LEARNING MADE EASY

2nd Edition

Algorithms for dummies®

A Wiley Brand

Understand how data drives algorithms

Create your own algorithms using Python

Discover how algorithms are used in the real world

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Author of *Artificial Intelligence For Dummies*

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Algorithms

2nd Edition

by John Paul Mueller and Luca Massaron

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Algorithms For Dummies®, 2nd Edition

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Contents at a Glance

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Introduction

You need to learn about algorithms for school or work. Yet, all the books you've tried on the subject end up being more along the lines of really good sleep-inducing aids rather than texts to teach you something. Assuming that you can get past the arcane symbols obviously written by a demented two-year-old with a penchant for squiggles, you end up having no idea of why you'd even want to know anything about them. Most math texts are boring! However, *Algorithms For Dummies,* 2nd Edition is different. The first thing you'll note is that this book has a definite lack of odd symbols (especially of the squiggly sort) floating about. Yes, you see a few (it is a math book, after all), but what you find instead are clear instructions for using algorithms that actually have names and a history behind them and that perform useful tasks. You'll encounter simple coding techniques to perform amazing tasks that will intrigue your friends. You can certainly make them jealous as you perform feats of math that they can't begin to understand. You get all this without having to strain your brain, even a little, and you won't even fall asleep (well, unless you really want to do so). New in this edition of the book are more details about how algorithms work, and you even get to create your own basic math package so that you know how to do it for that next job interview.

About This Book

Algorithms For Dummies, 2nd Edition is the math book that you wanted in college but didn't get. You discover, for example, that algorithms aren't new. After all, the Babylonians used algorithms to perform simple tasks as early as 1,600 BC. If the Babylonians could figure this stuff out, certainly you can, too! This book actually has three things that you won't find in most math books:

- Algorithms that have actual names and a historical basis so that you can remember the algorithm and know why someone took time to create it
- Simple explanations of how the algorithm performs awesome feats of data manipulation, data analysis, or probability prediction
- Code that shows how to use the algorithm without actually dealing with arcane symbols that no one without a math degree can understand

Part of the emphasis of this book is on using the right tools. This book uses Python to perform various tasks. Python has special features that make working with algorithms significantly easier. For example, Python provides access to a huge array of packages that let you do just about anything you can imagine, and more than a few that you can't. However, unlike many texts that use Python, this one doesn't bury you in packages. We use a select group of packages that provide great flexibility with a lot of functionality but don't require you to pay anything. You can go through this entire book without forking over a cent of your hard-earned money.

You also discover some interesting techniques in this book. The most important is that you don't just see the algorithms used to perform tasks; you also get an explanation of how the algorithms work. Unlike many other books, *Algorithms For Dummies*, 2nd Edition enables you to fully understand what you're doing, but without requiring you to have a PhD in math. Every one of the examples shows the expected output and tells you why that output is important. You aren't left with the feeling that something is missing.

Of course, you might still be worried about the whole programming environment issue, and this book doesn't leave you in the dark there, either. This book relies on Google Colab to provide a programming environment (although you can use Jupyter Notebook quite easily, too). Because you access Colab through a browser, you can program anywhere and at any time that you have access to a browser, even on your smartphone while at the dentist's office or possibly while standing on your head watching reruns of your favorite show.

To help you absorb the concepts, this book uses the following conventions:

- Text that you're meant to type just as it appears in the book is in **bold**. The exception is when you're working through a step list: Because each step is bold, the text to type is not bold.
- Words that we want you to type in that are also in *italics* are used as placeholders, which means that you need to replace them with something that works for you. For example, if you see "Type ***Your Name*** and press Enter," you need to replace *Your Name* with your actual name.
- We also use *italics* for terms we define. This means that you don't have to rely on other sources to provide the definitions you need.
- Web addresses and programming code appear in `monofont`. If you're reading a digital version of this book on a device connected to the Internet, you can click the live link to visit that website, like this: `http://www.dummies.com`.
- When you need to click command sequences, you see them separated by a special arrow, like this: File ➪ New File, which tells you to click File and then New File.

Foolish Assumptions

You might find it difficult to believe that we've assumed anything about you — after all, we haven't even met you yet! Although most assumptions are indeed foolish, we made certain assumptions to provide a starting point for the book.

The first assumption is that you're familiar with the platform you want to use, because the book doesn't provide any guidance in this regard. (Chapter 3 does, however, tell you how to access Google Colab from your browser and use it to work with the code examples in the book.) To give you the maximum information about Python with regard to algorithms, this book doesn't discuss any platform-specific issues. You really do need to know how to install applications, use applications, and generally work with your chosen platform before you begin working with this book.

This book isn't a math primer. Yes, you see lots of examples of complex math, but the emphasis is on helping you use Python to perform common tasks using algorithms rather than learning math theory. However, you do get explanations of many of the algorithms used in the book so that you can understand how the algorithms work. Chapters 1 and 2 guide you through a what you need to know in order to use this book successfully. Chapter 5 is a special chapter that discusses how to create your own math library, which significantly aids you in understanding how math works with code to create a reusable package. It also looks dandy on your resume to say that you've created your own math library.

This book also assumes that you can access items on the Internet. Sprinkled throughout are numerous references to online material that will enhance your learning experience. However, these added sources are useful only if you actually find and use them. You must also have Internet access to use Google Colab.

Icons Used in This Book

As you read this book, you encounter icons in the margins that indicate material of interest (or not, as the case may be). Here's what the icons mean:

TIP

Tips are nice because they help you save time or perform some task without a lot of extra work. The tips in this book are time-saving techniques or pointers to resources that you should try so that you can get the maximum benefit from Python, or in performing algorithm-related or data analysis–related tasks.

WARNING

We don't want to sound like angry parents or some kind of maniacs, but you should avoid doing anything that's marked with a Warning icon. Otherwise, you might find that your application fails to work as expected, you get incorrect answers from seemingly bulletproof algorithms, or (in the worst-case scenario) you lose data.

TECHNICAL STUFF

Whenever you see this icon, think advanced tip or technique. You might find these tidbits of useful information just too boring for words, or they could contain the solution you need to get a program running. Skip these bits of information whenever you like.

REMEMBER

If you don't get anything else out of a particular chapter or section, remember the material marked by this icon. This text usually contains an essential process or a bit of information that you must know to work with Python, or to perform algorithm-related or data analysis–related tasks successfully.

Beyond the Book

This book isn't the end of your Python or algorithm learning experience — it's really just the beginning. We provide online content to make this book more flexible and better able to meet your needs. That way, as we receive email from you, we can address questions and tell you how updates to Python, or its associated add-ons affect book content. In fact, you gain access to all these cool additions:

- **Cheat sheet:** You remember using crib notes in school to make a better mark on a test, don't you? You do? Well, a cheat sheet is sort of like that. It provides you with some special notes about tasks that you can do with Python, Google Colab, and algorithms that not every other person knows. To find the cheat sheet for this book, go to `www.dummies.com` and enter *Algorithms For Dummies, 2nd Edition Cheat Sheet* in the search box. The cheat sheet contains really neat information such as finding the algorithms that you commonly need to perform specific tasks.
- **Updates:** Sometimes changes happen. For example, we might not have seen an upcoming change when we looked into our crystal ball during the writing of this book. In the past, this possibility simply meant that the book became outdated and less useful, but you can now find updates to the book, if we make any, by going to `www.dummies.com` and entering *Algorithms For Dummies, 2nd Edition* in the search box.

  In addition to these updates, check out the blog posts with answers to reader questions and demonstrations of useful book-related techniques at `http://blog.johnmuellerbooks.com/`.

- **Companion files:** Hey! Who really wants to type all the code in the book and reconstruct all those plots manually? Most readers prefer to spend their time actually working with Python, performing tasks using algorithms, and seeing the interesting things they can do, rather than typing. Fortunately for you, the examples used in the book are available for download, so all you need to do is read the book to learn algorithm usage techniques. You can find these files by searching *Algorithms For Dummies,* 2nd Edition at `www.dummies.com` and scrolling down the left side of the page that opens. The source code is also at `http://www.johnmuellerbooks.com/source-code/`, and `https://github.com/lmassaron/algo4d_2ed`.

Where to Go from Here

It's time to start your algorithm learning adventure! If you're completely new to algorithms, you should start with Chapter 1 and progress through the book at a pace that allows you to absorb as much of the material as possible. Make sure to read about Python, because the book uses this language as needed for the examples.

If you're a novice who's in an absolute rush to get going with algorithms as quickly as possible, you can skip to Chapter 3 with the understanding that you may find some topics a bit confusing later.

Readers who have some exposure to Python, and have the appropriate language versions installed, can save reading time by moving directly to Chapter 5. You can always go back to earlier chapters as necessary when you have questions. However, you do need to understand how each technique works before moving to the next one. Every technique, coding example, and procedure has important lessons for you, and you could miss vital content if you start skipping too much information.

1 Getting Started with Algorithms

IN THIS PART . . .

Defining algorithms and their design

Using Google Colab to work with algorithms

Performing essential data manipulations

Building a matrix manipulation class

IN THIS CHAPTER

» Defining what is meant by *algorithm*

» Relying on computers to use algorithms to provide solutions

» Determining how issues differ from solutions

» Performing data manipulation so that you can find a solution

Chapter 1 Introducing Algorithms

If you're in the majority of people, you're likely confused as you open this book and begin your adventure with algorithms, because most texts never tell you what an algorithm is, much less why you'd want to use one. Hearing about algorithms is like being in school again with the teacher droning on; you're falling asleep from lack of interest because algorithms don't seem particularly useful to understand at the moment.

The first section of this chapter is dedicated to helping you understand precisely what the term *algorithm* means and why you benefit from knowing how to use algorithms. Far from being arcane, algorithms are actually used all over the place, and you have probably used or been helped by them for years without really knowing it. So, they're stealth knowledge! In truth, algorithms are becoming the spine that supports and regulates what is important in an increasingly complex and technological society like ours.

The second section of this chapter discusses how you use computers to create solutions to problems using algorithms, how to distinguish between issues and solutions, and what you need to do to manipulate data to discover a solution. The goal is to help you differentiate between algorithms and other tasks that people confuse with algorithms. In short, you discover why you really want to know about algorithms, as well as how to apply them to data.

The third section of the chapter discusses algorithms in a real-world manner, that is, by viewing the terminologies used to understand algorithms and to present algorithms in a way that shows that the real world is often less than perfect. Understanding how to describe an algorithm in a realistic manner also helps to temper expectations to reflect the realities of what an algorithm can actually do.

The final section of the chapter discusses data. The algorithms you work with in this book require data input in a specific form, which sometimes means changing the data to match the algorithm's requirements. Data manipulation doesn't change the content of the data. Instead, it changes the presentation and form of the data so that an algorithm can help you see new patterns that weren't apparent before (but were actually present in the data all along).

Describing Algorithms

Even though people have solved algorithms manually for thousands of years, doing so can consume huge amounts of time and require many numeric computations, depending on the complexity of the problem you want to solve. Algorithms are all about finding solutions, and the speedier and easier, the better. A huge gap exists between mathematical algorithms historically created by geniuses of their time, such as Euclid (`https://www.britannica.com/biography/Euclid-Greek-mathematician`), Sir Isaac Newton (`https://www.britannica.com/biography/Isaac-Newton`), or Carl Friedrich Gauss (`https://www.britannica.com/biography/Carl-Friedrich-Gauss`), and modern algorithms created in universities as well as private research and development laboratories. The main reason for this gap is the use of computers. Using computers to solve problems by employing the appropriate algorithm speeds up the task significantly. You may notice that more problem solutions appear quickly today, in part, because computer power is both cheap and constantly increasing.

When working with algorithms, you consider the inputs, desired outputs, and the process (a sequence of actions) used to obtain a desired output from a given input. However, you can get the terminology wrong and view algorithms in the wrong way because you haven't really considered how they work in a real-world setting.

Sources of information about algorithms often present them in a way that proves confusing because they're too sophisticated or even downright incorrect. Although you may find other definitions, this book uses the following definitions for terms that people often confuse with algorithms (but aren't):

- **Equation:** Numbers and symbols that, when taken as a whole, equate to a specific value. An equation always contains an equals sign so that you know that the numbers and symbols represent the specific value on the other side of the equals sign. Equations generally contain variable information presented as a symbol, but they're not required to use variables.
- **Formula:** A combination of numbers and symbols used to express information or ideas. Formulas normally present mathematical or logical concepts, such as defining the Greatest Common Divisor (GCD) of two integers (the video at `https://www.khanacademy.org/math/cc-sixth-grade-math/cc-6th-factors-and-multiples/cc-6th-gcf/v/greatest-common-divisor` tells how this works). Generally, they show the relationship between two or more variables.
- REMEMBER **Algorithm:** A sequence of steps used to solve a problem. The sequence presents a unique method of addressing an issue by providing a particular solution. An algorithm need not represent mathematical or logical concepts, even though the presentations in this book often do fall into those categories because people most commonly use algorithms in this manner. In order for a process to represent an algorithm, it must be:
  - **Finite:** The algorithm must eventually solve the problem. This book discusses problems with a known solution so that you can evaluate whether an algorithm solves the problem correctly.
  - **Well-defined:** The series of steps must be precise and present steps that are understandable. Especially because computers are involved in algorithm use, the computer must be able to understand the steps to create a usable algorithm.
  - **Effective:** An algorithm must solve all cases of the problem for which someone defined it. An algorithm should always solve the problem it has to solve. Even though you should anticipate some failures, the incidence of failure is rare and occurs only in situations that are acceptable for the intended algorithm use.

With these definitions in mind, the following sections help to clarify the precise nature of algorithms. The goal isn't to provide a precise definition for algorithms, but rather to help you understand how algorithms fit into the grand scheme of things so that you can develop your own understanding of what algorithms are and why they're so important.

The right way to make toast: Defining algorithm uses

An algorithm always presents a series of steps and doesn't necessarily perform these steps to solve a math formula. The scope of algorithms is incredibly large. You can find algorithms that solve problems in science, medicine, finance, industrial production and supply, and communication. Algorithms provide support for all parts of a person's daily life. Anytime a sequence of actions achieving something in our life is finite, well-defined, and effective, you can view it as an algorithm. For example, you can turn even something as trivial and simple as making toast into an algorithm. In fact, the making toast procedure often appears in computer science classes, as discussed at `http://brianaspinall.com/now-thats-how-you-make-toast-using-computer-algorithms/`.

