glass as half-full, you can claim that cutting the work by half is nothing to sneeze at, even if you solve a small instance of the problem, especially by hand. Also note that had we not limited our investigation to the circuits starting at the same vertex, the number of permutations would have been even larger, by a factor of n.

Knapsack Problem

Here is another well-known problem in algorithmics. Given n items of known weights $w_1, w_2, \ldots, w_n$ and values $v_1, v_2, \ldots, v_n$ and a knapsack of capacity W, find the most valuable subset of the items that fit into the knapsack. If you do not like the idea of putting yourself in the shoes of a thief who wants to steal the most



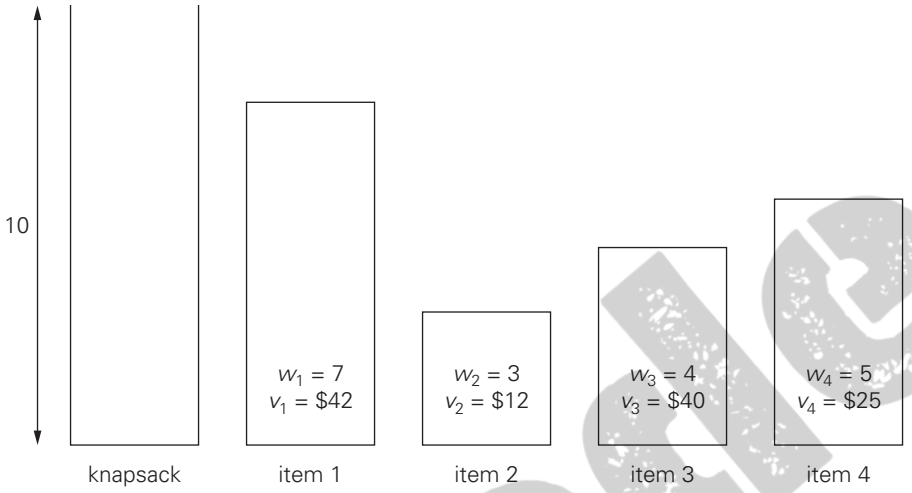
Tour	Length	
$a \rightarrow b \rightarrow c \rightarrow d \rightarrow a$	$l = 2 + 8 + 1 + 7 = 18$	
$a \rightarrow b \rightarrow d \rightarrow c \rightarrow a$	$l = 2 + 3 + 1 + 5 = 11$	optimal
$a \rightarrow c \rightarrow b \rightarrow d \rightarrow a$	$l = 5 + 8 + 3 + 7 = 23$	
$a \rightarrow c \rightarrow d \rightarrow b \rightarrow a$	$l = 5 + 1 + 3 + 2 = 11$	optimal
$a \rightarrow d \rightarrow b \rightarrow c \rightarrow a$	$l = 7 + 3 + 8 + 5 = 23$	
$a \rightarrow d \rightarrow c \rightarrow b \rightarrow a$	$l = 7 + 1 + 8 + 2 = 18$	

FIGURE 3.7 Solution to a small instance of the traveling salesman problem by exhaustive search.

valuable loot that fits into his knapsack, think about a transport plane that has to deliver the most valuable set of items to a remote location without exceeding the plane's capacity. Figure 3.8a presents a small instance of the knapsack problem.

The exhaustive-search approach to this problem leads to generating all the subsets of the set of n items given, computing the total weight of each subset in order to identify feasible subsets (i.e., the ones with the total weight not exceeding the knapsack capacity), and finding a subset of the largest value among them. As an example, the solution to the instance of Figure 3.8a is given in Figure 3.8b. Since the number of subsets of an n-element set is 2^n, the exhaustive search leads to a $\Omega(2^n)$ algorithm, no matter how efficiently individual subsets are generated.

Thus, for both the traveling salesman and knapsack problems considered above, exhaustive search leads to algorithms that are extremely inefficient on every input. In fact, these two problems are the best-known examples of so-called ***NP-hard problems***. No polynomial-time algorithm is known for any *NP*-hard problem. Moreover, most computer scientists believe that such algorithms do not exist, although this very important conjecture has never been proven. More-sophisticated approaches—backtracking and branch-and-bound (see Sections 12.1 and 12.2)—enable us to solve some but not all instances of these and



(a)

Subset	Total weight	Total value
$\varnothing$	0	$ 0
{1}	7	$42
{2}	3	$12
{3}	4	$40
{4}	5	$25
{1, 2}	10	$54
{1, 3}	11	not feasible
{1, 4}	12	not feasible
{2, 3}	7	$52
{2, 4}	8	$37
{3, 4}	**9**	**$65**
{1, 2, 3}	14	not feasible
{1, 2, 4}	15	not feasible
{1, 3, 4}	16	not feasible
{2, 3, 4}	12	not feasible
{1, 2, 3, 4}	19	not feasible

(b)

FIGURE 3.8 (a) Instance of the knapsack problem. (b) Its solution by exhaustive search. The information about the optimal selection is in bold.

similar problems in less than exponential time. Alternatively, we can use one of many approximation algorithms, such as those described in Section 12.3.

Assignment Problem

In our third example of a problem that can be solved by exhaustive search, there are n people who need to be assigned to execute n jobs, one person per job. (That is, each person is assigned to exactly one job and each job is assigned to exactly one person.) The cost that would accrue if the ith person is assigned to the jth job is a known quantity $C[i, j]$ for each pair $i, j = 1, 2, \ldots, n$. The problem is to find an assignment with the minimum total cost.

A small instance of this problem follows, with the table entries representing the assignment costs $C[i, j]$:

	Job 1	**Job 2**	**Job 3**	**Job 4**
Person 1	9	2	7	8
Person 2	6	4	3	7
Person 3	5	8	1	8
Person 4	7	6	9	4

It is easy to see that an instance of the assignment problem is completely specified by its cost matrix C. In terms of this matrix, the problem is to select one element in each row of the matrix so that all selected elements are in different columns and the total sum of the selected elements is the smallest possible. Note that no obvious strategy for finding a solution works here. For example, we cannot select the smallest element in each row, because the smallest elements may happen to be in the same column. In fact, the smallest element in the entire matrix need not be a component of an optimal solution. Thus, opting for the exhaustive search may appear as an unavoidable evil.

We can describe feasible solutions to the assignment problem as n-tuples $\langle j_1, \ldots, j_n \rangle$ in which the ith component, $i = 1, \ldots, n$, indicates the column of the element selected in the ith row (i.e., the job number assigned to the ith person). For example, for the cost matrix above, $\langle 2, 3, 4, 1 \rangle$ indicates the assignment of Person 1 to Job 2, Person 2 to Job 3, Person 3 to Job 4, and Person 4 to Job 1. The requirements of the assignment problem imply that there is a one-to-one correspondence between feasible assignments and permutations of the first n integers. Therefore, the exhaustive-search approach to the assignment problem would require generating all the permutations of integers $1, 2, \ldots, n$, computing the total cost of each assignment by summing up the corresponding elements of the cost matrix, and finally selecting the one with the smallest sum. A few first iterations of applying this algorithm to the instance given above are shown in Figure 3.9; you are asked to complete it in the exercises.

$$C = \begin{bmatrix} 9 & 2 & 7 & 8 \\ 6 & 4 & 3 & 7 \\ 5 & 8 & 1 & 8 \\ 7 & 6 & 9 & 4 \end{bmatrix}$$

<1, 2, 3, 4> cost = 9 + 4 + 1 + 4 = 18
<1, 2, 4, 3> cost = 9 + 4 + 8 + 9 = 30
<1, 3, 2, 4> cost = 9 + 3 + 8 + 4 = 24
<1, 3, 4, 2> cost = 9 + 3 + 8 + 6 = 26
<1, 4, 2, 3> cost = 9 + 7 + 8 + 9 = 33
<1, 4, 3, 2> cost = 9 + 7 + 1 + 6 = 23
etc.

FIGURE 3.9 First few iterations of solving a small instance of the assignment problem by exhaustive search.

Since the number of permutations to be considered for the general case of the assignment problem is $n!$, exhaustive search is impractical for all but very small instances of the problem. Fortunately, there is a much more efficient algorithm for this problem called the ***Hungarian method*** after the Hungarian mathematicians König and Egerváry, whose work underlies the method (see, e.g., [Kol95]).

This is good news: the fact that a problem domain grows exponentially or faster does not necessarily imply that there can be no efficient algorithm for solving it. In fact, we present several other examples of such problems later in the book. However, such examples are more of an exception to the rule. More often than not, there are no known polynomial-time algorithms for problems whose domain grows exponentially with instance size, provided we want to solve them exactly. And, as we mentioned above, such algorithms quite possibly do not exist.

4

Decrease-and-Conquer

The ***decrease-and-conquer*** technique is based on exploiting the relationship between a solution to a given instance of a problem and a solution to its smaller instance. Once such a relationship is established, it can be exploited either top down or bottom up. The former leads naturally to a recursive implementation, although, as one can see from several examples in this chapter, an ultimate implementation may well be nonrecursive. The bottom-up variation is usually implemented iteratively, starting with a solution to the smallest instance of the problem; it is called sometimes the ***incremental approach***.