Unfortunately, the algorithm on the site is flawed. The instructor never removes the bread from the wrapper and never plugs the toaster in, so the result is damaged plain bread still in its wrapper stuffed into a nonfunctional toaster (see the discussion at `http://blog.johnmuellerbooks.com/2013/03/04/procedures-in-technical-writing/` for details). Even so, the idea is the correct one, yet it requires some slight, but essential, adjustments to make the algorithm finite and effective.

One of the most common uses of algorithms is as a means of solving formulas. For example, when working with the GCD of two integer values, you can perform the task manually by listing each of the factors for the two integers and then selecting the greatest factor that is common to both. For example, GCD (20, 25) is 5 because 5 is the largest number that divides evenly into both 20 and 25. However, processing every GCD manually is time consuming and error prone, so the Greek mathematician Euclid created a better algorithm to perform the task. You can see the Euclidean method demonstrated at `https://www.khanacademy.org/computing/computer-science/cryptography/modarithmetic/a/the-euclidean-algorithm`.

However, a single formula, which is a presentation of symbols and numbers used to express information or ideas, can have multiple solutions, each of which is an algorithm. In the case of GCD, another common algorithm is one created by Derrick Henry Lehmer (`https://www.imsc.res.in/~kapil/crypto/notes/node11.html`). Because you can solve any formula multiple ways, people spend a great deal of time comparing algorithms to determine which one works best in a given situation. (See a comparison of Euclid to Lehmer at `http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.31.693&rep=rep1&type=pdf`.)

Because our society and its accompanying technology are changing quickly, we need algorithms that can keep the pace. Scientific achievements such as sequencing the human genome were possible in our age because scientists found algorithms that run fast enough to complete the task. Measuring which algorithm is better in a given situation, or in an average usage situation, is really serious stuff and is a topic of discussion among computer scientists.

When it comes to computer science, the same algorithm can have multiple presentations; why do it one way when you can invent multiple methods just for fun? For example, you can *present* the Euclidean algorithm in both recursive and iterative forms, as explained at `http://cs.stackexchange.com/questions/1447/what-is-most-efficient-for-gcd`. In short, algorithms present a method of solving formulas, but it would be a mistake to say that just one acceptable algorithm exists for any given formula or that only one acceptable presentation of an algorithm exists. Using algorithms to solve problems of various sorts has a long history — it isn't something that has just happened.

Even if you limit your gaze to computer science, data science, artificial intelligence, and other technical areas, you find many kinds of algorithms — too many for a single book. For example, *The Art of Computer Programming*, by Donald E. Knuth (Addison-Wesley), spans 3,168 pages in four volumes (see `http://www.amazon.com/exec/obidos/ASIN/0321751043/datacservip0f-20/`) and still doesn't manage to cover the topic (the author intended to write more volumes). However, here are some interesting uses for you to consider:

» **Searching:** Locating information or verifying that the information you see is the information you want is an essential task. Without this ability, you couldn't perform many tasks online, such as finding the website on the Internet selling the perfect coffee pot for your office. These algorithms change constantly, as shown by Google's recent change in its algorithm (`https://www.youaretech.com/blog/2021/1/26/webpage-experience-a-major-google-algorithm-update-in-2021nbsp`).

» **Sorting:** Determining which order to use to present information is important because most people today suffer from information overload, and putting information in order is one way to reduce the onrush of data. Imagine going to Amazon, finding that more than a thousand coffee pots are for sale there, and yet not being able to sort them in order of price or the most positive review. Moreover, many complex algorithms require data in the proper order to work dependably, so ordering is an important requisite for solving more problems.

» **Transforming:** Converting one sort of data to another sort of data is critical to understanding and using the data effectively. For example, you might understand imperial weights just fine, but all your sources use the metric system. Converting between the two systems helps you understand the data.

- **Scheduling:** Making the use of resources fair to all concerned is another way in which algorithms make their presence known in a big way. For example, timing lights at intersections are no longer simple devices that count down the seconds between light changes. Modern devices consider all sorts of issues, such as the time of day, weather conditions, and flow of traffic.
- **Graph analysis:** Deciding on the shortest path between two points finds all sorts of uses. For example, in a routing problem, your GPS couldn't function without this particular algorithm because it could never direct you along city streets using the shortest route from point A to point B. And even then, your GPS might direct you to drive into a lake (`https://theweek.com/articles/464674/8-drivers-who-blindly-followed-gps-into-disaster`).
- **Cryptography:** Keeping data safe is an ongoing battle with hackers constantly attacking data sources. Algorithms make it possible to analyze data, put it into some other form, and then return it to its original form later.
- **Pseudorandom number generation:** Imagine playing games that never varied. You start at the same place; perform the same steps, in the same manner, every time you play. Without the capability to generate seemingly random numbers, many computer tasks become impossible.

REMEMBER

This list presents an incredibly short overview. People use algorithms for many different tasks and in many different ways, and constantly create new algorithms to solve both existing problems and new problems. The most important issue to consider when working with algorithms is that given a particular input, you should expect a specific output. Secondary issues include how many resources the algorithm requires to perform its task and how long it takes to complete the task. Depending on the kind of issue and the sort of algorithm used, you may also need to consider issues of accuracy and consistency.

Finding algorithms everywhere

The previous section mentions the toast algorithm for a specific reason. For some reason, making toast is probably the most popular algorithm ever created. Many grade-school children write their equivalent of the toast algorithm long before they can even solve the most basic math. It's not hard to imagine how many variations of the toast algorithm exist and what the precise output is of each of them. The results likely vary by individual and the level of creativity employed. There are also websites dedicated to telling children about algorithms, such as the one at `https://www.idtech.com/blog/algorithms-for-kids`. In short, algorithms appear in great variety and often in unexpected places.

Every task you perform on a computer involves algorithms. Some algorithms appear as part of the computer hardware. The very act of booting a computer involves the use of an algorithm. You also find algorithms in operating systems, applications, and every other piece of software. Even users rely on algorithms. Scripts help direct users to perform tasks in a specific way, but those same steps could appear as written instructions or as part of an organizational policy statement.

Daily routines often devolve into algorithms. Think about how you spend your day. If you're like most people, you perform essentially the same tasks every day in the same order, making your day an algorithm that solves the problem of how to live successfully while expending the least amount of energy possible. After all, that's what a routine does; it makes us efficient.

Throughout this book, you see the same three elements for every algorithm:

1. Describe the problem.
2. Create a series of steps to solve the problem (well defined).
3. Perform the steps to obtain a desired result (finite and effective).

Using Computers to Solve Problems

The term *computer* sounds quite technical and possibly a bit overwhelming to some people, but people today are neck deep (possibly even deeper) in computers. You wear at least one computer, your smartphone, most of the time. If you have any sort of special device, such as a pacemaker, it also includes a computer. A car can contain as many as 150 computers in the form of embedded microprocessors that regulate fuel consumption, engine combustion, transmission, steering, and stability (see `https://spectrum.ieee.org/software-eating-car` for details), provide Advanced Driver-Assist Systems (ADAS), and more lines of code than a jet fighter. A computer exists to solve problems quickly and with less effort than solving them manually. Consequently, it shouldn't surprise you that this book uses still more computers to help you understand algorithms better.

Computers vary in a number of ways. The computer in a watch is quite small; the one on a desktop quite large. Supercomputers are immense and contain many smaller computers all tasked to work together to solve complex issues, such as predicting tomorrow's weather. The most complex algorithms rely on special computer functionality to obtain solutions to the issues people design them to solve. Yes, you could use lesser resources to perform the task, but the trade-off is waiting a lot longer for an answer, or getting an answer that lacks sufficient accuracy to provide a useful solution. In some cases, you wait so long that the answer is no longer important. With the need for both speed and accuracy in mind, the following sections discuss some special computer features that can affect algorithms.

Getting the most out of modern CPUs and GPUs

General-purpose processors, CPUs, started out as a means to solve problems using algorithms. However, their general-purpose nature also means that a CPU can perform a great many other tasks, such as moving data around or interacting with external devices. A general-purpose processor does many things well, which means that it can perform the steps required to complete an algorithm, but not necessarily fast. Owners of early general-purpose processors could add math coprocessors (special math-specific chips) to their systems to gain a speed advantage (see `https://www.computerhope.com/jargon/m/mathcopr.htm` for details). Today, general-purpose processors have the math coprocessor embedded into them, so when you get an Intel i9 processor, you actually get multiple processors in a single package.

A *GPU* is a special-purpose processor with capabilities that lend themselves to faster algorithm execution. For most people, GPUs are supposed to take data, manipulate it in a special way, and then display a pretty picture onscreen. However, any computer hardware can serve more than one purpose. It turns out that GPUs are particularly adept at performing data transformations, which is a key task for solving algorithms in many cases. It shouldn't surprise you to discover that people who create algorithms spend a lot of time thinking outside the box, which means that they often see methods of solving issues in nontraditional approaches.

The point is that CPUs and GPUs form the most commonly used chips for performing algorithm-related tasks. The first performs general-purpose tasks quite well, and the second specializes in providing support for math-intensive tasks, especially those that involve data transformations. Using multiple cores makes parallel processing (performing more than one algorithmic step at a time) possible. Adding multiple chips increases the number of cores available. Having more cores adds speed, but a number of factors keeps the speed gain to a minimum. Using two i9 chips won't produce double the speed of just one i9 chip.

Working with special-purpose chips

A math coprocessor and a GPU are two examples of common special-purpose chips in that you don't see them used to perform tasks such as booting the system. However, algorithms often require the use of uncommon special-purpose chips to solve problems. This isn't a hardware book, but it pays to spend time showing you all sorts of interesting chips, such as the artificial neurons that UCSD is working on (`https://www.marktechpost.com/2021/06/03/ucsd-researchers-develop-an-artificial-neuron-device-that-could-reduce-energy-use-and-size-of-neural-network-hardware/`). Imagine performing algorithmic processing using devices that simulate the human brain. It would create an interesting environment for performing tasks that might not otherwise be possible today.

Neural networks, a technology that is used to simulate human thought and make deep learning techniques possible for machine learning scenarios, are now benefitting from the use of specialized chips (the article at `https://analyticsindiamag.com/top-10-gpus-for-deep-learning-in-2021/` outlines ten of them). These kinds of chips not only perform algorithmic processing extremely fast but also learn as they perform the tasks, making them faster still with each iteration. Learning computers will eventually power robots that can move (after a fashion) on their own, akin to the robots seen in the movie *I Robot.* Some robots even sport facial expressions now (`https://www.sciencedaily.com/releases/2021/05/210527145244.htm`).

REMEMBER

No matter how they work, specialized processors will eventually power all sorts of algorithms that will have real-world consequences. You can already find many of these real-world applications in a relatively simple form. For example, imagine the tasks that a pizza-making robot would have to solve — the variables it would have to consider on a real-time basis. This sort of robot already exists (this is just one example of the many industrial robots used to produce material goods by employing algorithms), and you can bet that it relies on algorithms to describe what to do, as well as on special chips to ensure that the tasks are done quickly (`https://www.therobotreport.com/picnic-pizza-making-robot-is-now-available/`).

TECHNICAL STUFF

Eventually, it might even be possible to use the human mind as a processor and output the information through a special interface. At one point, people experimented with putting processors directly into the brain, but the latest innovation relies on the use of veins to make the connection (`https://www.independent.co.uk/life-style/gadgets-and-tech/brain-computer-interface-vein-als-stent-neuralink-b1556167.html`). Imagine a system in which humans can solve problems using algorithms at the speed of computers, but with the creative "what if" potential of humans.

Networks: Sharing is more than caring

Unless you have unlimited funds, using some algorithms effectively may not be possible, even with specialized chips. In that case, you can network computers together. Using special software, one computer, a host, can use the processors of all client computers running an *agent* (a kind of in-memory background application that makes the processor available). Using this approach, you can solve incredibly complex problems by offloading pieces of the problem to a number of client computers. As each computer in the network solves its part of the problem, it sends the results back to the host, which puts the pieces together to create a consolidated answer, a technique called *cluster computing.*

Lest you think this is the stuff of science fiction, people are using cluster computing techniques (`https://www.geeksforgeeks.org/an-overview-of-cluster-computing/`) in all sorts of interesting ways. For example, the article at `https://turingpi.com/12-amazing-raspberry-pi-cluster-use-cases/` details how you can build your own supercomputer (among other tasks) by combining multiple Raspberry Pi (`https://www.raspberrypi.org/`) boards into a single cluster.

Distributed computing, another version of cluster computing (but with a looser organization) is also popular. In fact, you can find a list of distributed computing projects at `https://en.wikipedia.org/wiki/List_of_distributed_computing_projects`. The list of projects includes some major endeavors, such as Search for Extraterrestrial Intelligence (SETI). You can also donate your computer's extra processing power to work on a cure for cancer. The list of potential projects is amazing. Most of these projects are hosted by Berkeley Open Infrastructure for Network Computing (`https://boinc.berkeley.edu/`), but you can find other sponsors.

Leveraging available data

Part of solving problem using an algorithm has nothing to do with processing power, creative thinking outside the box, or anything of a physical nature. To create a solution to most problems, you also need data on which to base a conclusion. For example, in the toast-making algorithm, you need to know about the availability of bread, a toaster, electricity to power the toaster, and so on before you can solve the problem of actually making toast. The data becomes important because you can't finish the algorithm when missing even one element of the required solution. Of course, you may need additional input data as well. For example, the person wanting the toast may not like rye. If this is the case and all you have is rye bread to use, the presence of bread still won't result in a successful result.

Data comes from all sorts of sources and in all kinds of forms. You can stream data from a source such as a real-time monitor, access a public data source, rely on private data in a database, scrape the data from websites, or get it in myriad other ways too numerous to mention here. The data may be static (unchanging) or dynamic (constantly changing). You may find that the data is complete or missing elements. The data may not appear in the right form (such as when you get imperial units and require metric units when solving a weight problem). The data may appear in a tabular format when you need it in some other form. It may reside in an unstructured way (for instance, in a NoSQL database or just in a bunch of different data files) when you need the formatting of a relational database. In short, you need to know all sorts of things about the data used with your algorithm in order to solve problems with it.

REMEMBER

Because data comes in so many forms and you need to work with it in so many ways, this book pays a lot of attention to data. Starting in Chapter 6, you discover just how data structure comes into play. Moving on to Chapter 7, you begin looking at how to search through data to find what you need. Chapters 12 through 14 help you work with big data. However, you can find some sort of data-specific information in just about every chapter of the book because without data, an algorithm can't solve any problems.

Distinguishing between Issues and Solutions

This book discusses two parts of the algorithmic view of the real world. On the one hand, you have *issues*, which are problems that you need to solve. An issue can describe the desired output of an algorithm, or it can describe a hurdle you must overcome to obtain the desired output. *Solutions* are the methods, or steps, used to address the issues. A solution can relate to just one step or many steps within the algorithm. In fact, the output of an algorithm, the response to the last step, is a solution. The following sections help you understand some of the important aspects of issues and solutions.

Being correct and efficient

Using algorithms is all about getting an acceptable answer. The reason you look for an acceptable answer is that some algorithms generate more than one answer in response to fuzzy input data. Life often makes precise answers impossible to get. Of course, getting a precise answer is always the goal, but often you end up with an acceptable answer instead.

Getting the most precise answer possible may take too much time. When you seek a precise answer that takes too long to obtain, the information becomes useless and you've wasted your time. Choosing between two algorithms that address the same issue may come down to a choice between speed and precision. A fast algorithm may not generate a precise answer, but the answer may still work well enough to provide useful output.

Wrong answers can be a problem. Creating a lot of wrong answers fast is just as bad as creating a lot of precisely correct answers slowly. Part of the focus of this book is helping you find the middle ground between too fast and too slow, and between inaccurate and too accurate. Even though your math teacher stressed the need for providing the correct answer in the way expressed by the book you used at the time, real-world math often involves weighing choices and making middle-ground decisions that affect you in ways you might not think possible.

Discovering there is no free lunch

You may have heard the common myth that you can have everything in the way of computer output without putting much effort into deriving the solution. Unfortunately, no absolute solution exists to any problem, and better answers are often quite costly. When working with algorithms, you quickly discover the need to provide additional resources when you require precise answers quickly. The size and complexity of the data sources you use greatly affect the solution resolution as well. As size and complexity increase, you find that the need to add resources increases as well.

Adapting the strategy to the problem

Part 5 of this book looks at strategies you can use to decrease the cost of working with algorithms. The best mathematicians use tricks to get more output from less computing. For example, you can create an ultimate algorithm to solve an issue, or you can use a host of simpler algorithms to solve the same issue, but using multiple processors. The host of simple algorithms will usually work faster and better than the single, complex algorithm, even though this approach seems counterintuitive.

Describing algorithms in a lingua franca

Algorithms do provide a basis for communication between people, even when those individuals have different perspectives and speak different languages. For example, Bayes' Theorem (the probability of an event occurring given certain premises; see `https://betterexplained.com/articles/an-intuitive-and-short-explanation-of-bayes-theorem/` for a quick explanation of this amazing theorem)

```
P(B|E) = P(E|B)*P(B)/P(E)
```

appears the same whether you speak English, Spanish, Chinese, German, French, or any other language. Regardless what language you speak, the algorithm looks the same and acts the same given the same data. Algorithms help cross all sorts of divides that serve to separate humans from each other by expressing ideas in a form that anyone can prove. As you go through this book, you discover the beauty and magic that algorithms can provide in communicating even subtle thoughts to others.

TIP

Apart from universal mathematical notations, algorithms take advantage of programming languages as a means for explaining and communicating the formulas they solve. You can find all the sorts of algorithms in C, C++, Java, Fortran, Python (as in this book), and other languages. *Pseudocode* is a way to describe computer operations by using common English words. Some writers rely on pseudocode to overcome the fact that an algorithm may be proposed in a programming language that you don't know. In addition, pseudocode can be more concise than a programming language because you can use intuitive ideas that the programming language may not capture well.

Facing problems that are like brick walls, only harder

An important consideration when working with algorithms is that you can use them to solve issues of any complexity. The algorithm doesn't think, have emotion, or care how you use it (or even abuse it). You can use algorithms in any way required to solve an issue. For example, the same group of algorithms used to perform facial recognition to act as an alternative to computer passwords (for security purposes) can find terrorists lurking in an airport or recognize a lost child wandering the streets. The same algorithm has different uses; how to use it depends on the interests of the user. Part of the reason you want to read this book carefully is to help you solve those hard problems that may require only a simple algorithm to address.

Structuring Data to Obtain a Solution

Humans think about data in nonspecific ways and apply various rules to the same data to understand it in ways that computers never can. A computer's view of data is structured, simple, uncompromising, and most definitely not creative. When humans prepare data for a computer to use, the data often interacts with the algorithms in unexpected ways and produces undesirable output. The problem is one in which the human fails to appreciate the limited view of data that a computer has. The following sections describe two aspects of data that you see illustrated in many of the chapters to follow.

Understanding a computer's point of view

A computer has a simple view of data, but it's also a view that humans typically don't understand. For one thing, everything is a number to a computer because computers aren't designed to work with any other kind of data. Humans see characters on the computer display and assume that the computer interacts with the data in that manner, but the computer doesn't understand the data or its implications. The letter *A* is simply the number 65 to the computer. In fact, it's not truly even the number 65. The computer sees a series of electrical impulses that equate to a binary value of 0100 0001.

Computers also don't understand the whole concept of uppercase and lowercase. To a human, the lowercase *a* is simply another form of the uppercase *A*, but to a computer they're two different values. A lowercase *a* appears as the number 97 (a binary value of 0110 0001).

If these simple sorts of single letter comparisons could cause such problems between humans and computers, it isn't hard to imagine what happens when humans start assuming too much about other kinds of data. For example, a computer can't hear or appreciate music. Yet, music comes out of the computer speakers. The same holds true for graphics. A computer sees a series of 0s and 1s, not a graphic containing a pretty scene of the countryside.

REMEMBER

It's important to consider data from the computer's perspective when using algorithms. The computer sees only 0s and 1s, nothing else. Consequently, when you start working through the needs of the algorithm, you must view the data in that manner. You may actually find it beneficial to know that the computer's view of data makes some solutions easier to find, not harder. You discover more about this oddity in viewing data as the book progresses.

Arranging data makes the difference

Computers also have a strict idea about the form and structure of data. When you begin working with algorithms, you find that a large part of the job involves making the data appear in a form that the computer can use when using the algorithm to find a solution to an issue. Although a human can mentally see patterns in data that isn't arranged precisely right, computers really do need the precision to find the same pattern. The benefit of this precision is that computers can often make new patterns visible. In fact, that's one of the main reasons to use algorithms with computers — to help locate new patterns and then use those patterns to perform other tasks. For example, a computer may recognize a customer's spending pattern so that you can use the information to generate more sales automatically.

IN THIS CHAPTER

» Considering how to solve a problem

» Using a divide-and-conquer approach to solving problems

» Understanding the greedy approach to solving problems

» Determining the costs of problem solutions

» Performing algorithm measurements

Chapter 2 Considering Algorithm Design

An algorithm consists of a series of steps used to solve a problem, that could include input data to provide the basis of solving the problem and sometimes constraints that any solution must consider before anyone will regard the algorithm as effective. The first section of this chapter helps you consider the *problem solution* (the solution to the problem you're trying to solve). It helps you understand the need to create algorithms that are both flexible (can handle a wide range of data inputs) and effective (yield the desired output).

The second section of this chapter considers how to derive a solution. Feeling overwhelmed by a problem is common and the most common way to solve the issue is to divide the problem into smaller, manageable pieces. This divide-and-conquer approach to problem solving originally referred to warfare (see a history of this approach at `https://classroom.synonym.com/civilization-invented-divide-conquer-strategy-12746.html`). However, people use the same ideas to cut problems of all sorts down to size.

REMEMBER

The third section of the chapter refers to the greedy approach to problem solving. Greed normally has a negative connotation (like stealing your friend's fruit cup from their plate), but not in this case. A *greedy algorithm* is one that makes an optimal choice at each problem-solving stage. By doing so, it hopes to obtain an overall optimal solution to solve the problem. Unfortunately, this strategy doesn't always work, but it's always worth a try. It often yields a *good enough* solution, making it a good baseline.

No matter what problem-solving approach you choose, every algorithm comes with costs. Being good shoppers, people who rely heavily on algorithms want the best possible deal, which means performing a cost/benefit analysis. Of course, getting the best deal also assumes that a person using the algorithm has some idea of what sort of solution is good enough. Getting a solution that is too precise (one that offers too much detail) or one that offers too much in the way of output is often wasteful, so part of keeping costs under control is getting what you need as output and nothing more.

To know what you have with an algorithm, you need to know how to measure it in various ways. Measurements create a picture of usability, size, resource usage, and cost in your mind. More important, measurements offer the means of making comparisons. You can't compare algorithms without measurements. Until you can compare the algorithms, you can't choose the best one for a task.

Starting to Solve a Problem

Before you can solve any problem, you must understand it. Doing so isn't just a matter of sizing up the problem, either. Knowing that you have certain inputs and require certain outputs is a start, but that's not really enough to create a solution. Part of the solution process is to

- Discover how other people have created new problem solutions
- Know what resources you have on hand
- Determine the sorts of solutions that worked for similar problems in the past
- Consider what sorts of solutions haven't produced a desirable result

The following sections help you understand these phases of solving a problem. Realize that you won't necessarily perform these phases in order and that sometimes you revisit a phase after getting more information. The process of starting a problem solution is iterative; you keep at it until you have a good understanding of the problem at hand.

Modeling real-world problems

Real-world problems differ from those found in textbooks, mostly because the real world has no imagination at all. When creating a textbook, the author often creates a simple example to help the reader understand the basic principles at work. The example models just one aspect of a more complex problem. A real-world problem may require that you combine several techniques to create a complete solution. For example, to locate the best answer to a problem, you may:

1. Need to sort the answer set by a specific criterion.
2. Perform some sort of filtering and transformation.
3. Search the result.

Without this sequence of steps, comparing each of the answers adequately may prove impossible, and you end up with a less-than-optimal result. A series of algorithms used together to create a desired result is an *ensemble*. You can read about their use in machine learning in *Machine Learning For Dummies*, 2nd Edition, by John Paul Mueller and Luca Massaron (Wiley). The article at `https://machinelearningmastery.com/tour-of-ensemble-learning-algorithms/` gives you a quick overview of how ensembles work.

However, real-world problems are even more complex than simply looking at static data or iterating that data only once. For example, anything that moves, such as a car, airplane, or robot, receives constant input. Each updated input includes error information that a real-world solution will need to incorporate into the result in order to keep these machines working properly. In addition to other algorithms, the constant calculations require the proportional integral derivative (PID) algorithm (see `https://www.ni.com/en-us/innovations/white-papers/06/pid-theory-explained.html` for a detailed explanation of this algorithm) to control the machine using a feedback loop. Every calculation brings the solution used to control the machine into better focus, which is why machines often go through a settling stage when you first turn them on.

When modeling a real-world problem, you must also consider non-obvious issues that crop up. An obvious solution, even one based on significant mathematical input and solid theory, may not work. For example, during WWII, the allies had a serious problem with bomber losses. Therefore, the engineers analyzed every bullet hole in every plane that came back. After the analysis, the engineers used their solution to armor the allied planes more heavily to ensure that more of them would come back. It didn't work. Enter Abraham Wald. This mathematician suggested a non-obvious solution: Put armor plating in all the places that lacked bullet holes (because the areas with bullet holes are already strong enough; otherwise the plane wouldn't have returned). The resulting solution did work and is now used as the basis for *survivor bias* (the fact that the survivors of an incident often don't show what actually caused a loss) in working with algorithms. You can read more about this fascinating bit of history at `https://medium.com/@penguinpress/an-excerpt-from-how-not-to-be-wrong-by-jordan-ellenberg-664e708cfc3d`.

Real-world modeling may also include the addition of what scientists normally consider undesirable traits. For example, scientists often consider noise undesirable because it hides the underlying data. Consider a hearing aid, which removes noise to enable someone to hear better (see the discussion at `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4111515/` for details). Many methods exist for removing noise, some of which you can find in this book starting with Chapter 9 as part of other topic discussions.

However, as counterintuitive as it might seem, adding noise to the data also requires an algorithm that provides useful output with that noise in place. For example, Ken Perlin wanted to get rid of the machine-like look of computer-generated graphics in 1983, and he created an algorithm to do so. The result is Perlin noise (see `https://catlikecoding.com/unity/tutorials/pseudorandom-noise/perlin-noise/` for details). The effect is so useful that Perlin won an Academy Award for his work (see `https://cs.nyu.edu/~perlin/doc/oscar.html` for details). A real-world scenario often requires choices that may not be obvious when working in the lab or during the learning process.

REMEMBER

The main gist of this section is that solutions often require several iterations to create, you may have to spend a lot of time refining them, and obvious solutions may not work at all. When modeling a real-world problem, you do begin with the solutions found in textbooks, but then you must move beyond theory to find the actual solution to your problem. As this book progresses, you're exposed to a wide variety of algorithms — all of which help you find solutions. The important thing to remember is that you may need to combine these examples in various ways and discover methods for interacting with data so that it lends itself to finding patterns that match the output you require.

Finding solutions and counterexamples

The previous section introduces you to the vagaries of discovering real-world solutions, ones that consider issues that solutions found in the lab can't take into account. However, just finding a solution — even a good one — isn't sufficient because even good solutions fail on occasion. Playing the devil's advocate by locating counterexamples is an important part of starting to solve a problem. The purpose of counterexamples is to

- Potentially disprove the solution
- Provide boundaries that define the solution better

- Consider situations in which the hypothesis used as a basis for the solution remains untested
- Help you understand the limits of the solution

A common scenario that illustrates a solution and counterexample is the statement that all prime numbers are odd. (*Prime numbers* are positive integers that can be evenly divided by themselves and 1 to produce an integer result.) Of course, the number 2 is prime, but it's also even, which makes the original statement false. Someone making the statement could then qualify it by saying that all prime numbers are odd except 2. The partial solution to the problem of finding all the prime numbers is that you need to find odd numbers, except in the case of 2, which is even. In this second case, disproving the solution is no longer possible, but adding to the original statement provides a boundary.