There are three major variations of decrease-and-conquer:

- decrease by a constant
- decrease by a constant factor
- variable size decrease

In the ***decrease-by-a-constant*** variation, the size of an instance is reduced by the same constant on each iteration of the algorithm. Typically, this constant is equal to one (Figure 4.1), although other constant size reductions do happen occasionally.

Consider, as an example, the exponentiation problem of computing a^n where $a \neq 0$ and n is a nonnegative integer. The relationship between a solution to an instance of size n and an instance of size $n - 1$ is obtained by the obvious formula $a^n = a^{n-1} \cdot a$. So the function $f(n) = a^n$ can be computed either "top down" by using its recursive definition

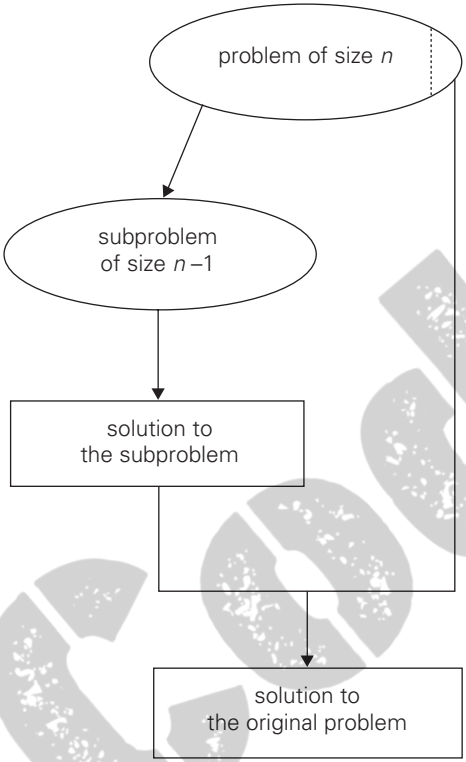


FIGURE 4.1 Decrease-(by one)-and-conquer technique.

$$f(n) = \begin{cases} f(n-1) \cdot a & \text{if } n > 0, \\ 1 & \text{if } n = 0, \end{cases} \tag{4.1}$$

or "bottom up" by multiplying 1 by a n times. (Yes, it is the same as the brute-force algorithm, but we have come to it by a different thought process.) More interesting examples of decrease-by-one algorithms appear in Sections 4.1–4.3.

The ***decrease-by-a-constant-factor*** technique suggests reducing a problem instance by the same constant factor on each iteration of the algorithm. In most applications, this constant factor is equal to two. (Can you give an example of such an algorithm?) The decrease-by-half idea is illustrated in Figure 4.2.

For an example, let us revisit the exponentiation problem. If the instance of size n is to compute a^n, the instance of half its size is to compute $a^{n/2}$, with the obvious relationship between the two: $a^n = (a^{n/2})^2$. But since we consider here instances with integer exponents only, the former does not work for odd n. If n is odd, we have to compute a^{n-1} by using the rule for even-valued exponents and then multiply the result by a. To summarize, we have the following formula:

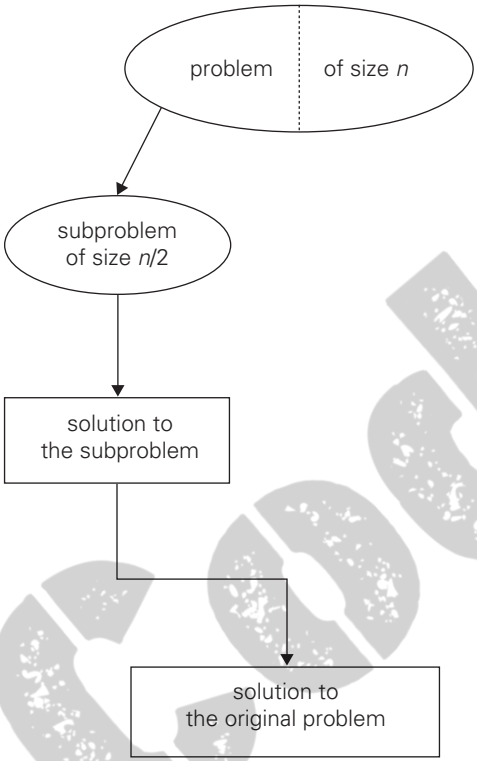


FIGURE 4.2 Decrease-(by half)-and-conquer technique.

$$a^n = \begin{cases} (a^{n/2})^2 & \text{if } n \text{ is even and positive,} \\ (a^{(n-1)/2})^2 \cdot a & \text{if } n \text{ is odd,} \\ 1 & \text{if } n = 0. \end{cases} \quad \textbf{(4.2)}$$

If we compute a^n recursively according to formula (4.2) and measure the algorithm's efficiency by the number of multiplications, we should expect the algorithm to be in $\Theta(\log n)$ because, on each iteration, the size is reduced by about a half at the expense of one or two multiplications.

A few other examples of decrease-by-a-constant-factor algorithms are given in Section 4.4 and its exercises. Such algorithms are so efficient, however, that there are few examples of this kind.

Finally, in the ***variable-size-decrease*** variety of decrease-and-conquer, the size-reduction pattern varies from one iteration of an algorithm to another. Euclid's algorithm for computing the greatest common divisor provides a good example of such a situation. Recall that this algorithm is based on the formula

$$\gcd(m, n) = \gcd(n, m \bmod n).$$

Though the value of the second argument is always smaller on the right-hand side than on the left-hand side, it decreases neither by a constant nor by a constant factor. A few other examples of such algorithms appear in Section 4.5.

4.1 Insertion Sort

In this section, we consider an application of the decrease-by-one technique to sorting an array $A[0..n-1]$. Following the technique's idea, we assume that the smaller problem of sorting the array $A[0..n-2]$ has already been solved to give us a sorted array of size $n-1$: $A[0] \le \cdots \le A[n-2]$. How can we take advantage of this solution to the smaller problem to get a solution to the original problem by taking into account the element $A[n-1]$? Obviously, all we need is to find an appropriate position for $A[n-1]$ among the sorted elements and insert it there. This is usually done by scanning the sorted subarray from right to left until the first element smaller than or equal to $A[n-1]$ is encountered to insert $A[n-1]$ right after that element. The resulting algorithm is called ***straight insertion sort*** or simply ***insertion sort***.

Though insertion sort is clearly based on a recursive idea, it is more efficient to implement this algorithm bottom up, i.e., iteratively. As shown in Figure 4.3, starting with $A[1]$ and ending with $A[n-1]$, $A[i]$ is inserted in its appropriate place among the first i elements of the array that have been already sorted (but, unlike selection sort, are generally not in their final positions).

Here is pseudocode of this algorithm.

ALGORITHM *InsertionSort*$(A[0..n-1])$

```
//Sorts a given array by insertion sort
//Input: An array A[0..n − 1] of n orderable elements
//Output: Array A[0..n − 1] sorted in nondecreasing order
for i ← 1 to n − 1 do
    v ← A[i]
    j ← i − 1
    while j ≥ 0 and A[j] > v do
        A[j + 1] ← A[j]
        j ← j − 1
    A[j + 1] ← v
```

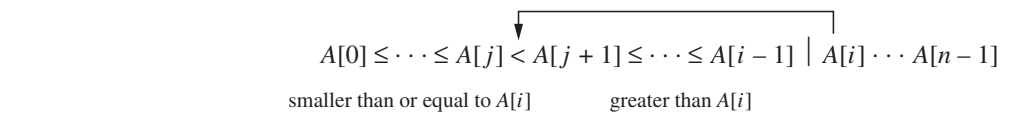


FIGURE 4.3 Iteration of insertion sort: $A[i]$ is inserted in its proper position among the preceding elements previously sorted.

89 | **45** 68 90 29 34 17
45 89 | **68** 90 29 34 17
45 68 89 | **90** 29 34 17
45 68 89 90 | **29** 34 17
29 45 68 89 90 | **34** 17
29 34 45 68 89 90 | **17**
17 29 34 45 68 89 90

FIGURE 4.4 Example of sorting with insertion sort. A vertical bar separates the sorted part of the array from the remaining elements; the element being inserted is in bold.

The operation of the algorithm is illustrated in Figure 4.4.

The basic operation of the algorithm is the key comparison $A[j] > v$. (Why not $j \geq 0$? Because it is almost certainly faster than the former in an actual computer implementation. Moreover, it is not germane to the algorithm: a better implementation with a sentinel—see Problem 8 in this section's exercises—eliminates it altogether.)

The number of key comparisons in this algorithm obviously depends on the nature of the input. In the worst case, $A[j] > v$ is executed the largest number of times, i.e., for every $j = i - 1, \ldots, 0$. Since $v = A[i]$, it happens if and only if $A[j] > A[i]$ for $j = i - 1, \ldots, 0$. (Note that we are using the fact that on the ith iteration of insertion sort all the elements preceding $A[i]$ are the first i elements in the input, albeit in the sorted order.) Thus, for the worst-case input, we get $A[0] > A[1]$ (for $i = 1$), $A[1] > A[2]$ (for $i = 2$), $\ldots$, $A[n-2] > A[n-1]$ (for $i = n - 1$). In other words, the worst-case input is an array of strictly decreasing values. The number of key comparisons for such an input is

$$C_{worst}(n) = \sum_{i=1}^{n-1} \sum_{j=0}^{i-1} 1 = \sum_{i=1}^{n-1} i = \frac{(n-1)n}{2} \in \Theta(n^2).$$

Thus, in the worst case, insertion sort makes exactly the same number of comparisons as selection sort (see Section 3.1).

In the best case, the comparison $A[j] > v$ is executed only once on every iteration of the outer loop. It happens if and only if $A[i-1] \leq A[i]$ for every $i = 1, \ldots, n-1$, i.e., if the input array is already sorted in nondecreasing order. (Though it "makes sense" that the best case of an algorithm happens when the problem is already solved, it is not always the case, as you are going to see in our discussion of quicksort in Chapter 5.) Thus, for sorted arrays, the number of key comparisons is

$$C_{best}(n) = \sum_{i=1}^{n-1} 1 = n - 1 \in \Theta(n).$$

This very good performance in the best case of sorted arrays is not very useful by itself, because we cannot expect such convenient inputs. However, almost-sorted files do arise in a variety of applications, and insertion sort preserves its excellent performance on such inputs.

A rigorous analysis of the algorithm's average-case efficiency is based on investigating the number of element pairs that are out of order (see Problem 11 in this section's exercises). It shows that on randomly ordered arrays, insertion sort makes on average half as many comparisons as on decreasing arrays, i.e.,

$$C_{avg}(n) \approx \frac{n^2}{4} \in \Theta(n^2).$$

This twice-as-fast average-case performance coupled with an excellent efficiency on almost-sorted arrays makes insertion sort stand out among its principal competitors among elementary sorting algorithms, selection sort and bubble sort. In addition, its extension named ***shellsort***, after its inventor D. L. Shell [She59], gives us an even better algorithm for sorting moderately large files (see Problem 12 in this section's exercises).

4.2 Topological Sorting

In this section, we discuss an important problem for directed graphs, with a variety of applications involving prerequisite-restricted tasks. Before we pose this problem, though, let us review a few basic facts about directed graphs themselves. A ***directed graph***, or ***digraph*** for short, is a graph with directions specified for all its edges (Figure 4.5a is an example). The adjacency matrix and adjacency lists are still two principal means of representing a digraph. There are only two notable differences between undirected and directed graphs in representing them: (1) the adjacency matrix of a directed graph does not have to be symmetric; (2) an edge in a directed graph has just one (not two) corresponding nodes in the digraph's adjacency lists.

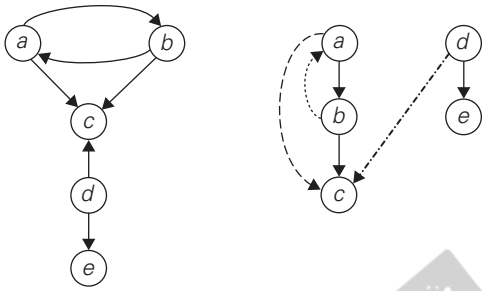


FIGURE 4.5 (a) Digraph. (b) DFS forest of the digraph for the DFS traversal started at a.

Depth-first search and breadth-first search are principal traversal algorithms for traversing digraphs as well, but the structure of corresponding forests can be more complex than for undirected graphs. Thus, even for the simple example of Figure 4.5a, the depth-first search forest (Figure 4.5b) exhibits all four types of edges possible in a DFS forest of a directed graph: ***tree edges*** (ab, bc, de), ***back edges*** (ba) from vertices to their ancestors, ***forward edges*** (ac) from vertices to their descendants in the tree other than their children, and ***cross edges*** (dc), which are none of the aforementioned types.

Note that a back edge in a DFS forest of a directed graph can connect a vertex to its parent. Whether or not it is the case, the presence of a back edge indicates that the digraph has a directed cycle. A ***directed cycle*** in a digraph is a sequence of three or more of its vertices that starts and ends with the same vertex and in which every vertex is connected to its immediate predecessor by an edge directed from the predecessor to the successor. For example, a, b, a is a directed cycle in the digraph in Figure 4.5a. Conversely, if a DFS forest of a digraph has no back edges, the digraph is a ***dag***, an acronym for ***directed acyclic graph***.

Edge directions lead to new questions about digraphs that are either meaningless or trivial for undirected graphs. In this section, we discuss one such question. As a motivating example, consider a set of five required courses {C1, C2, C3, C4, C5} a part-time student has to take in some degree program. The courses can be taken in any order as long as the following course prerequisites are met: C1 and C2 have no prerequisites, C3 requires C1 and C2, C4 requires C3, and C5 requires C3 and C4. The student can take only one course per term. In which order should the student take the courses?

The situation can be modeled by a digraph in which vertices represent courses and directed edges indicate prerequisite requirements (Figure 4.6). In terms of this digraph, the question is whether we can list its vertices in such an order that for every edge in the graph, the vertex where the edge starts is listed before the vertex where the edge ends. (Can you find such an ordering of this digraph's vertices?) This problem is called ***topological sorting***. It can be posed for an

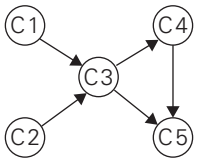


FIGURE 4.6 Digraph representing the prerequisite structure of five courses.

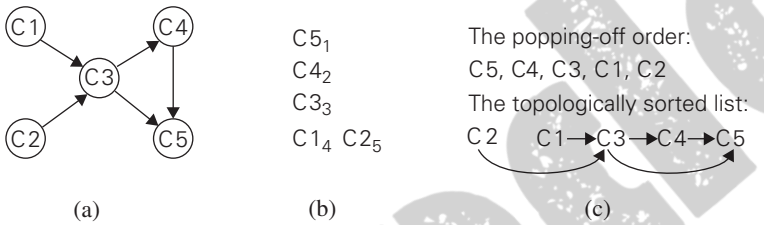


FIGURE 4.7 (a) Digraph for which the topological sorting problem needs to be solved. (b) DFS traversal stack with the subscript numbers indicating the popping-off order. (c) Solution to the problem.

arbitrary digraph, but it is easy to see that the problem cannot have a solution if a digraph has a directed cycle. Thus, for topological sorting to be possible, a digraph in question must be a dag. It turns out that being a dag is not only necessary but also sufficient for topological sorting to be possible; i.e., if a digraph has no directed cycles, the topological sorting problem for it has a solution. Moreover, there are two efficient algorithms that both verify whether a digraph is a dag and, if it is, produce an ordering of vertices that solves the topological sorting problem.

The first algorithm is a simple application of depth-first search: perform a DFS traversal and note the order in which vertices become dead-ends (i.e., popped off the traversal stack). Reversing this order yields a solution to the topological sorting problem, provided, of course, no back edge has been encountered during the traversal. If a back edge has been encountered, the digraph is not a dag, and topological sorting of its vertices is impossible.

Why does the algorithm work? When a vertex v is popped off a DFS stack, no vertex u with an edge from u to v can be among the vertices popped off before v. (Otherwise, (u, v) would have been a back edge.) Hence, any such vertex u will be listed after v in the popped-off order list, and before v in the reversed list.

Figure 4.7 illustrates an application of this algorithm to the digraph in Figure 4.6. Note that in Figure 4.7c, we have drawn the edges of the digraph, and they all point from left to right as the problem's statement requires. It is a convenient way to check visually the correctness of a solution to an instance of the topological sorting problem.

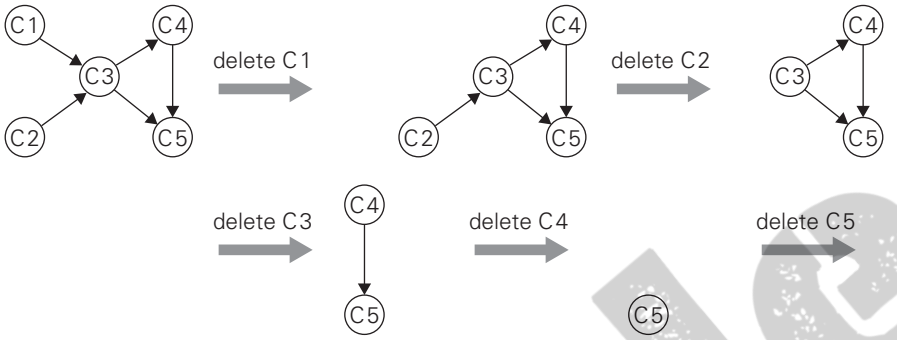


FIGURE 4.8 Illustration of the source-removal algorithm for the topological sorting problem. On each iteration, a vertex with no incoming edges is deleted from the digraph.