By casting doubt on the original assertion, you can also consider situations in which the hypothesis, all prime numbers except 2 are odd, may not hold true. For example, 1 is an odd number but isn't considered prime (see the discussion at `https://primes.utm.edu/notes/faq/one.html` for details). So now the original statement has two boundaries, and you must restate it as follows: Prime numbers are greater than 1 and usually odd, except for 2, which is even. The boundaries for prime numbers are better defined by locating and considering counterexamples.

TIP

As the complexity of a problem grows, the potential for finding counterexamples grows as well. An essential rule to consider is that, as with reliability, having more failure points means greater potential for a failure to occur. Thinking of algorithms in this way is important. Ensembles of simple algorithms can produce better results with fewer potential counterexamples than a single complex algorithm.

Standing on the shoulders of giants

A myth that defies explanation is that the techniques currently used to process huge quantities of data are somehow new. Yes, new algorithms do appear all the time, but the basis for these algorithms is all of the algorithms that have gone before. In fact, when you think about Sir Isaac Newton, you might think of someone who invented something new, yet even he stated (using correct spelling for his time), "If I have seen further it is by standing on the sholders of Giants" (see `https://en.wikiquote.org/wiki/Isaac_Newton` for additional quotes and insights).

The algorithms you use today weren't even new in the days of Aristotle (see `https://plato.stanford.edu/entries/aristotle-mathematics/`) and Plato (see `https://www.storyofmathematics.com/greek_plato.html`). The origins of algorithms in use today are so hidden in history that the best anyone can say is that math relies on adaptations of knowledge from ancient times. The use of algorithms since antiquity should give you a certain feeling of comfort because the algorithms in use today are based on knowledge tested for thousands of years.

This isn't to say that some mathematicians haven't overturned the apple cart over the years. For example, John Nash's theory, Nash Equilibrium, significantly changed how economics is considered today (see `https://www.masterclass.com/articles/nash-equilibrium-explained`). Of course, recognition for such work comes slowly. Nash had to wait for a long time before he received much in the way of professional recognition (see the story at `https://www.princeton.edu/main/news/archive/S42/72/29C63/index.xml`) despite having won a Nobel Prize in economics for his contributions. Just in case you're interested, John Nash's story is depicted in the movie *A Beautiful Mind,* which contains some much-debated scenes, including one containing a claim that the Nash Equilibrium somehow overturns some of the work of Adam Smith, another contributor to economic theories. (See one such discussion at `https://www.quora.com/Was-Adam-Smith-wrong-as-claimed-by-John-Nash-in-the-movie-A-Beautiful-Mind`.)

Dividing and Conquering

If solving problems were easy, everyone would do it. However, the world is still filled with unsolved problems and the condition isn't likely to change anytime soon, for one simple reason: Problems often appear so large that no solution is imaginable. Ancient warriors faced a similar problem. An opposing army would seem so large and their forces so small as to make the problem of winning a war unimaginably hard, perhaps impossible. Yet, by dividing the opposing army into small pieces and attacking it a little at a time, a small army could potentially defeat a much larger opponent. (The ancient Greeks, Romans, and Napoleon Bonaparte were all great users of the divide-and-conquer strategy; see *Napoleon For Dummies,* by J. David Markham [Wiley], for details.)

You face the same problem as those ancient warriors. Often, the resources at your disposal seem quite small and inadequate. However, by dividing a huge problem into small pieces so that you can understand each piece, you can eventually create a solution that works for the problem as a whole. Algorithms have this premise at their core: to use steps to solve problems one small piece at a time. The following sections help you understand the divide-and-conquer approach to problem solving in more detail.

Avoiding brute-force solutions

A *brute-force solution* is one in which you try each possible answer, one at a time, to locate the best possible answer. (This is also called an *exhaustive approach*, mostly because you're so tired when you finish.) It's thorough, this much is certain, but it also wastes time and resources in most cases. Testing every answer, even when it's easy to prove that a particular answer has no chance of success, wastes time that an algorithm can use on answers that have a better chance of success. In addition, testing the various answers using this approach generally wastes resources, such as memory. Think of it this way: You want to break the combination for a lock, so you begin at 0, 0, 0, even though you know that this particular combination has no chance of success given the physical characteristics of combination locks. A brute-force solution would proceed with testing 0, 0, 0 anyway and then move on to the equally ridiculous 0, 0, 1.

REMEMBER

Every solution type does come with advantages, although sometimes quite small. A brute-force solution has one such advantage. Because you test every answer, you don't need to perform any sort of preprocessing. The time saved in skipping the preprocessing, though, is unlikely to ever pay back the time lost in trying every answer. However, you may find occasion to use a brute-force solution when

- Finding a perfect solution, if one exists, is essential.
- The problem size is limited.
- You can use heuristics to reduce the size of the solution set.
- Simplicity of implementation is more important than speed.

Keeping it simple, silly (KISS)

The brute-force solution, described in the previous section, has a serious drawback. It looks at the entire problem at one time. It's sort of like going into a library and hunting book by book through the shelves without ever considering any method of making your search simpler. The divide-and-conquer approach to book searches is different. In this case, you begin by dividing the library into children's and adults' sections. After that, you divide the adults' section into categories. Finally, you search just the part of the category that contains the book of interest. This is the purpose of classification systems such as the Dewey Decimal System (see `https://mcpl.info/childrens/how-use-dewey-decimal-system`). The point is that divide and conquer simplifies the problem.

The divide part of divide and conquer is an essential way to understand a problem better as well. Trying to understand the layout of an entire library could prove difficult. However, knowing that the book you want to find on comparative psychology appears as part of Class 100 in Division 150 of Section 156 makes your job easier. You can understand this smaller problem because you know that every Section 156 book will contain something about the topic you want to know about. Algorithms work the same way. By making the problem simpler, you can create a set of simpler steps to finding a problem solution, which reduces the time to find the solution, reduces the number of resources used, and improves your chances of finding precisely the solution you need.

Breaking down a problem is usually better

After you have divided a problem into manageable pieces, you need to conquer the piece in question. This means creating a precise problem definition. You don't want just any book on comparative psychology; you want one written by George Romanes. Knowing that the book you want appears in Section 156 of the Dewey Decimal System is a good start, but it doesn't solve the problem. Now you need a process for reviewing every book in Section 156 for the specific book you need. The process might go further still and look for books with specific content. To make this process viable, you must break the problem down completely, define precisely what you need, and then, after you understand the problem thoroughly, use the correct set of steps (algorithm) to find what you need.

Learning that Greed Can Be Good

In some cases, you can't see the end of a solution process or even know whether you're winning the war. All you can really do is ensure that you win the individual battles to create a problem solution in hopes of also winning the war. A greedy method to problem solving uses this approach. It looks for an overall solution by choosing the best possible outcome at each problem solution stage.

REMEMBER

It seems that winning each battle would necessarily mean winning the war as well, but sometimes the real world doesn't work that way. A *Pyrrhic victory* is one in which someone wins every battle but ends up losing the war because the cost of the victory exceeds the gains of winning by such a large margin. You can read about five Pyrrhic victories at `https://www.history.com/news/5-famous-pyrrhic-victories`. These histories show that a greedy algorithm often does work, but not always, so you need to consider the best overall solution to a problem rather than become blinded by interim wins. The following sections describe how to avoid the Pyrrhic victory when working with algorithms.

Applying greedy reasoning

Greedy reasoning is often used as part of an optimization process. The algorithm views the problem one step at a time and focuses just on the step at hand. Every greedy algorithm makes two assumptions:

- You can make a single optimal choice at a given step.
- By choosing the optimal selection at each step, you can find an optimal solution for the overall problem.

You can find many greedy algorithms, each optimized to perform particular tasks. Here are some common examples of greedy algorithms used for graph analysis (see Chapter 9 for more about graphs) and data compression (see Chapter 14 for more about data compression) and the reason you might want to use them:

- **Kruskal's Minimum Spanning Tree (MST):** The algorithm chooses the edge between two nodes with the smallest value, not the greatest value as the word *greedy* might initially convey. This sort of algorithm might help you find the shortest path between two locations on a map or perform other graph-related tasks.
- **Prim's MST:** This algorithm splits an undirected graph (one in which direction isn't considered) in half. It then selects the edge that connects the two halves to make the total weight of the two halves the smallest it can be. You might find this algorithm used in a maze game to locate the shortest distance between the start and finish of the maze.
- **Huffman Encoding:** The algorithm assigns a code to every unique data entry in a stream of entries, with the most commonly used data entry receiving the shortest code. For example, the letter *E* would normally receive the shortest code when compressing English text, because you use it more often than any other letter in the alphabet. By changing the encoding technique, you can compress the text and make it considerably smaller, reducing transmission time.

Reaching a good solution

Scientists and mathematicians use greedy algorithms so often that Chapter 15 covers them in depth. However, what you really want is a *good* solution, not just a particular solution. In most cases, a good solution provides optimal results of the sort you can measure, but the word *good* can include many meanings, depending on the problem domain. You must ask what problem you want to solve and which solution solves the problem in a manner that best meets your needs. For example, when working in engineering, you might need to weigh solutions that consider weight, size, cost, or other considerations, or perhaps some combination of all these outputs that meet a specific requirement.

To put this issue in context, say that you build a coin machine that creates change for particular monetary amounts using the fewest coins possible (maybe as part of an automatic checkout at a store). The reason to use the fewest coins possible is to reduce equipment wear, the weight of coins needed, and the time required to make change (your customers are always in a hurry, after all). A greedy solution solves the problem by using the largest coins possible. For example, to output $0.16 in change, you use a dime ($0.10), a nickel ($0.05), and a penny ($0.01).

REMEMBER

A problem occurs when you can't use every coin type in creating a solution. The change machine might be out of nickels, for example. To provide $0.40 in change, a greedy solution would start with a quarter ($0.25) and a dime ($0.10). Unfortunately, there are no nickels, so the coin machine then outputs five pennies (5 × $0.01) for a total of seven coins. The optimal solution in this case is to use four dimes instead (4 × $0.10). As a result, the greedy algorithm provides a particular solution, but not an optimal solution. The change-making problem receives considerable attention because it's so hard to solve. You can find additional discussions such as "Combinatorics of the Change-Making Problem," by Anna Adamaszeka and Michal Adamaszek (`https://www.sciencedirect.com/science/article/pii/S0195669809001292`) and "Coin Change" by Mayukh Sinha (`https://www.geeksforgeeks.org/coin-change-dp-7/`).

Computing Costs and Following Heuristics

Even when you find a good solution, one that is both efficient and effective, you still need to know precisely what the solution costs. You may find that the cost of using a particular solution is still too high, even when everything else is considered. Perhaps the answer comes almost, but not quite, on time or it uses too many computing resources. The search for a good solution involves creating an environment in which you can fully test the algorithm, the states it creates, the operators it uses to change those states, and the time required to derive a solution.

Often, you find that a *heuristic approach,* one that relies on self-discovery and produces sufficiently useful results (not necessarily optimal, but good enough) is the method you actually need to solve a problem. Getting the algorithm to perform some of the required work for you saves time and effort because you can create algorithms that see patterns better than humans do. Consequently, self-discovery is the process of allowing the algorithm to show you a potentially useful path to a solution (but you still have to count on human intuition and understanding to know whether the solution is the right one). The following sections describe techniques you can use to compute the cost of an algorithm using heuristics as a method of discovering the actual usefulness of any given solution.

Representing the problem as a space

A *problem space* is an environment in which a search for a solution takes place. A set of states and the operators used to change those states represent the problem space. For example, consider a tile game that has eight tiles in a 3-x-3 frame. Each tile shows one part of a picture, and the tiles start in some random order so that the picture is scrambled. The goal is to move one tile at a time to place all the tiles in the right order and reveal the picture. You can see an example of this sort of puzzle at `https://www.proprofsgames.com/puzzle/sliding/`.

The combination of the start state, the randomized tiles, and the goal state — the tiles in a particular order — is the *problem instance.* You could represent the puzzle graphically using a *problem space graph.* Each node of the problem space graph presents a state (the eight tiles in a particular position). The edges represent operations, such as to move tile number eight up. When you move tile eight up, the picture changes — it moves to another state.

Winning the game by moving from the start state to the goal state isn't the only consideration. To solve the game efficiently, you need to perform the task in the least number of moves possible, which means using the smallest number of operations. The minimum number of moves used to solve the puzzle is the *problem depth.*

You must consider several factors when representing a problem as a space. For example, you must consider the maximum number of nodes that will fit in memory, and whether the number of nodes that memory can support matches the expected number of nodes necessary to solve the problem, which represents the *space complexity.* When you can't fit all the nodes in memory at one time, the computer must generate them only when necessary and then discard the previous nodes to free memory or store some nodes in other locations. To determine whether the nodes will fit in memory, you must consider *time complexity* because longer algorithm runs determinate the maximum number of nodes created to solve the problem. In addition, it's important to consider the *branching factor,* which is the average number of nodes created at each step in the problem space graph to solve a problem. For the same solution, an algorithm with a higher branching factor will generate more nodes than one with a lower branching factor.

Going random and being blessed by luck

Solving a search problem using brute-force techniques (described in "Avoiding brute-force solutions," earlier in this chapter) is possible. The advantage of this approach is that you don't need any domain-specific knowledge to use one of these algorithms. A brute-force algorithm tends to use the simplest possible approach to solving the problem. The disadvantage is that a brute-force approach works well only for a small number of nodes. Here are some of the common brute-force search algorithms:

Technique	Description	Cons	Pros
Breadth-first search	Begins at the root node, explores each of the child nodes first, then moves down to the next level. It progresses level by level until it finds a solution.	Must store every node in memory, which means that it uses a considerable amount of memory for a large number of nodes.	Can check for duplicate nodes to save time and always comes up with a solution.
Depth-first search	Begins at the root node and explores a set of connected child nodes until it reaches a leaf node. It progresses branch by branch until it finds a solution.	Can't check for duplicate nodes, which means that it might traverse the same node paths more than once.	It's memory efficient.
Bidirectional search	Searches simultaneously from the root node and the goal node until the two search paths meet in the middle.	It's time efficient and uses memory more efficiently than other approaches, and it always finds a solution.	Complexity of implementation, translating into a longer development cycle.