The second algorithm is based on a direct implementation of the decrease-(by one)-and-conquer technique: repeatedly, identify in a remaining digraph a ***source***, which is a vertex with no incoming edges, and delete it along with all the edges outgoing from it. (If there are several sources, break the tie arbitrarily. If there are none, stop because the problem cannot be solved—see Problem 6a in this section's exercises.) The order in which the vertices are deleted yields a solution to the topological sorting problem. The application of this algorithm to the same digraph representing the five courses is given in Figure 4.8.

Note that the solution obtained by the source-removal algorithm is different from the one obtained by the DFS-based algorithm. Both of them are correct, of course; the topological sorting problem may have several alternative solutions.

The tiny size of the example we used might create a wrong impression about the topological sorting problem. But imagine a large project—e.g., in construction, research, or software development—that involves a multitude of interrelated tasks with known prerequisites. The first thing to do in such a situation is to make sure that the set of given prerequisites is not contradictory. The convenient way of doing this is to solve the topological sorting problem for the project's digraph. Only then can one start thinking about scheduling tasks to, say, minimize the total completion time of the project. This would require, of course, other algorithms that you can find in general books on operations research or in special ones on CPM (Critical Path Method) and PERT (Program Evaluation and Review Technique) methodologies.

As to applications of topological sorting in computer science, they include instruction scheduling in program compilation, cell evaluation ordering in spreadsheet formulas, and resolving symbol dependencies in linkers.

5

Divide-and-Conquer

Divide-and-conquer is probably the best-known general algorithm design technique. Though its fame may have something to do with its catchy name, it is well deserved: quite a few very efficient algorithms are specific implementations of this general strategy. Divide-and-conquer algorithms work according to the following general plan:

1. A problem is divided into several subproblems of the same type, ideally of about equal size.
2. The subproblems are solved (typically recursively, though sometimes a different algorithm is employed, especially when subproblems become small enough).
3. If necessary, the solutions to the subproblems are combined to get a solution to the original problem.

The divide-and-conquer technique is diagrammed in Figure 5.1, which depicts the case of dividing a problem into two smaller subproblems, by far the most widely occurring case (at least for divide-and-conquer algorithms designed to be executed on a single-processor computer).

As an example, let us consider the problem of computing the sum of n numbers $a_0, \ldots, a_{n-1}$. If $n > 1$, we can divide the problem into two instances of the same problem: to compute the sum of the first $\lfloor n/2 \rfloor$ numbers and to compute the sum of the remaining $\lceil n/2 \rceil$ numbers. (Of course, if $n = 1$, we simply return a_0 as the answer.) Once each of these two sums is computed by applying the same method recursively, we can add their values to get the sum in question:

$$a_0 + \cdots + a_{n-1} = (a_0 + \cdots + a_{\lfloor n/2 \rfloor - 1}) + (a_{\lfloor n/2 \rfloor} + \cdots + a_{n-1}).$$

Is this an efficient way to compute the sum of n numbers? A moment of reflection (why could it be more efficient than the brute-force summation?), a

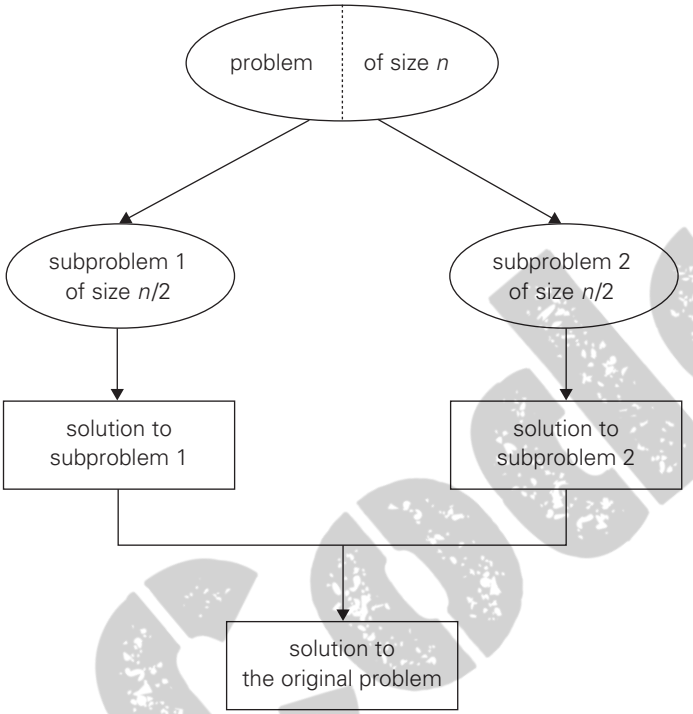


FIGURE 5.1 Divide-and-conquer technique (typical case).

small example of summing, say, four numbers by this algorithm, a formal analysis (which follows), and common sense (we do not normally compute sums this way, do we?) all lead to a negative answer to this question.[1]

Thus, not every divide-and-conquer algorithm is necessarily more efficient than even a brute-force solution. But often our prayers to the Goddess of Algorithmics—see the chapter's epigraph—*are* answered, and the time spent on executing the divide-and-conquer plan turns out to be significantly smaller than solving a problem by a different method. In fact, the divide-and-conquer approach yields some of the most important and efficient algorithms in computer science. We discuss a few classic examples of such algorithms in this chapter. Though we consider only sequential algorithms here, it is worth keeping in mind that the divide-and-conquer technique is ideally suited for parallel computations, in which each subproblem can be solved simultaneously by its own processor.

As mentioned above, in the most typical case of divide-and-conquer a problem's instance of size n is divided into two instances of size $n/2$. More generally, an instance of size n can be divided into b instances of size n/b, with a of them needing to be solved. (Here, a and b are constants; $a \geq 1$ and $b > 1$.) Assuming that size n is a power of b to simplify our analysis, we get the following recurrence for the running time $T(n)$:

$$T(n) = aT(n/b) + f(n), \tag{5.1}$$

where $f(n)$ is a function that accounts for the time spent on dividing an instance of size n into instances of size n/b and combining their solutions. (For the sum example above, $a = b = 2$ and $f(n) = 1$.) Recurrence (5.1) is called the ***general divide-and-conquer recurrence***. Obviously, the order of growth of its solution $T(n)$ depends on the values of the constants a and b and the order of growth of the function $f(n)$. The efficiency analysis of many divide-and-conquer algorithms is greatly simplified by the following theorem (see Appendix B).

Master Theorem If $f(n) \in \Theta(n^d)$ where $d \geq 0$ in recurrence (5.1), then

$$T(n) \in \begin{cases} \Theta(n^d) & \text{if } a < b^d, \\ \Theta(n^d \log n) & \text{if } a = b^d, \\ \Theta(n^{\log_b a}) & \text{if } a > b^d. \end{cases}$$

Analogous results hold for the O and Ω notations, too.

For example, the recurrence for the number of additions $A(n)$ made by the divide-and-conquer sum-computation algorithm (see above) on inputs of size $n = 2^k$ is

$$A(n) = 2A(n/2) + 1.$$

Thus, for this example, $a = 2$, $b = 2$, and $d = 0$; hence, since $a > b^d$,

$$A(n) \in \Theta(n^{\log_b a}) = \Theta(n^{\log_2 2}) = \Theta(n).$$

Note that we were able to find the solution's efficiency class without going through the drudgery of solving the recurrence. But, of course, this approach can only establish a solution's order of growth to within an unknown multiplicative constant, whereas solving a recurrence equation with a specific initial condition yields an exact answer (at least for n's that are powers of b).

It is also worth pointing out that if $a = 1$, recurrence (5.1) covers decrease-by-a-constant-factor algorithms discussed in the previous chapter. In fact, some people consider such algorithms as binary search degenerate cases of divide-and-conquer, where just one of two subproblems of half the size needs to be solved. It is better not to do this and consider decrease-by-a-constant-factor and divide-and-conquer as different design paradigms.

5.1 Mergesort

Mergesort is a perfect example of a successful application of the divide-and-conquer technique. It sorts a given array $A[0..n-1]$ by dividing it into two halves $A[0..\lfloor n/2 \rfloor - 1]$ and $A[\lfloor n/2 \rfloor..n-1]$, sorting each of them recursively, and then merging the two smaller sorted arrays into a single sorted one.

ALGORITHM *Mergesort*$(A[0..n-1])$

```
//Sorts array A[0..n − 1] by recursive mergesort
//Input: An array A[0..n − 1] of orderable elements
//Output: Array A[0..n − 1] sorted in nondecreasing order
if n > 1
    copy A[0..⌊n/2⌋ − 1] to B[0..⌊n/2⌋ − 1]
    copy A[⌊n/2⌋..n − 1] to C[0..⌈n/2⌉ − 1]
    Mergesort(B[0..⌊n/2⌋ − 1])
    Mergesort(C[0..⌈n/2⌉ − 1])
    Merge(B, C, A)    //see below
```

The ***merging*** of two sorted arrays can be done as follows. Two pointers (array indices) are initialized to point to the first elements of the arrays being merged. The elements pointed to are compared, and the smaller of them is added to a new array being constructed; after that, the index of the smaller element is incremented to point to its immediate successor in the array it was copied from. This operation is repeated until one of the two given arrays is exhausted, and then the remaining elements of the other array are copied to the end of the new array.

ALGORITHM *Merge*$(B[0..p-1], C[0..q-1], A[0..p+q-1])$

```
//Merges two sorted arrays into one sorted array
//Input: Arrays B[0..p − 1] and C[0..q − 1] both sorted
//Output: Sorted array A[0..p + q − 1] of the elements of B and C
i ← 0; j ← 0; k ← 0
while i < p and j < q do
    if B[i] ≤ C[j]
        A[k] ← B[i]; i ← i + 1
    else A[k] ← C[j]; j ← j + 1
    k ← k + 1
if i = p
    copy C[j..q − 1] to A[k..p + q − 1]
else copy B[i..p − 1] to A[k..p + q − 1]
```

The operation of the algorithm on the list 8, 3, 2, 9, 7, 1, 5, 4 is illustrated in Figure 5.2.

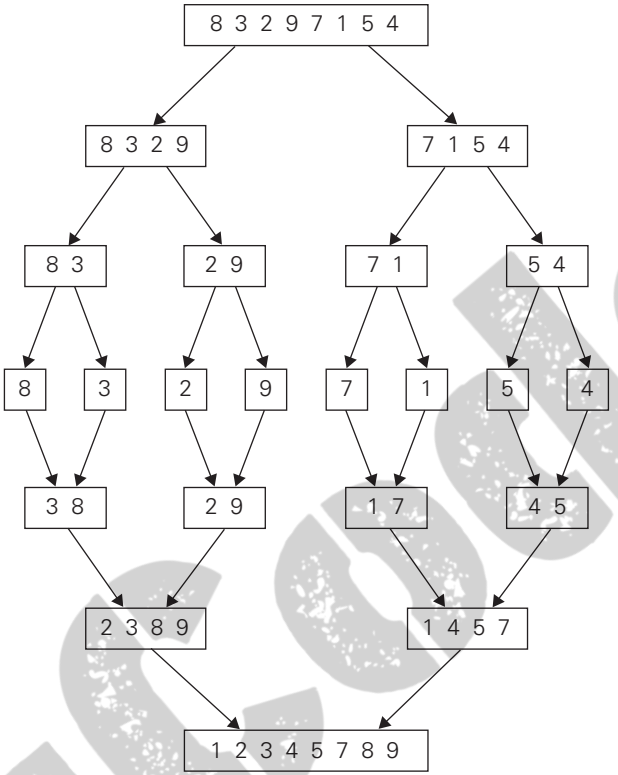


FIGURE 5.2 Example of mergesort operation.

How efficient is mergesort? Assuming for simplicity that n is a power of 2, the recurrence relation for the number of key comparisons $C(n)$ is

$$C(n) = 2C(n/2) + C_{merge}(n) \quad \text{for } n > 1, \quad C(1) = 0.$$

Let us analyze $C_{merge}(n)$, the number of key comparisons performed during the merging stage. At each step, exactly one comparison is made, after which the total number of elements in the two arrays still needing to be processed is reduced by 1. In the worst case, neither of the two arrays becomes empty before the other one contains just one element (e.g., smaller elements may come from the alternating arrays). Therefore, for the worst case, $C_{merge}(n) = n - 1$, and we have the recurrence

$$C_{worst}(n) = 2C_{worst}(n/2) + n - 1 \quad \text{for } n > 1, \quad C_{worst}(1) = 0.$$

Hence, according to the Master Theorem, $C_{worst}(n) \in \Theta(n \log n)$ (why?). In fact, it is easy to find the exact solution to the worst-case recurrence for $n = 2^k$:

$$C_{worst}(n) = n \log_2 n - n + 1.$$

The number of key comparisons made by mergesort in the worst case comes very close to the theoretical minimum[2] that any general comparison-based sorting algorithm can have. For large n, the number of comparisons made by this algorithm in the average case turns out to be about $0.25n$ less (see [Gon91, p. 173]) and hence is also in $\Theta(n \log n)$. A noteworthy advantage of mergesort over quicksort and heapsort—the two important advanced sorting algorithms to be discussed later—is its stability (see Problem 7 in this section's exercises). The principal shortcoming of mergesort is the linear amount of extra storage the algorithm requires. Though merging can be done in-place, the resulting algorithm is quite complicated and of theoretical interest only.

There are two main ideas leading to several variations of mergesort. First, the algorithm can be implemented bottom up by merging pairs of the array's elements, then merging the sorted pairs, and so on. (If n is not a power of 2, only slight bookkeeping complications arise.) This avoids the time and space overhead of using a stack to handle recursive calls. Second, we can divide a list to be sorted in more than two parts, sort each recursively, and then merge them together. This scheme, which is particularly useful for sorting files residing on secondary memory devices, is called ***multiway mergesort***.

5.2 Quicksort

Quicksort is the other important sorting algorithm that is based on the divide-and-conquer approach. Unlike mergesort, which divides its input elements according to their position in the array, quicksort divides them according to their value. We already encountered this idea of an array partition in Section 4.5, where we discussed the selection problem. A partition is an arrangement of the array's elements so that all the elements to the left of some element $A[s]$ are less than or equal to $A[s]$, and all the elements to the right of $A[s]$ are greater than or equal to it:

$$\underbrace{A[0] \dots A[s-1]}_{\text{all are} \le A[s]} \quad A[s] \quad \underbrace{A[s+1] \dots A[n-1]}_{\text{all are} \ge A[s]}$$

Obviously, after a partition is achieved, $A[s]$ will be in its final position in the sorted array, and we can continue sorting the two subarrays to the left and to the right of $A[s]$ independently (e.g., by the same method). Note the difference with mergesort: there, the division of the problem into two subproblems is immediate and the entire work happens in combining their solutions; here, the entire work happens in the division stage, with no work required to combine the solutions to the subproblems.

Here is pseudocode of quicksort: call $Quicksort(A[0..n-1])$ where

ALGORITHM $Quicksort(A[l..r])$

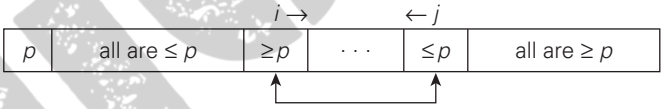
```
//Sorts a subarray by quicksort
//Input: Subarray of array A[0..n − 1], defined by its left and right
//       indices l and r
//Output: Subarray A[l..r] sorted in nondecreasing order
if l < r
    s ←Partition(A[l..r])  //s is a split position
    Quicksort(A[l..s − 1])
    Quicksort(A[s + 1..r])
```

As a partition algorithm, we can certainly use the Lomuto partition discussed in Section 4.5. Alternatively, we can partition $A[0..n-1]$ and, more generally, its subarray $A[l..r]$ $(0 \le l < r \le n-1)$ by the more sophisticated method suggested by C.A.R. Hoare, the prominent British computer scientist who invented quicksort.[3]

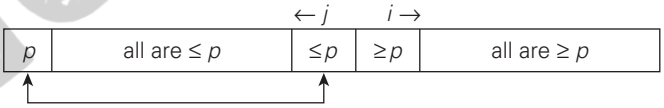
As before, we start by selecting a pivot—an element with respect to whose value we are going to divide the subarray. There are several different strategies for selecting a pivot; we will return to this issue when we analyze the algorithm's efficiency. For now, we use the simplest strategy of selecting the subarray's first element: $p = A[l]$.

Unlike the Lomuto algorithm, we will now scan the subarray from both ends, comparing the subarray's elements to the pivot. The left-to-right scan, denoted below by index pointer i, starts with the second element. Since we want elements smaller than the pivot to be in the left part of the subarray, this scan skips over elements that are smaller than the pivot and stops upon encountering the first element greater than or equal to the pivot. The right-to-left scan, denoted below by index pointer j, starts with the last element of the subarray. Since we want elements larger than the pivot to be in the right part of the subarray, this scan skips over elements that are larger than the pivot and stops on encountering the first element smaller than or equal to the pivot. (Why is it worth stopping the scans after encountering an element equal to the pivot? Because doing this tends to yield more even splits for arrays with a lot of duplicates, which makes the algorithm run faster. For example, if we did otherwise for an array of n equal elements, we would have gotten a split into subarrays of sizes $n - 1$ and 0, reducing the problem size just by 1 after scanning the entire array.)