Using a heuristic and a cost function

For some people, the word *heuristic* just sounds complicated. It would be just as easy to say that the algorithm makes an educated guess and then tries again when it fails. Unlike brute-force methods, heuristic algorithms learn by iteratively trying to improve the solution over time. They also use cost functions to make better choices. Consequently, heuristic algorithms are more complex, but they have a distinct advantage in solving complex problems. As with brute-force algorithms, there are many heuristic algorithms, and each comes with its own set of advantages, disadvantages, and special requirements. The following list describes a few of the most common heuristic algorithms:

- **Pure heuristic search:** Expands nodes in order of their cost. It maintains two lists. The closed list contains the nodes it has already explored; the open list contains the nodes it must yet explore. In each iteration, the algorithm expands the node with the lowest possible cost. All its child nodes are placed in the closed list and the individual child node costs are calculated. The algorithm sends the child nodes with a low cost back to the open list and deletes the child nodes with a high cost.
- **A * search:** Tracks the cost of nodes as it explores them (and choosing the least expensive ones) using this equation: `f(n) = g(n) + h(n)`, where
  - `n` is the node identifier.
  - `g(n)` is the cost of reaching the node so far.
  - `h(n)` is the estimated cost to reach the goal from the node.
  - `f(n)` is the estimated cost of the path from n to the goal.
- **Greedy best-first search:** Chooses the path that is closest to the goal using the equation `f(n) = h(n)`. It can find solutions quite quickly, but it can also get stuck in loops, so many people don't consider it an optimal approach to finding a solution.

Evaluating Algorithms

Gaining insights into precisely how algorithms work is important because otherwise you can't determine whether an algorithm actually performs in the way you need it to. Also, without good measurements, you can't perform accurate comparisons to know whether you really do need to discover a new method of solving a problem when an older solution works too slowly or uses too many resources. Knowing the basis to use to compare different solutions and deciding between them is an essential skill when dealing with algorithms.

The issue of efficiency has been part of discovering and designing new algorithms since the concept of algorithms first came into being, which is why you see so many different algorithms competing to solve the same problem. The concept of measuring the size of the functions within an algorithm and analyzing how the algorithm works isn't new; both Ada Lovelace and Charles Babbage considered the problems of algorithm efficiency in reference to computers as early as 1843 (see `https://www.computerhistory.org/babbage/adalovelace/`).

Donald Knuth (`https://www-cs-faculty.stanford.edu/~knuth/`), computer scientist, mathematician, professor emeritus at Stanford University, and author of the milestone, multivolume book *The Art of Computer Programming* (Addison-Wesley), devoted much of his research and studies to comparing algorithms. He strove to formalize how to estimate the resource needs of algorithms in a mathematical way and to allow a correct comparison between alternative solutions. He coined the term *analysis of algorithms,* which is the branch of computer science devoted to understanding how algorithms work in a formal way. The analysis measures resources required in terms of the number of operations an algorithm requires to reach a solution or by its occupied space (such as the storage an algorithm requires in computer memory).

Analysis of algorithms requires some mathematical understanding and some computations, but it's extremely beneficial in your journey to discover, appreciate, and effectively use algorithms. This topic is considerably more abstract than other topics in this book. To make the discussion less theoretical, later chapters present more practicalities of such measurement by examining algorithms together in detail. The following sections give you the basics.

Simulating using abstract machines

The more operations an algorithm requires, the more complex it is. Complexity is a measure of algorithm efficiency in terms of time usage because each operation takes some time. Given the same problem, complex algorithms are generally less favorable than simple algorithms because complex algorithms require more time. Think about those times when speed of execution makes the difference, such as in the medical or financial sector, or when flying on automatic pilot on an airplane or space rocket. Measuring algorithm complexity is a challenging task, though a necessary one if you want to employ the right solution. The first measurement technique uses abstract machines like the Random Access Machine (RAM).

Abstract machines aren't real computers but rather theoretical ones — computers that are imagined in their functioning. It's sort of like daydreaming for computer scientists. You use abstract machines to consider how well an algorithm would work on a computer without testing it on the real thing, yet is bound by the type of hardware you'd use. A RAM computer performs basic arithmetic operations and interacts with information in memory, and that's all. Every time a RAM computer does anything, it takes a time step (a time unit). When you evaluate an algorithm in a RAM simulation, you count time steps using the following procedure:

1. Count each simple operation (arithmetic ones) as a time step.
2. Break complex operations into simple arithmetic operations and count time steps as defined in Step 1.
3. Count every data access from memory as one time step.

To perform this accounting, you write a pseudocode version of your algorithm (as mentioned in Chapter 1) and perform these steps using paper and pencil. In the end, it's a simple approach based on a basic idea of how computers work, a useful approximation that you can use to compare solutions regardless of the power and speed of your hardware or the programming language you use.

REMEMBER

Using a simulation is different from running the algorithm on a computer because you use a standard and predefined input. Real computer measurements require that you run the code and verify the time required to run it. Running code on a computer is actually a *benchmark*, another form of efficiency measurement, in which you also account for the application environment (such as the type of hardware used and the software implementation). A benchmark is useful but lacks generalization. Consider, for instance, how newer hardware can quickly execute an algorithm that took ages on your previous computer.

Getting even more abstract

If you thought things were abstract before, this section makes those previous sections seem concrete, but grit your teeth and move on because you really are up to the task! Measuring a series of steps devised to achieve a solution to a problem poses quite a few challenges. The previous section discusses counting time steps (number of operations), but sometimes you also need to compute space (such as the memory an algorithm consumes). You consider space when your problem is greedy for resources. Depending on the problem, you may consider an algorithm to be better when it works efficiently with regard to one of these resource consumption aspects:

- Running time
- Computer memory requirements
- Hard-disk usage
- Power consumption
- Data-transmission speed in a network

Some of these aspects relate to others in an inverse manner, so if, for instance, you want speedier execution time, you can sometimes increase memory or power consumption to get it. Not only can you have different efficiency configurations when running an algorithm, you can also change the hardware characteristics and software implementation to accomplish your goals. In terms of hardware, using a supercomputer or a general-purpose computer does matter, and the software, or language used to write the algorithm, is definitely a game changer. In addition, the quantity and kind of data you feed the algorithm could result in better or worse performance measurements.

RAM simulations count time because when you can employ a solution in so many environments, and its resource usage depends on so many factors, you have to find a way to simplify comparisons so that they become standard. Otherwise, you can't compare possible alternatives. The solution is, as so often happens with many other problems, to use a single measure and say that one size fits all. In this case, the measure is time, which you make equal to the number of operations, that is, the complexity of the algorithm.

A RAM simulation places the algorithm in a situation that's both language and machine-agnostic (it's independent of programming language and computer type). However, explaining how a RAM simulation works to others requires quite an effort. The analysis of algorithms proposes to use the number of operations you get from a RAM simulation and turn them into a mathematical function expressing how your algorithm behaves in terms of time, which is a quantification of the steps or operations required when the number of data inputs grows. For instance, if your algorithm sorts objects, you can express complexity using a function that reports how many operations it needs depending on the number of objects it receives.

Working with functions

A *function* in mathematics is simply a way to map some inputs to a response. Expressed in a different way, a *function* is a transformation (based on math operations) that transforms (maps) your input to an answer. For certain values of input (usually denoted by the letters *x* or *n*), you have a corresponding answer using the math that defines the function. For instance, a function like `f(n) = 2n` tells you that when your input is a number *n,* your answer is the number *n* multiplied by 2.

A function describing how an algorithm relates its solution to the quantity of data it receives is something you can analyze without specific hardware or software support. It's also easy to compare with other solutions, given the size of your problem. Analysis of algorithms is really a mind-blowing concept because it reduces a complex series of steps into a mathematical formula.

In most cases, an analysis of algorithms isn't interested in defining the function exactly. What you really need is a comparison of a target function with one or more other functions. These comparison functions appear within a set of proposed functions that perform poorly when contrasted to the target function. In this way, you don't have to plug numbers into functions of greater or lesser complexity; instead, you deal with simple, premade, and well-known functions. It's more effective and is similar to classifying the performance of algorithms into categories, rather than obtaining an exact performance measurement.

The set of generalized functions is called *Big O* notation, and in this book, you often encounter this small set of functions (put into parentheses and preceded by a capital O) used to represent the performance of algorithms. Figure 2-1 shows the analysis of an algorithm. A Cartesian coordinate system can represent its function as measured by RAM simulation, where the *abscissa* (the x coordinate) is the size of the input and the *ordinate* (the y coordinate) is its resulting number of operations. You can see three curves represented. Input size matters. However, quality also matters (for instance, when ordering problems, it's faster to order an input that's already almost ordered). Consequently, the analysis shows a worst case, `f1(n)`, an average case, `f2(n)`, and a best case, `f3(n)`. Even though the average case might give you a general idea, what you really care about is the worst case, because problems may arise when your algorithm struggles to reach a solution. The Big O function is the one that, after a certain `n0` value (the threshold for considering an input big), always results in a larger number of operations given the same input than the worst-case function `f1`. Thus, the Big O function is even more pessimistic than the one representing your algorithm, so no matter the quality of input, you can be sure that things can't get worse than that.

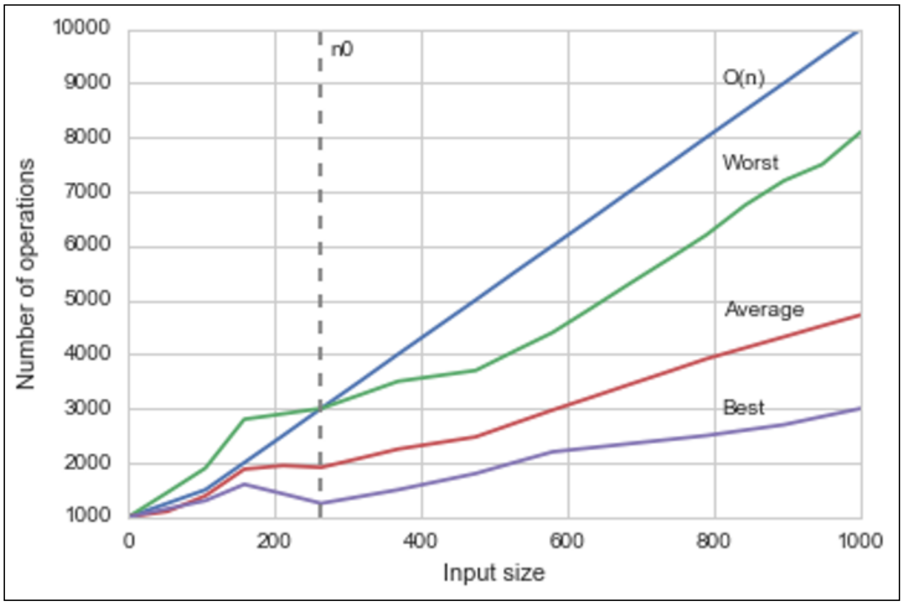


FIGURE 2-1: Complexity of an algorithm in case of best, average, and worst input case.

Many possible functions can result in worse results, but the choice of functions offered by the Big O notation that you can use is restricted because its purpose is to simplify complexity measurement by proposing a standard. This section contains just the few functions that are part of the Big O notation. The following list describes them in growing order of complexity:

- **Constant complexity O(1):** The same time, no matter how much input you provide. In the end, it is a constant number of operations, no matter how long the input data is.
- **Logarithmic complexity O(log n):** The number of operations grows at a slower rate than the input, making the algorithm less efficient with small inputs and more efficient with larger ones. A typical algorithm of this class is the binary search, as described in Chapter 7 on arranging and searching data.
- **Linear complexity O(n):** Operations grow with the input in a 1:1 ratio. A typical algorithm is iteration, which is when you scan input once and apply an operation to each element of it. Chapter 4 discusses iterations.
- **Linearithmic complexity O(n log n):** Complexity is a mix between logarithmic and linear complexity. It is typical of some smart algorithms used to order data, such as merge sort, heapsort, and quicksort. Chapter 7 tells you about most of them.
- **Quadratic complexity O(n^2):** Operations grow as a square of the number of inputs. When one iteration is nested inside another iteration, you have quadratic complexity. For instance, you have a list of names and, in order to find the most similar ones, you compare each name against all the other names. Some less efficient ordering algorithms present such complexity: bubble sort, selection sort, and insertion sort.
- **Cubic complexity O(n^3):** Operations grow even faster than quadratic complexity because there are multiple nested iterations. When an algorithm has this order of complexity and processes a modest amount of data (100,000 elements) it may run for years. When you have a number of operations that is a power of the input, it is common to refer to the algorithm as *running in polynomial time.*
- **Exponential complexity O(2^n):** The algorithm takes twice the number of previous operations for every new element added. When an algorithm has this complexity, even small problems may take forever. Many algorithms doing exhaustive searches have exponential complexity. However, the classic example for this level of complexity is the calculation of Fibonacci numbers (which, being a recursive algorithm, is dealt with in Chapter 4).
- **Factorial complexity O(n!):** If the input is 100 objects and an operation on a computer takes 10^{-6} seconds (a reasonable speed for computers today), completing the task will require about 10^{140} years (an impossible amount of time because the age of the universe is estimated as being 10^{14} years). A famous factorial complexity problem is the traveling salesman problem, in which a salesman has to find the shortest route for visiting many cities and coming back to the starting city (presented in Chapter 18).