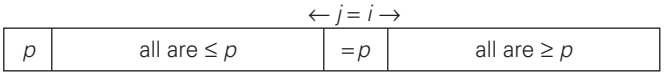
After both scans stop, three situations may arise, depending on whether or not the scanning indices have crossed. If scanning indices i and j have not crossed, i.e., $i < j$, we simply exchange $A[i]$ and $A[j]$ and resume the scans by incrementing i and decrementing j, respectively:



If the scanning indices have crossed over, i.e., $i > j$, we will have partitioned the subarray after exchanging the pivot with $A[j]$:



Finally, if the scanning indices stop while pointing to the same element, i.e., $i = j$, the value they are pointing to must be equal to p (why?). Thus, we have the subarray partitioned, with the split position $s = i = j$:



We can combine the last case with the case of crossed-over indices ($i > j$) by exchanging the pivot with $A[j]$ whenever $i \geq j$.

Here is pseudocode implementing this partitioning procedure.

ALGORITHM *HoarePartition*$(A[l..r])$

```
//Partitions a subarray by Hoare's algorithm, using the first element
//        as a pivot
//Input: Subarray of array A[0..n − 1], defined by its left and right
//        indices l and r (l < r)
//Output: Partition of A[l..r], with the split position returned as
//        this function's value
p ← A[l]
i ← l; j ← r + 1
repeat
    repeat i ← i + 1 until A[i] ≥ p
    repeat j ← j − 1 until A[j] ≤ p
    swap(A[i], A[j])
until i ≥ j
swap(A[i], A[j])  //undo last swap when i ≥ j
swap(A[l], A[j])
return j
```

Note that index i can go out of the subarray's bounds in this pseudocode. Rather than checking for this possibility every time index i is incremented, we can append to array $A[0..n-1]$ a "sentinel" that would prevent index i from advancing beyond position n. Note that the more sophisticated method of pivot selection mentioned at the end of the section makes such a sentinel unnecessary.

An example of sorting an array by quicksort is given in Figure 5.3.

We start our discussion of quicksort's efficiency by noting that the number of key comparisons made before a partition is achieved is $n + 1$ if the scanning indices cross over and n if they coincide (why?). If all the splits happen in the middle of corresponding subarrays, we will have the best case. The number of key comparisons in the best case satisfies the recurrence

$$C_{best}(n) = 2C_{best}(n/2) + n \quad \text{for } n > 1, \quad C_{best}(1) = 0.$$

According to the Master Theorem, $C_{best}(n) \in \Theta(n \log_2 n)$; solving it exactly for $n = 2^k$ yields $C_{best}(n) = n \log_2 n$.

In the worst case, all the splits will be skewed to the extreme: one of the two subarrays will be empty, and the size of the other will be just 1 less than the size of the subarray being partitioned. This unfortunate situation will happen, in particular, for increasing arrays, i.e., for inputs for which the problem is already solved! Indeed, if $A[0..n-1]$ is a strictly increasing array and we use $A[0]$ as the pivot, the left-to-right scan will stop on $A[1]$ while the right-to-left scan will go all the way to reach $A[0]$, indicating the split at position 0:

0	1	2	3	4	5	6	7
	i						*j*
5	3	1	9	8	2	4	7
			i			*j*	
5	3	1	9	8	2	4	7
			i			*j*	
5	3	1	4	8	2	9	7
				i	*j*		
5	3	1	4	8	2	9	7
				i	*j*		
5	3	1	4	2	8	9	7
				j	*i*		
5	3	1	4	2	8	9	7
2	3	1	4	**5**	8	9	7
	i		*j*				
2	3	1	4				
	i	*j*					
2	3	1	4				
	i	*j*					
2	1	3	4				
	j	*i*					
2	1	3	4				
1	**2**	3	4				
1							
			i j				
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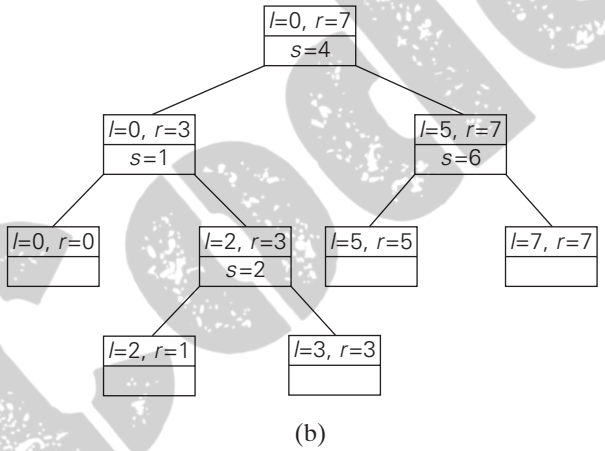
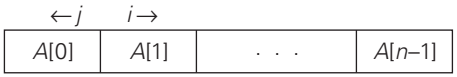
						i	*j*
					8	9	7
						i	*j*
					8	7	9
						j	*i*
					8	7	9
					7	**8**	9
					7		
							9

(a)



(b)

FIGURE 5.3 Example of quicksort operation. (a) Array's transformations with pivots shown in bold. (b) Tree of recursive calls to *Quicksort* with input values l and r of subarray bounds and split position s of a partition obtained.



So, after making $n + 1$ comparisons to get to this partition and exchanging the pivot $A[0]$ with itself, the algorithm will be left with the strictly increasing array $A[1..n-1]$ to sort. This sorting of strictly increasing arrays of diminishing sizes will

continue until the last one $A[n-2..n-1]$ has been processed. The total number of key comparisons made will be equal to

$$C_{worst}(n) = (n+1) + n + \cdots + 3 = \frac{(n+1)(n+2)}{2} - 3 \in \Theta(n^2).$$

Thus, the question about the utility of quicksort comes down to its average-case behavior. Let $C_{avg}(n)$ be the average number of key comparisons made by quicksort on a randomly ordered array of size n. A partition can happen in any position s ($0 \le s \le n-1$) after $n+1$ comparisons are made to achieve the partition. After the partition, the left and right subarrays will have s and $n-1-s$ elements, respectively. Assuming that the partition split can happen in each position s with the same probability $1/n$, we get the following recurrence relation:

$$C_{avg}(n) = \frac{1}{n}\sum_{s=0}^{n-1}[(n+1) + C_{avg}(s) + C_{avg}(n-1-s)] \quad \text{for } n > 1,$$
$$C_{avg}(0) = 0, \quad C_{avg}(1) = 0.$$

Its solution, which is much trickier than the worst- and best-case analyses, turns out to be

$$C_{avg}(n) \approx 2n \ln n \approx 1.39n \log_2 n.$$

Thus, on the average, quicksort makes only 39% more comparisons than in the best case. Moreover, its innermost loop is so efficient that it usually runs faster than mergesort (and heapsort, another $n \log n$ algorithm that we discuss in Chapter 6) on randomly ordered arrays of nontrivial sizes. This certainly justifies the name given to the algorithm by its inventor.

Because of quicksort's importance, there have been persistent efforts over the years to refine the basic algorithm. Among several improvements discovered by researchers are:

- better pivot selection methods such as ***randomized quicksort*** that uses a random element or the ***median-of-three*** method that uses the median of the leftmost, rightmost, and the middle element of the array
- switching to insertion sort on very small subarrays (between 5 and 15 elements for most computer systems) or not sorting small subarrays at all and finishing the algorithm with insertion sort applied to the entire nearly sorted array
- modifications of the partitioning algorithm such as the three-way partition into segments smaller than, equal to, and larger than the pivot (see Problem 9 in this section's exercises)

According to Robert Sedgewick [Sed11, p. 296], the world's leading expert on quicksort, such improvements in combination can cut the running time of the algorithm by 20%–30%.

Like any sorting algorithm, quicksort has weaknesses. It is not stable. It requires a stack to store parameters of subarrays that are yet to be sorted. While

the size of this stack can be made to be in $O(\log n)$ by always sorting first the smaller of two subarrays obtained by partitioning, it is worse than the $O(1)$ space efficiency of heapsort. Although more sophisticated ways of choosing a pivot make the quadratic running time of the worst case very unlikely, they do not eliminate it completely. And even the performance on randomly ordered arrays is known to be sensitive not only to implementation details of the algorithm but also to both computer architecture and data type. Still, the January/February 2000 issue of *Computing in Science & Engineering,* a joint publication of the American Institute of Physics and the IEEE Computer Society, selected quicksort as one of the 10 algorithms "with the greatest influence on the development and practice of science and engineering in the 20th century."

5.3 Binary Tree Traversals and Related Properties

In this section, we see how the divide-and-conquer technique can be applied to binary trees. A ***binary tree*** T is defined as a finite set of nodes that is either empty or consists of a root and two disjoint binary trees T_L and T_R called, respectively, the left and right subtree of the root. We usually think of a binary tree as a special case of an ordered tree (Figure 5.4). (This standard interpretation was an alternative definition of a binary tree in Section 1.4.)