IN THIS CHAPTER

» **Considering what Google Colab provides**

» **Using Google Colab to perform common development tasks**

» **Making applications run in Google Colab**

» **Getting help when you need it**

Chapter 3 Working with Google Colab

Colaboratory (`https://colab.research.google.com/notebooks/welcome.ipynb`), or Colab for short, is a Google cloud-based service that lets you write Python code using a notebook-like environment, rather than the usual IDE. (Jupyter Notebook, `https://jupyter.org/`, provides a similar environment to Colab on the desktop if you don't have an Internet connection.) You don't have to install anything on your system to use it. The benefit of this approach is that you can work with code in small pieces and obtain nearly instant results from any work you do. A notebook format also lends itself to output in a report format that works well for presentations and reports. The first section of this chapter helps you work through some Colab basics and understand how Colab differs from a standard IDE (and why this difference has a significant benefit when learning algorithms).

You can use Colab to perform specific tasks in a cell-oriented paradigm. The next sections of the chapter go through a range of task-related topics that start with the use of notebooks. Of course, you also want to perform other sorts of tasks, such as creating various cell types and using them to create notebooks that have a report-like appearance with functional code.

Part of working with Colab is knowing how to run the example code, making it run as quickly as possible. Two sections of the chapter are dedicated to using hardware acceleration and running the example code in various ways.

Finally, this chapter can't address every aspect of Colab, so the final section of the chapter serves as a handy resource for locating the most reliable information about Colab.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `\A4D2E\ A4D2E; 03; Colab Examples.ipynb` file of the downloadable source. See the Introduction for details on how to find these source files.

Defining Google Colab

Colab is designed to mimic a desktop application called Jupyter Notebook (`https://jupyter.org/`). In fact, it's somewhat difficult to tell the two applications apart in the functionality they provide. Google Colab is the cloud version of Notebook, and the Welcome page makes this fact apparent. It even uses IPython (the previous name for Jupyter) Notebook (`.ipynb`) files for the site.

Even though the two applications are similar and they both use `.ipynb` files, they do have some differences that you need to know about. The previous edition of this book used Jupyter Notebook, but Colab offers the ability to compute anywhere on any device that sports a browser, so this edition of the book focuses on Colab instead. The following sections help you understand the Colab differences.

Understanding what Google Colab does

You can use Colab to perform many tasks, but for the purpose of this book, you use it to write and run code, create its associated documentation, and display graphics. The downloadable source for this book is designed to run on Colab, but you can also use it with Jupyter Notebook if you want.

Jupyter Notebook is a localized application in that you use local resources with it. You could potentially use other sources, but doing so could prove inconvenient or impossible in some cases. For example, according to `https://docs.github.com/repositories/working-with-files/using-files/working-with-non-code-files`, your Notebook files will appear as static HTML pages when you use a GitHub repository (*GitHub* is a cloud-based storage technology specifically oriented to working with code.) In fact, some features won't work at all. Colab enables you to fully interact with your Notebook files using GitHub as a repository, and Colab supports a number of other online storage options as well, so you can regard Colab as your online partner in creating Python code.

The other reason that you really need to know about Colab is that you can use it with your alternative device. During the writing process, some of the example code was tested on an Android-based tablet (an ASUS ZenPad 3S 10). The target tablet has Chrome installed and executes the code well enough to follow the examples. All this said, you likely won't want to try to write code using a tablet of that size — the text was incredibly small, for one thing, and the lack of a keyboard could be a problem, too. The point is that you don't absolutely have to have a Windows, Linux, or OS X system to try the code, but the alternatives might not provide quite the performance you expect.

REMEMBER

Google Colab generally doesn't work with browsers other than Chrome (the browser used in this chapter), Firefox, or Safari (initial tests with Microsoft Edge have also been encouraging). In most cases, you see an error message, such as `This site may not work in your browser. Please use a supported browser`, and no other display if you try to start Colab in a browser that it doesn't support. The included More Info link takes you to `https://research.google.com/colaboratory/faq.html#browsers`, where you can learn more information.

SOME FIREFOX ODDITIES

Even with online help, you may still find that your copy of Firefox displays a `SecurityError: The operation is insecure.` error message. The initial error dialog box points to some unrelated issue, such as cookies, but you see this error message when you click Details. Simply dismissing the dialog box by clicking OK makes Colab appear to be working because it displays your code, but you won't see results from running the code.

As a first step toward fixing this problem, make sure that your copy of Firefox is current; older versions don't provide the required support. After you've updated your copy, setting the `network.websocket.allowInsecureFromHTTPS` preference using `About:Config` to `True` should resolve the problem, but sometimes it doesn't. In this case, verify that Firefox actually does allow third-party cookies by selecting both the Always for the Accept Third Party Cookies and Site Data option and the Remember History option in the History section on the Privacy & Security tab of the Options dialog box. Restart Firefox after each change and then try Colab again. If none of these fixes works, you must use Chrome to work with Colab on your system.

Getting familiar with Google Colab features

Google Colab provides access to a number of features through the menu system. One of these features, hardware acceleration, appears in the "Using Hardware Acceleration" section, later in this chapter. The features in this section all appear on the Tools menu.

Locating commands

The Tools ➪ Command Palette option displays a list of commands you can execute, as shown in Figure 3-1. Some of these commands also have shortcut keys, such as Ctrl+Alt+M for adding a comment to a cell. All these commands help you to perform tasks associated with Notebook content, such as adding forms.

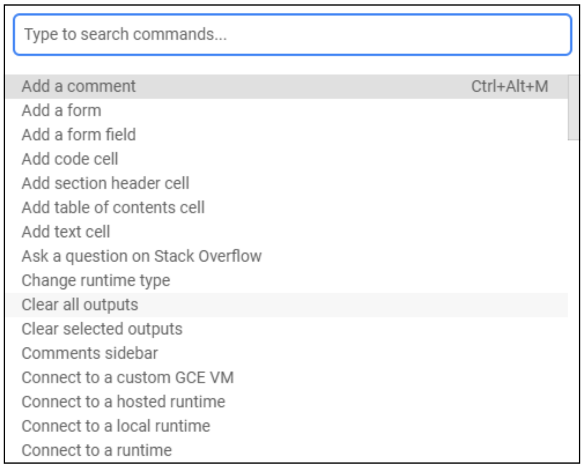


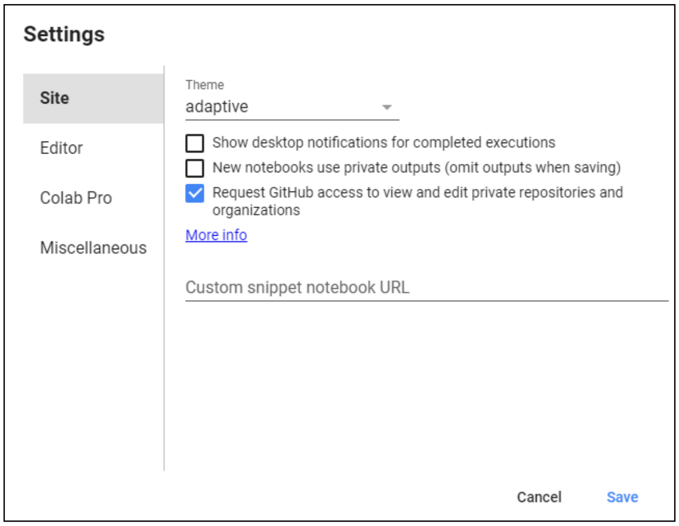
FIGURE 3-1: Using Colab commands makes configuring your Notebook easy.

Configuring settings

The Tools ➪ Settings option displays the Settings dialog box, shown in Figure 3-2. The four settings tabs perform these tasks:

- **Site:** Configures how the site works. The most interesting setting is the theme. Selecting Adaptive lets Colab choose the interface colors based on lighting conditions. You can also configure display and access settings on this tab.
- **Editor:** Determines how text appears onscreen and how the interface works. For example, you can set the key bindings to work like those in *Vim* (a text editor included on Unix and Linux systems, generally as the vi utility; see `https://www.vim.org/`) if desired. You can also select font size, spaces for each level of indentation, and a plethora of other settings.

- **Colab Pro:** Provides an advertisement for Colab Pro (`https://colab.research.google.com/signup`), which gives you some significant benefits like faster GPUs, longer runtimes, and more memory — all of which let you get more work done in a shorter time.
- **Miscellaneous:** Contains fun settings. You can choose from three visual effects: adding thunder and lightning using the Power Level setting; letting a Corgi run across the top of the display; and allowing a kitten to run across the top of the display. You can choose any mix of these visual effects.


Settings

Site | Editor | Colab Pro | Miscellaneous

Theme: adaptive

- [ ] Show desktop notifications for completed executions
- [ ] New notebooks use private outputs (omit outputs when saving)
- [✓] Request GitHub access to view and edit private repositories and organizations

More info

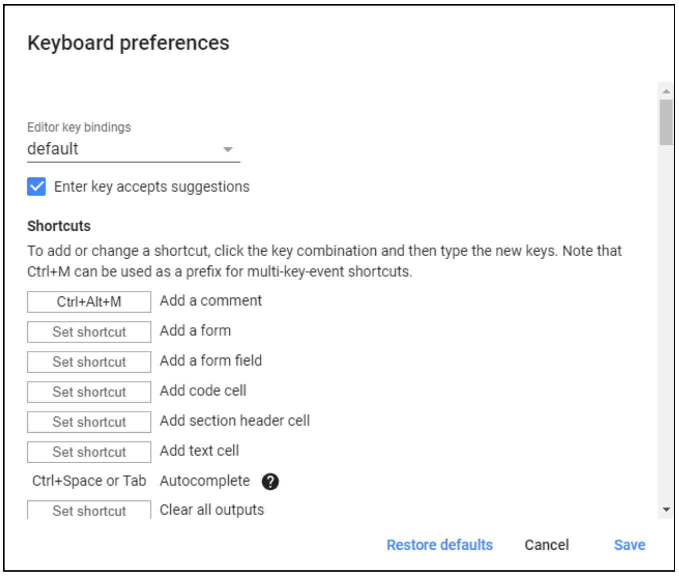
Custom snippet notebook URL

FIGURE 3-2: The Settings dialog box helps you configure the Colab IDE.

Customizing keyboard shortcuts

If you don't like the default keyboard shortcuts, you can customize them to match your needs. To do so, choose Tools ➪ Keyboard Shortcuts, and you see the Keyboard Preferences dialog box, shown in Figure 3-3. If you see Set Shortcut, it means that the command doesn't currently have a shortcut, so you can add one if desired. Here's how you work with shortcuts:

- To add or change a shortcut, place the cursor in the box next to the command and press the shortcut key you want to use for that command.
- To remove a shortcut, press Delete.



Keyboard preferences

Editor key bindings: default

[✓] Enter key accepts suggestions

Shortcuts

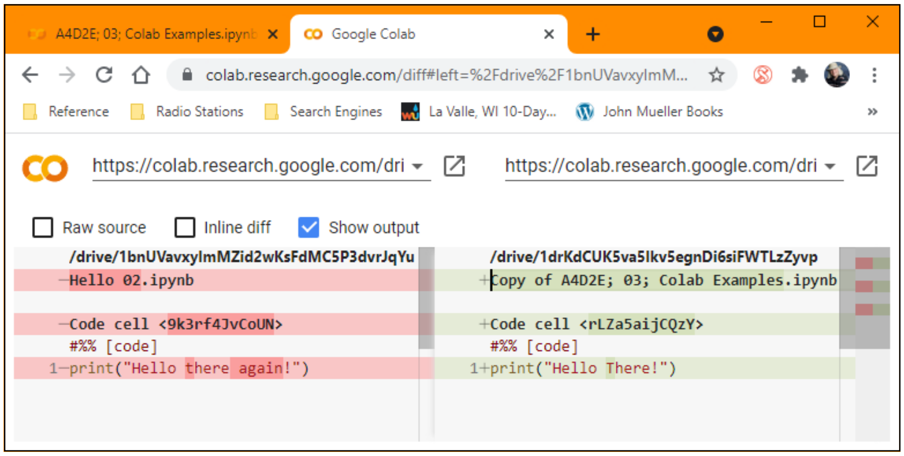
To add or change a shortcut, click the key combination and then type the new keys. Note that Ctrl+M can be used as a prefix for multi-key-event shortcuts.

Ctrl+Alt+M	Add a comment
Set shortcut	Add a form
Set shortcut	Add a form field
Set shortcut	Add code cell
Set shortcut	Add section header cell
Set shortcut	Add text cell
Ctrl+Space or Tab	Autocomplete
Set shortcut	Clear all outputs

FIGURE 3-3: Customize shortcut keys for speed of access to commands.

Comparing files

Sometimes you need to compare two files to see how they differ. When you select Tools ➪ Diff Notebooks, Colab opens a new browser tab and shows you two notebooks side by side, as shown in Figure 3-4. These are files selected by random from your Google Drive. To select the files you actually want to work with, click the down arrow next to the file path in each pane. The differences appear onscreen.



A4D2E; 03; Colab Examples.ipynb
Google Colab
colab.research.google.com/diff#left=%2Fdrive%2F1bnUVavxylmM...
Reference
Radio Stations
Search Engines
La Valle, WI 10-Day...
John Mueller Books
https://colab.research.google.com/dri
https://colab.research.google.com/dri

☐ Raw source ☐ Inline diff [✓] Show output

```
/drive/1bnUVavxylmMZid2wKsFdMC5P3dvrJqYu     /drive/1drKdCUK5va5lkv5egnDi6siFWTLzZyvp
−Hello 02.ipynb                              +Copy of A4D2E; 03; Colab Examples.ipynb

−Code cell <9k3rf4JvCoUN>                    +Code cell <rLZa5aijCQzY>
 #%% [code]                                   #%% [code]
1−print("Hello there again!")               1+print("Hello There!")
```

FIGURE 3-4: Colab lets you compare two files to see how they differ.

Working with Notebooks

The notebook forms the basis for interactions with Colab. In fact, Colab is built on notebooks, as previously mentioned. When you place the mouse on certain parts of the Welcome page at `https://colab.research.google.com/notebooks/welcome.ipynb`, you see opportunities for interacting with the page by adding either code or text entries (which you can use for notes as needed). These entries are active, so you can interact with them. You can also move cells around and copy the resulting material to your Google Drive. Of course, although interacting with the Welcome page is both unexpected and fun, the real purpose of this chapter is to demonstrate how to interact with Colab notebooks. The following sections describe how to perform basic notebook-related tasks with Colab.

Creating a new notebook

To create a new notebook, choose File➪New Notebook. You see a new Python 3 notebook like the one shown in Figure 3-5. (The latest version of Colab doesn't provide support for Python 2, so you can't use Python 2 with it.)

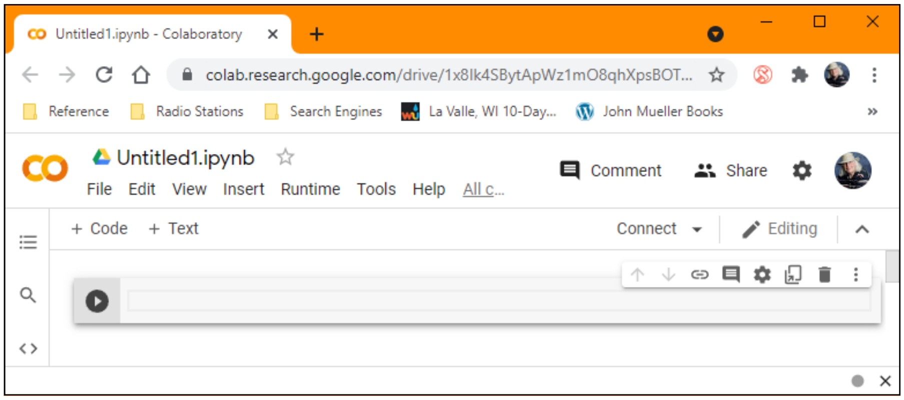
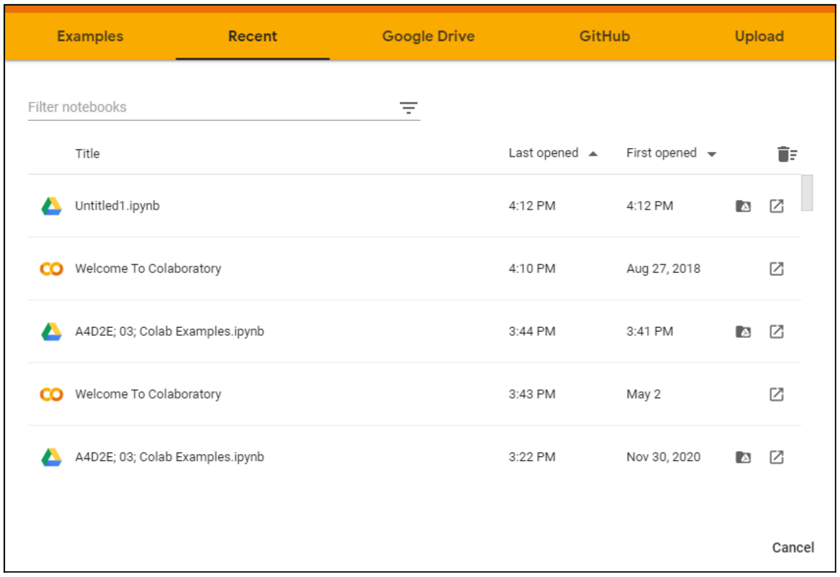


FIGURE 3-5: Create a new Python 3 Notebook.

The notebook shown in Figure 3-5 lets you change the filename by clicking it. To run the code in a particular cell, you click the right-pointing arrow on the left side of that cell. After you run the code, you must choose the next cell directly.

Opening existing notebooks

You can open existing notebooks found in local storage, on Google Drive, or on GitHub. You can also open any of the Colab examples or upload files from sources that you can access, such as a network drive on your system. In all cases, you begin by choosing File➪Open Notebook. You see the dialog box shown in Figure 3-6.



Title	Last opened	First opened
Untitled1.ipynb	4:12 PM	4:12 PM
Welcome To Colaboratory	4:10 PM	Aug 27, 2018
A4D2E; 03; Colab Examples.ipynb	3:44 PM	3:41 PM
Welcome To Colaboratory	3:43 PM	May 2
A4D2E; 03; Colab Examples.ipynb	3:22 PM	Nov 30, 2020

FIGURE 3-6: Use this dialog box to open existing notebooks.

The default view shows all the files you opened recently, regardless of location. The files appear in alphabetical order. You can filter the number of items displayed by typing a string into the Filter Notebooks field. Across the top are other options for opening notebooks.

TIP

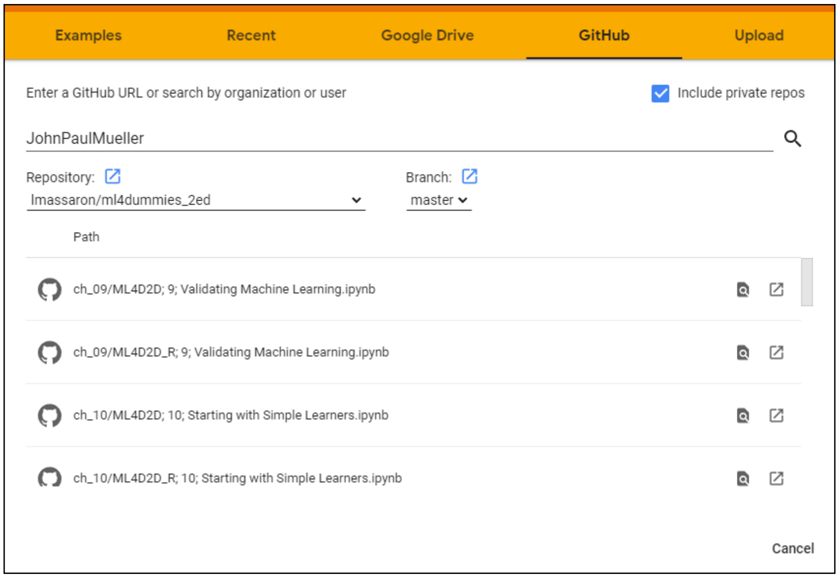
Even if you're not logged in, you can still access the Colab example projects. These projects help you understand Colab but won't allow you to do anything with your own projects. Even so, you can still experiment with Colab without logging into Google first. The following sections tell you more details about these options.

Using Google Drive for existing notebooks

Google Drive is the default location for many operations in Colab, and you can always choose it as a destination. When working with Google Drive, you see a list of files similar to those shown in Figure 3-6. To open a particular file, you click its link in the dialog box. The file opens in the current tab of your browser.

Using GitHub for existing notebooks

When working with GitHub, you initially need to provide the location of the source code online, as shown in Figure 3-7. The location must point to a public project; you can't use Colab to access private projects.



Enter a GitHub URL or search by organization or user

✓ Include private repos

JohnPaulMueller

Repository: lmassaron/ml4dummies_2ed

Branch: master

Path

ch_09/ML4D2D; 9; Validating Machine Learning.ipynb

ch_09/ML4D2D_R; 9; Validating Machine Learning.ipynb

ch_10/ML4D2D; 10; Starting with Simple Learners.ipynb

ch_10/ML4D2D_R; 10; Starting with Simple Learners.ipynb

FIGURE 3-7: When using GitHub, you must provide the location of the source code.

After you make the connection to GitHub, you see two lists: repositories, which are containers for code related to a particular project; and branches, a particular implementation of the code. Selecting a repository and branch displays a list of notebook files that you can load into Colab. Simply click the required link, and it loads as if you were using a *Google Drive* (`https://drive.google.com/`), which is another type of online storage.

Using local storage for existing notebooks

If you want to use the downloadable source for this book, or any local source for that matter, you select the Upload tab of the dialog box. In the center is a single button, Choose File. Clicking this button opens the File Open dialog box for your browser. You locate the file you want to upload, just as you normally would for opening any file.

REMEMBER

Selecting a file and clicking Open uploads the file to Google Drive. If you make changes to the file, those changes appear on Google Drive, not on your local drive. Depending on your browser, you usually see a new window open with the code loaded. However, you could also simply see a success message, in which case you must now open the file using the same technique as you would when using Google Drive. In some cases, your browser asks whether you want to leave the current page. You should tell the browser to do so.

TIP

The File ➪ Upload Notebook command also uploads a file to Google Drive. In fact, uploading a notebook works like uploading any other kind of file, and you see the same dialog box. If you want to upload other kinds of files, using the File ➪ Upload Notebook command is likely faster.

Saving notebooks

Colab provides a significant number of options for saving your notebook. However, none of these options works with your local drive. After you upload content from your local drive to Google Drive or GitHub, Colab manages the content in the cloud and not on your local drive. To save updates to your local drive, you must download the file to your local drive. The following sections review the cloud-based options for saving notebooks.

Using Drive to save notebooks

The default location for storing your data is Google Drive. When you choose File ➪ Save, the content you create goes to the root directory of your Google Drive. If you want to save the content to a different folder, you need to select that folder in Google Drive (`https://drive.google.com/`).

REMEMBER

Colab tracks the versions of your project as you perform saves. However, as these revisions age, Colab removes them. To save a version that won't age, you use the File ➪ Save and Pin Revision command. To see the revisions for your project, choose File ➪ Revision History.

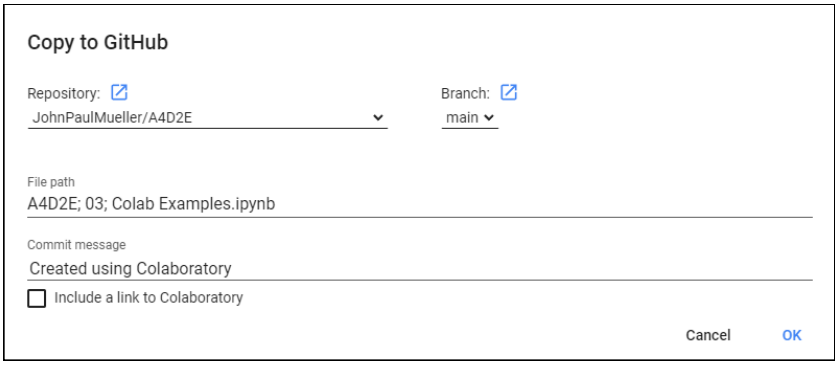
You can also save a copy of your project by choosing File ➪ Save a Copy In Drive. The copy receives the word *Copy* as part of its name. Of course, you can rename it later. Colab stores the copy in the current Google Drive folder.

Using GitHub to save notebooks

GitHub provides an alternative to Google Drive for saving content. It offers an organized method of sharing code for the purpose of discussion, review, and distribution. You can find GitHub at `https://github.com/`. The source code for this book appears at `https://github.com/lmassaron/algo4d_2ed`, so you can access it easily from Colab.

REMEMBER

You may use only public repositories when working with GitHub from Colab, even though GitHub also supports private repositories. To save a file to GitHub, choose File ➪ Save a Copy in GitHub. If you aren't already signed into GitHub, Colab displays a window that requests your sign-in information. After you sign in, you see a dialog box similar to the one shown in Figure 3-8.


Copy to GitHub

Repository: JohnPaulMueller/A4D2E

Branch: main

File path
A4D2E; 03; Colab Examples.ipynb

Commit message
Created using Colaboratory

☐ Include a link to Colaboratory

FIGURE 3-8: Using GitHub means storing your data in a repository.

If your account doesn't currently have a repository, you must either create a new repository or choose an existing repository in which to store your data. After you save the file, it appears in the GitHub repository of your choice. The repository includes a link to open the data in Colab by default, unless you choose not to include this feature.

Using GitHub gists to save notebooks

You use GitHub gists as a means of sharing single files or other resources with other people. Some people use them for full projects as well, but the idea is that you have a concept that you want to share — something that isn't quite fully formed and doesn't represent a usable application. You can read more about gists at `https://help.github.com/articles/about-gists/`.

Performing Common Tasks

Most tasks in Colab and Notebook work the same. Each has both code cells and noncode cells, and you can create code cells in both Colab and Notebook by using the options on the Insert menu. Likewise, both environments have noncode cells that come in three forms:

- Text
- Section header
- Form field, which comes in these types:
  - Dropdown
  - Input

- Slider
- Markdown

Noncode cells in Colab work somewhat differently from the Markdown cells found in Notebook, but the idea is the same. Two interesting additions in Colab that aren't found in Notepad are the scratch code cell, which allows you to experiment with code in real time, and code snippets, which are canned code for performing specific tasks (you just insert them where needed).

You can also edit and move cells. One important difference between the two environments is that you can't change a cell type in Colab, but you can in Notebook. A cell that you create as a section header can't suddenly transform into a code cell. The following sections offer a brief overview of the various features.

Creating code cells

The first cell that Colab creates for you is a code cell. Colab and Notebook share the same features with regard to code, so code you write in Colab also works in Notepad (and vice versa). However, off to the side of the cell, you see a menu of extras that you can use with Colab (see Figure 3-9); these aren't present in Notebook.

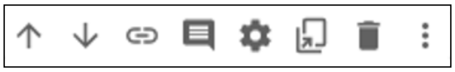


FIGURE 3-9: Colab code cells contain a few extras not found in Notebook.

You use the icons shown in Figure 3-9 to augment your Colab code experience. Here's what these features do (in order of appearance, left to right, in the figure):

- **Move cell up:** Moves the cell up one position in the cell hierarchy.
- **Move cell down:** Moves the cell down one position in the cell hierarchy.
- **Link to cell:** Displays a dialog box containing a link you can use to access a specific cell within the notebook. You can embed this link anywhere on a web page or within a notebook to allow someone to access that specific cell. The person still sees the entire notebook but doesn't have to search for the cell you want to discuss.
- **(Optional) Add a comment (assuming that you have the right to make a comment):** Creates a comment balloon to the right of the cell. This is not the same as a code comment, which exists inline with the code but affects the entire cell. You can edit, delete, or resolve comments. A resolved comment is one that receives attention and is no longer applicable.