Since the definition itself divides a binary tree into two smaller structures of the same type, the left subtree and the right subtree, many problems about binary trees can be solved by applying the divide-and-conquer technique. As an example, let us consider a recursive algorithm for computing the height of a binary tree. Recall that the height is defined as the length of the longest path from the root to a leaf. Hence, it can be computed as the maximum of the heights of the root's left

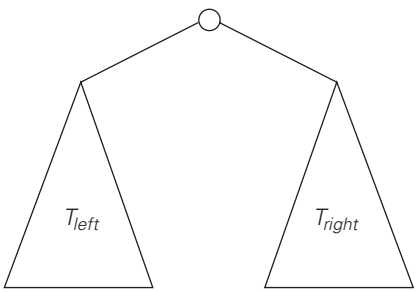


FIGURE 5.4 Standard representation of a binary tree.

and right subtrees plus 1. (We have to add 1 to account for the extra level of the root.) Also note that it is convenient to define the height of the empty tree as -1. Thus, we have the following recursive algorithm.

ALGORITHM *Height*(T)

//Computes recursively the height of a binary tree
//Input: A binary tree T
//Output: The height of T
if $T = \varnothing$ **return** -1
else return $\max\{Height(T_{left}), Height(T_{right})\} + 1$

We measure the problem's instance size by the number of nodes $n(T)$ in a given binary tree T. Obviously, the number of comparisons made to compute the maximum of two numbers and the number of additions $A(n(T))$ made by the algorithm are the same. We have the following recurrence relation for $A(n(T))$:

$$A(n(T)) = A(n(T_{left})) + A(n(T_{right})) + 1 \quad \text{for } n(T) > 0,$$
$$A(0) = 0.$$

Before we solve this recurrence (can you tell what its solution is?), let us note that addition is not the most frequently executed operation of this algorithm. What is? Checking—and this is very typical for binary tree algorithms—that the tree is not empty. For example, for the empty tree, the comparison $T = \varnothing$ is executed once but there are no additions, and for a single-node tree, the comparison and addition numbers are 3 and 1, respectively.

It helps in the analysis of tree algorithms to draw the tree's extension by replacing the empty subtrees by special nodes. The extra nodes (shown by little squares in Figure 5.5) are called ***external***; the original nodes (shown by little circles) are called ***internal***. By definition, the extension of the empty binary tree is a single external node.

It is easy to see that the *Height* algorithm makes exactly one addition for every internal node of the extended tree, and it makes one comparison to check whether

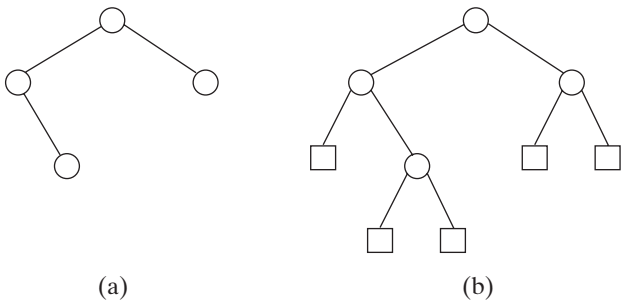


FIGURE 5.5 Binary tree (on the left) and its extension (on the right). Internal nodes are shown as circles; external nodes are shown as squares.

the tree is empty for every internal and external node. Therefore, to ascertain the algorithm's efficiency, we need to know how many external nodes an extended binary tree with n internal nodes can have. After checking Figure 5.5 and a few similar examples, it is easy to hypothesize that the number of external nodes x is always 1 more than the number of internal nodes n:

$$x = n + 1. \tag{5.2}$$

To prove this equality, consider the total number of nodes, both internal and external. Since every node, except the root, is one of the two children of an internal node, we have the equation

$$2n + 1 = x + n,$$

which immediately implies equality (5.2).

Note that equality (5.2) also applies to any nonempty ***full binary tree***, in which, by definition, every node has either zero or two children: for a full binary tree, n and x denote the numbers of parental nodes and leaves, respectively.

Returning to algorithm *Height,* the number of comparisons to check whether the tree is empty is

$$C(n) = n + x = 2n + 1,$$

and the number of additions is

$$A(n) = n.$$

The most important divide-and-conquer algorithms for binary trees are the three classic traversals: preorder, inorder, and postorder. All three traversals visit nodes of a binary tree recursively, i.e., by visiting the tree's root and its left and right subtrees. They differ only by the timing of the root's visit:

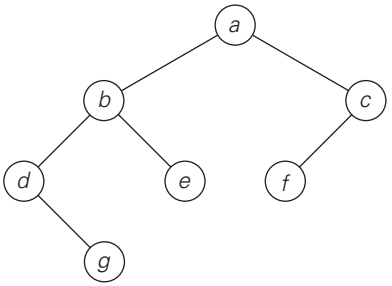
In the ***preorder traversal***, the root is visited before the left and right subtrees are visited (in that order).

In the ***inorder traversal***, the root is visited after visiting its left subtree but before visiting the right subtree.

In the ***postorder traversal***, the root is visited after visiting the left and right subtrees (in that order).

These traversals are illustrated in Figure 5.6. Their pseudocodes are quite straightforward, repeating the descriptions given above. (These traversals are also a standard feature of data structures textbooks.) As to their efficiency analysis, it is identical to the above analysis of the *Height* algorithm because a recursive call is made for each node of an extended binary tree.

Finally, we should note that, obviously, not all questions about binary trees require traversals of both left and right subtrees. For example, the search and insert operations for a binary search tree require processing only one of the two subtrees. Accordingly, we considered them in Section 4.5 not as applications of divide-and-conquer but rather as examples of the variable-size-decrease technique.



preorder: *a, b, d, g, e, c, f*
inorder: *d, g, b, e, a, f, c*
postorder: *g, d, e, b, f, c, a*

FIGURE 5.6 Binary tree and its traversals.

5.4 Multiplication of Large Integers and Strassen's Matrix Multiplication

In this section, we examine two surprising algorithms for seemingly straightforward tasks: multiplying two integers and multiplying two square matrices. Both

achieve a better asymptotic efficiency by ingenious application of the divide-and-conquer technique.

Multiplication of Large Integers

Some applications, notably modern cryptography, require manipulation of integers that are over 100 decimal digits long. Since such integers are too long to fit in a single word of a modern computer, they require special treatment. This practical need supports investigations of algorithms for efficient manipulation of large integers. In this section, we outline an interesting algorithm for multiplying such numbers. Obviously, if we use the conventional pen-and-pencil algorithm for multiplying two n-digit integers, each of the n digits of the first number is multiplied by each of the n digits of the second number for the total of n^2 digit multiplications. (If one of the numbers has fewer digits than the other, we can pad the shorter number with leading zeros to equalize their lengths.) Though it might appear that it would be impossible to design an algorithm with fewer than n^2 digit multiplications, this turns out not to be the case. The miracle of divide-and-conquer comes to the rescue to accomplish this feat.

To demonstrate the basic idea of the algorithm, let us start with a case of two-digit integers, say, 23 and 14. These numbers can be represented as follows:

$$23 = 2 \cdot 10^1 + 3 \cdot 10^0 \quad \text{and} \quad 14 = 1 \cdot 10^1 + 4 \cdot 10^0.$$

Now let us multiply them:

$$\begin{aligned} 23 * 14 &= (2 \cdot 10^1 + 3 \cdot 10^0) * (1 \cdot 10^1 + 4 \cdot 10^0) \\ &= (2 * 1)10^2 + (2 * 4 + 3 * 1)10^1 + (3 * 4)10^0. \end{aligned}$$

The last formula yields the correct answer of 322, of course, but it uses the same four digit multiplications as the pen-and-pencil algorithm. Fortunately, we can compute the middle term with just one digit multiplication by taking advantage of the products $2 * 1$ and $3 * 4$ that need to be computed anyway:

$$2 * 4 + 3 * 1 = (2 + 3) * (1 + 4) - 2 * 1 - 3 * 4.$$

Of course, there is nothing special about the numbers we just multiplied. For any pair of two-digit numbers $a = a_1a_0$ and $b = b_1b_0$, their product c can be computed by the formula

$$c = a * b = c_2 10^2 + c_1 10^1 + c_0,$$

where

$c_2 = a_1 * b_1$ is the product of their first digits,

$c_0 = a_0 * b_0$ is the product of their second digits,

$c_1 = (a_1 + a_0) * (b_1 + b_0) - (c_2 + c_0)$ is the product of the sum of the a's digits and the sum of the b's digits minus the sum of c_2 and c_0.

Now we apply this trick to multiplying two n-digit integers a and b where n is a positive even number. Let us divide both numbers in the middle—after all, we promised to take advantage of the divide-and-conquer technique. We denote the first half of the a's digits by a_1 and the second half by a_0; for b, the notations are b_1 and b_0, respectively. In these notations, $a = a_1a_0$ implies that $a = a_1 10^{n/2} + a_0$ and $b = b_1b_0$ implies that $b = b_1 10^{n/2} + b_0$. Therefore, taking advantage of the same trick we used for two-digit numbers, we get

$$\begin{aligned} c = a * b &= (a_1 10^{n/2} + a_0) * (b_1 10^{n/2} + b_0) \\ &= (a_1 * b_1)10^n + (a_1 * b_0 + a_0 * b_1)10^{n/2} + (a_0 * b_0) \\ &= c_2 10^n + c_1 10^{n/2} + c_0, \end{aligned}$$

where

$c_2 = a_1 * b_1$ is the product of their first halves,

$c_0 = a_0 * b_0$ is the product of their second halves,

$c_1 = (a_1 + a_0) * (b_1 + b_0) - (c_2 + c_0)$ is the product of the sum of the a's halves and the sum of the b's halves minus the sum of c_2 and c_0.

If $n/2$ is even, we can apply the same method for computing the products c_2, c_0, and c_1. Thus, if n is a power of 2, we have a recursive algorithm for computing the product of two n-digit integers. In its pure form, the recursion is stopped when n becomes 1. It can also be stopped when we deem n small enough to multiply the numbers of that size directly.

How many digit multiplications does this algorithm make? Since multiplication of n-digit numbers requires three multiplications of $n/2$-digit numbers, the recurrence for the number of multiplications $M(n)$ is

$$M(n) = 3M(n/2) \quad \text{for } n > 1, \quad M(1) = 1.$$

Solving it by backward substitutions for $n = 2^k$ yields

$$\begin{aligned} M(2^k) &= 3M(2^{k-1}) = 3[3M(2^{k-2})] = 3^2 M(2^{k-2}) \\ &= \cdots = 3^i M(2^{k-i}) = \cdots = 3^k M(2^{k-k}) = 3^k. \end{aligned}$$

Since $k = \log_2 n$,

$$M(n) = 3^{\log_2 n} = n^{\log_2 3} \approx n^{1.585}.$$

(On the last step, we took advantage of the following property of logarithms: $a^{\log_b c} = c^{\log_b a}$.)

But what about additions and subtractions? Have we not decreased the number of multiplications by requiring more of those operations? Let $A(n)$ be the number of digit additions and subtractions executed by the above algorithm in multiplying two n-digit decimal integers. Besides $3A(n/2)$ of these operations needed to compute the three products of $n/2$-digit numbers, the above formulas

require five additions and one subtraction. Hence, we have the recurrence

$$A(n) = 3A(n/2) + cn \quad \text{for } n > 1, \quad A(1) = 1.$$

Applying the Master Theorem, which was stated in the beginning of the chapter, we obtain $A(n) \in \Theta(n^{\log_2 3})$, which means that the total number of additions and subtractions have the same asymptotic order of growth as the number of multiplications.

The asymptotic advantage of this algorithm notwithstanding, how practical is it? The answer depends, of course, on the computer system and program quality implementing the algorithm, which might explain the rather wide disparity of reported results. On some machines, the divide-and-conquer algorithm has been reported to outperform the conventional method on numbers only 8 decimal digits long and to run more than twice faster with numbers over 300 decimal digits long—the area of particular importance for modern cryptography. Whatever this outperformance "crossover point" happens to be on a particular machine, it is worth switching to the conventional algorithm after the multiplicands become smaller than the crossover point. Finally, if you program in an object-oriented language such as Java, C++, or Smalltalk, you should also be aware that these languages have special classes for dealing with large integers.

Discovered by 23-year-old Russian mathematician Anatoly Karatsuba in 1960, the divide-and-conquer algorithm proved wrong the then-prevailing opinion that the time efficiency of any integer multiplication algorithm must be in $\Omega(n^2)$. The discovery encouraged researchers to look for even (asymptotically) faster algorithms for this and other algebraic problems. We will see such an algorithm in the next section.

Strassen's Matrix Multiplication

Now that we have seen that the divide-and-conquer approach can reduce the number of one-digit multiplications in multiplying two integers, we should not be surprised that a similar feat can be accomplished for multiplying matrices. Such an algorithm was published by V. Strassen in 1969 [Str69]. The principal insight of the algorithm lies in the discovery that we can find the product C of two 2×2 matrices A and B with just seven multiplications as opposed to the eight required by the brute-force algorithm (see Example 3 in Section 2.3). This is accomplished by using the following formulas:

$$\begin{bmatrix} c_{00} & c_{01} \\ c_{10} & c_{11} \end{bmatrix} = \begin{bmatrix} a_{00} & a_{01} \\ a_{10} & a_{11} \end{bmatrix} * \begin{bmatrix} b_{00} & b_{01} \\ b_{10} & b_{11} \end{bmatrix}$$
$$= \begin{bmatrix} m_1 + m_4 - m_5 + m_7 & m_3 + m_5 \\ m_2 + m_4 & m_1 + m_3 - m_2 + m_6 \end{bmatrix},$$

where

$$
\begin{aligned}
m_1 &= (a_{00} + a_{11}) * (b_{00} + b_{11}),\\
m_2 &= (a_{10} + a_{11}) * b_{00},\\
m_3 &= a_{00} * (b_{01} - b_{11}),\\
m_4 &= a_{11} * (b_{10} - b_{00}),\\
m_5 &= (a_{00} + a_{01}) * b_{11},\\
m_6 &= (a_{10} - a_{00}) * (b_{00} + b_{01}),\\
m_7 &= (a_{01} - a_{11}) * (b_{10} + b_{11}).
\end{aligned}
$$

Thus, to multiply two 2×2 matrices, Strassen's algorithm makes seven multiplications and 18 additions/subtractions, whereas the brute-force algorithm requires eight multiplications and four additions. These numbers should not lead us to multiplying 2×2 matrices by Strassen's algorithm. Its importance stems from its *asymptotic* superiority as matrix order n goes to infinity.

Let A and B be two $n \times n$ matrices where n is a power of 2. (If n is not a power of 2, matrices can be padded with rows and columns of zeros.) We can divide A, B, and their product C into four $n/2 \times n/2$ submatrices each as follows:

$$
\left[\begin{array}{c|c} C_{00} & C_{01} \\ \hline C_{10} & C_{11} \end{array}\right] = \left[\begin{array}{c|c} A_{00} & A_{01} \\ \hline A_{10} & A_{11} \end{array}\right] * \left[\begin{array}{c|c} B_{00} & B_{01} \\ \hline B_{10} & B_{11} \end{array}\right].
$$

It is not difficult to verify that one can treat these submatrices as numbers to get the correct product. For example, C_{00} can be computed either as $A_{00} * B_{00} + A_{01} * B_{10}$ or as $M_1 + M_4 - M_5 + M_7$ where M_1, M_4, M_5, and M_7 are found by Strassen's formulas, with the numbers replaced by the corresponding submatrices. If the seven products of $n/2 \times n/2$ matrices are computed recursively by the same method, we have Strassen's algorithm for matrix multiplication.

Let us evaluate the asymptotic efficiency of this algorithm. If $M(n)$ is the number of multiplications made by Strassen's algorithm in multiplying two $n \times n$ matrices (where n is a power of 2), we get the following recurrence relation for it:

$$M(n) = 7M(n/2) \quad \text{for } n > 1, \quad M(1) = 1.$$

Since $n = 2^k$,

$$
\begin{aligned}
M(2^k) &= 7M(2^{k-1}) = 7[7M(2^{k-2})] = 7^2 M(2^{k-2}) = \cdots\\
&= 7^i M(2^{k-i}) \cdots = 7^k M(2^{k-k}) = 7^k.
\end{aligned}
$$

Since $k = \log_2 n$,

$$M(n) = 7^{\log_2 n} = n^{\log_2 7} \approx n^{2.807},$$

which is smaller than n^3 required by the brute-force algorithm.

Since this savings in the number of multiplications was achieved at the expense of making extra additions, we must check the number of additions $A(n)$ made by Strassen's algorithm. To multiply two matrices of order $n > 1$, the algorithm needs to multiply seven matrices of order $n/2$ and make 18 additions/subtractions of matrices of size $n/2$; when $n = 1$, no additions are made since two numbers are

simply multiplied. These observations yield the following recurrence relation:

$$A(n) = 7A(n/2) + 18(n/2)^2 \quad \text{for } n > 1, \quad A(1) = 0.$$

Though one can obtain a closed-form solution to this recurrence (see Problem 8 in this section's exercises), here we simply establish the solution's order of growth. According to the Master Theorem, $A(n) \in \Theta(n^{\log_2 7})$. In other words, the number of additions has the same order of growth as the number of multiplications. This puts Strassen's algorithm in $\Theta(n^{\log_2 7})$, which is a better efficiency class than $\Theta(n^3)$ of the brute-force method.

Since the time of Strassen's discovery, several other algorithms for multiplying two $n \times n$ matrices of real numbers in $O(n^\alpha)$ time with progressively smaller constants α have been invented. The fastest algorithm so far is that of Coopersmith and Winograd [Coo87] with its efficiency in $O(n^{2.376})$. The decreasing values of the exponents have been obtained at the expense of the increasing complexity of these algorithms. Because of large multiplicative constants, none of them is of practical value. However, they are interesting from a theoretical point of view. On one hand, they get closer and closer to the best theoretical lower bound known for matrix multiplication, which is n^2 multiplications, though the gap between this bound and the best available algorithm remains unresolved. On the other hand, matrix multiplication is known to be computationally equivalent to some other important problems, such as solving systems of linear equations (discussed in the next chapter).