- **Open editor settings:** Opens the same dialog box shown in Figure 3-2 and discussed in the "Getting familiar with Google Colab features" section, earlier in this chapter. You need to select some code before this option appears.
- **Mirror cell in tab:** Mirrors the currently selected cell in a Cell pane that appears on the right side of the window. You can scroll wherever you want within the code in the left pane and keep this code accessible. The right-pointing arrow lets you execute the cell at any time after making changes in left-pane code. A pair of double-pointing arrows lets you move the focus back to the selected code in the left pane with a single click. You can also move the cell code to a scratch cell, where you can play with it without modifying your original code. You can have more than one Cell pane. You simply select the one you want and move between them as needed, which lets you move easily from place to place in your code. Close a Cell pane by clicking the *X* next to the word *Cell.*
- **Delete Cell:** Removes the cell from the notebook.
- **Vertical ellipses:** Contains a number of additional features in a menu (not all of which may appear because they depend on the file you have opened, the tasks you have performed, and your rights to work with the file content):
  - **Copy Cell:** Copies the content of the currently selected cell to the clipboard.
  - **Cut Cell:** Deletes the content of the currently selected cell and places it on the Clipboard.
  - **Clear Output:** Removes the output from the cell. You must run the code again to regenerate the output.
  - **View Output Fullscreen:** Displays the output (not the entire cell or any other part of the notebook) in full-screen mode on the host device. This option is useful when displaying a significant amount of content, or when a detailed view of graphics helps explain a topic. Press Esc to exit full-screen mode.
  - **Add a Form:** Inserts a form into the cell to the right of the code. You use forms to provide a graphical input for parameters. Forms don't appear in Notebook, but because of how you create them, they won't prevent you from running the code in Notebook. You can read more about forms at `https://colab.research.google.com/notebooks/forms.ipynb`.

Code cells also tell you about the code and its execution. The little icon next to the output displays information about the execution when you hover your mouse over it. Clicking the icon clears the output. You must run the code again to regenerate the output.

Creating text cells

Text cells work much like Markup cells in Notebook. However, Figure 3-10 shows that you receive additional help in formatting the text using a graphical interface. The markup is the same, but you have the option of allowing the GUI to help you create the markup. For example, in this case, to create the hash sign (#) for a heading, you click the double T icon that appears first in the list. Clicking the double T icon again would increase the header level. To the right, you see how the text will appear in the notebook.

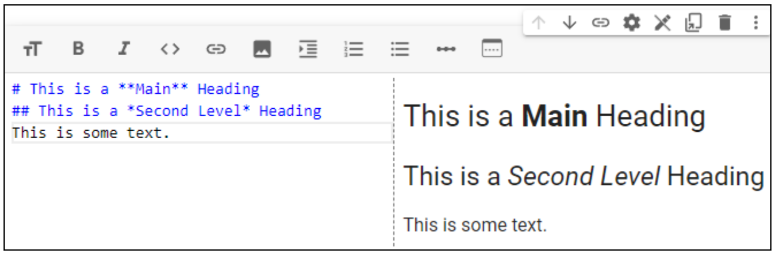
Notice the menu to the right of the text cell. This menu contains many of the same options that a code cell does. For example, you can create a list of links to help people access specific parts of your notebook through an index. In contrast to Notebook, you can't execute text cells to resolve the markup they contain.

Creating special cells

The special cells that Colab provides are variations of the text cell. These special cells, which you access using the Insert menu option, make creating the required cells faster. However, you shouldn't use these special cells if you need to maintain compatibility between Colab and Notebook. The following sections describe each of these special cell types.

Working with headings

When you choose Insert➪Section Header Cell, you see a new cell created below the currently selected cell that has the appropriate header level 1 entry in it. You can increase the heading level by clicking the double T icon. The GUI looks the same as the one in Figure 3-10, so you have all the standard formatting features for your text.



```
# This is a **Main** Heading
## This is a *Second Level* Heading
This is some text.
```

This is a **Main** Heading

This is a *Second Level* Heading

This is some text.

FIGURE 3-10: Use the GUI to make formatting your text easier.

Working with a table of contents

An interesting addition to Colab is the automatic generation of a table of content for your notebook. To use this feature, click the Table of Contents icon on the left side of the window. The table of contents contains one entry for each heading you provide in your code. The entries are automatically organized according to level, so you see the hierarchy of your code. Clicking an entry automatically takes you to that location in your code.

Editing cells

Both Colab and Notebook have Edit menus that contain the options you expect, such as the ability to cut, copy, and paste cells. The two products also have some interesting differences. For example, Notebook allows you to split and merge cells. Colab contains an option to show or hide the code as a toggle. These differences give each product a slightly different flavor but don't really change your ability to use each one to create and modify Python code.

Moving cells

The same technique you use for moving cells in Notebook also works with Colab. The only difference is that Colab relies exclusively on toolbar buttons (refer to in Figure 3-9); Notebook also has cell movement options on the Edit menu. To move a cell, select it and then click the Move cell up or Move cell down buttons as needed.

Using Hardware Acceleration

Even though you won't need it for the examples in this book, Colab does offer hardware acceleration in the form of a Graphics Processing Unit (GPU) or Tensor Processing Unit (TPU). Both of these special processors offer the ability to process multiple sets of data in parallel at high speed. When working with big data (see Chapter 12) in a machine learning or deep learning environment, a GPU or TPU can make a huge difference in the time required to accomplish a task. The main difference between a GPU and a TPU is that a GPU appears as part of most high-end display adapters today and can double for rendering complex graphics, while a TPU is a custom processor designed by Google specifically for machine learning and deep learning tasks. (There are other differences, but they aren't important for this book.)

GPU and TPU support are disabled by default in Colab. To enable GPU or TPU support, choose Runtime ➪ Change Runtime Type. A Notebook Settings dialog box appears. In this dialog box is the Hardware Accelerator drop-down list, from which you can choose None (the default), GPU, or TPU.

Executing the Code

For your code to be useful, you need to run it at some point. Previous sections have mentioned the right-pointing arrow that appears in the current cell. Clicking it runs just the current cell. Of course, you have other options than clicking the right-pointing arrow, and all these options appear on the Runtime menu (the Cell menu in Notebook). The following list summarizes these options:

- **Running the current cell:** Instead of clicking the right-pointing arrow, you can also choose Runtime ➪ Run the Focused Cell to execute the code in the current cell.
- **Running other cells:** Colab provides options on the Runtime menu for executing the code in the next cell, the previous cell, or a selection of cells. Simply choose the option that matches the cell or set of cells you want to execute.
- **Running all the cells:** In some cases, you want to execute all the code in a notebook. In this case, choose Runtime ➪ Run All. Execution starts at the top of the notebook, in the first cell containing code, and continues to the last cell that contains code in the notebook. You can stop execution at any time by choosing Runtime ➪ Interrupt Execution.

TIP

Choosing Runtime ➪ Manage Sessions displays a dialog box containing a list of all the sessions that are currently executing for your account on Colab. You can use this dialog box to determine when the code in that notebook last executed and how much memory the notebook consumes. Click the trash can icon to end execution for a particular notebook.

Getting Help

The most obvious place to obtain help with Colab is from the Colab Help menu. The menu doesn't have a general help link, but you can find it at `https://colab.research.google.com/notebooks/welcome.ipynb` (which requires you to log into the Colab site). This menu does contain all the usual entries:

- **Frequently Asked Questions (FAQs):** Takes you to a page containing questions that other people have asked.
- **Search Code Snippets:** Opens a pane showing common tasks, such as working with a camera, in which you can search for example code that could meet your needs with a little modification. Clicking the Insert button inserts the code at the current cursor location in the cell that has focus. Each of the entries also shows an example of the code.
- **Report a Bug:** Takes you to a page where you can report Colab errors.
- **Ask a Question on Stack Overflow:** Displays a new browser tab, where you can ask questions from other users. You see a login screen if you haven't already logged in to Stack Overflow.
- **Send Feedback:** Displays a dialog box with links for locations where you can obtain additional information. If you really do want to send feedback, then you click the Continue Anyway link at the bottom of the dialog box.

IN THIS CHAPTER

» **Using matrixes and vectors to perform calculations**

» **Obtaining the correct combinations**

» **Employing recursive techniques to obtain specific results**

» **Considering ways to speed calculations**

Chapter 4 Performing Essential Data Manipulations Using Python

You've probably used online tutorials or other methods to learn the basics of the Python language — the arcane symbols you use to communicate with your computer. (If not, you can find good basic tutorials at `https://www.w3schools.com/python/` and `https://www.tutorialspoint.com/python/index.htm`). However, simply knowing how to control a language by using its constructs to perform tasks isn't enough to create a useful application. The goal of mathematical algorithms is to turn one kind of data into another kind of data. *Manipulating data* means taking raw input and doing something with it to achieve a desired result. (This is a topic covered in *Python for Data Science For Dummies,* by John Paul Mueller and Luca Massaron [Wiley].) For example, until you do something with traffic data, you can't see the patterns that emerge that tell you where to spend additional money in improvements. The traffic data in its raw form does nothing to inform you — you must manipulate it to see the pattern in a useful manner.

In times past, people performed the various manipulations to make data useful by hand, which required advanced math knowledge. Fortunately, you can find Python packages to perform most of these manipulations using a little code. You don't have to memorize arcane manipulations anymore — just know which Python features to use. That's what this chapter helps you achieve. You discover the means to perform various kinds of data manipulations using easily accessed Python packages designed especially for the purpose. (Chapter 5 takes the next step and shows you how to create your own library of hand-coded algorithms.) This chapter begins with vector and matrix manipulations. Later sections discuss techniques such as recursion that can make the tasks even simpler, plus perform some tasks that are nearly impossible using other means. You also discover how to speed up the calculations so that you spend less time manipulating the data and more time doing something really interesting with it.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `\A4D2E\A4D2E; 04; Basic Vectors and Matrixes.ipynb`, `\A4D2E\A4D2E; 04; Binary Search.ipynb`, and `\A4D2E\A4D2E; 04; Recursion.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Performing Calculations Using Vectors and Matrixes

To perform useful work with Python, you often need to work with larger amounts of data that come in specific forms. These forms have odd-sounding names, but the names are quite important. The three terms you need to know for this chapter are as follows:

- **Scalar:** A single base data item. For example, the number 2 shown by itself is a scalar.
- **Vector:** A one-dimensional array (essentially a list) of data items. For example, an array containing the numbers 2, 3, 4, and 5 would be a vector.
- **Matrix:** A two-or-more-dimensional array (essentially a table) of data items. For example, an array containing the numbers 2, 3, 4, and 5 in the first row and 6, 7, 8, and 9 in the second row is a matrix.

Python provides an interesting assortment of features on its own, but you'd still need to do a lot of work to perform some tasks. To reduce the amount of work you do, you can rely on code written by other people and found in packages. The following sections describe how to use the NumPy package (`https://numpy.org/`) to perform various tasks on scalars, vectors, and matrixes. This chapter provides an overview of NumPy by emphasizing the features you use later (see `https://www.w3schools.com/python/numpy/default.asp` for more details).

Understanding scalar and vector operations

The NumPy package provides essential functionality for scientific computing in Python. To use `numpy`, you import it using a command such as `import numpy as np`. Now you can access `numpy` using the common two-letter abbreviation `np`.

REMEMBER

Python provides access to just one data type in any particular category. For example, if you need to create a variable that represents a number without a decimal portion, you use the integer data type. Using a generic designation like this is useful because it simplifies code and gives the developer a lot less to worry about. However, in scientific calculations, you often need better control over how data appears in memory, which means having more data types, something that `numpy` provides for you. For example, you might need to define a particular scalar as a `short` (a value that is 16 bits long). Using `numpy`, you could define it as `myShort = np.short(15)`. The NumPy package provides access to an assortment of data types (`https://numpy.org/doc/stable/reference/arrays.scalars.html`).

Use the `numpy array()` function to create a vector. For example, `myVect = np.array([1, 2, 3, 4])` creates a vector with four elements. In this case, the vector contains standard Python integers. You can also use the `arrange()` function to produce vectors, such as `myVect = np.arange(1, 10, 2)`, which fills `myVect` with `[1, 3, 5, 7, 9]`. The first input tells the starting point, the second the stopping point, and the third the step between each number. A fourth argument lets you define the data type for the vector.

You can also create a vector with a specific data type. All you need to do is specify the data type like this: `myVect = np.int16([1, 2, 3, 4])` to fill `myVect` with a vector containing 16-bit integer values. To verify this for yourself, you can use `print(type(myVect[0]))`, which outputs `<class 'numpy.int16'>`.

TIP

You can perform basic math functions on vectors as a whole, which makes `numpy` incredibly useful and less prone to errors that can occur when using programming constructs such as loops to perform the same task. For example, when starting with `myVect = np.array([1, 2, 3, 4])`, `myVect + 1` produces an output of `array([2, 3, 4, 5], dtype=int16)`. Note that the output tells you specifically which data type is in use. As you might expect, `myVect - 1` produces an output of `array([0, 1, 2, 3], dtype=int16)`.

As a final thought on scalar and vector operations, you can also perform both logical and comparison tasks. For example, the following code performs comparison operations on two arrays:

```
a = np.array([1, 2, 3, 4])
b = np.array([2, 2, 4, 4])

print(a == b)
print(a < b)
```

The output in this case is:

```
[False  True False  True]
[ True False  True False]
```

Starting with two vectors, `a` and `b`, the code checks whether the individual elements in `a` equal those in `b`. In this case, `a[0]` doesn't equal `b[0]`. However, `a[1]` does equal `b[1]`. The output is a vector of type `bool` that contains `True` or `False` values based on the individual comparisons.

Logical operations rely on special functions. You check the logical output of the Boolean operators AND, OR, XOR, and NOT. Here is an example of the logical functions:

```
a = np.array([True, False, True, False])
b = np.array([True, True, False, False])

print(np.logical_or(a, b))
print(np.logical_and(a, b))
print(np.logical_not(a))
print(np.logical_xor(a, b))
```

When you run this code, you see these outputs:

```
[ True  True  True False]
[ True False False False]
[False  True False  True]
[False  True  True False]
```

You can read more about the logic functions at `https://numpy.org/doc/stable/reference/routines.logic.html`.

Performing vector multiplication

Adding, subtracting, or dividing vectors occurs on an element-by-element basis, as described in the previous section. However, when it comes to multiplication, things get a little odd. In fact, depending on what you really want to do, things can become quite odd indeed. Consider the sort of multiplication discussed in the previous section. Both `myVect * myVect` and `np.multiply(myVect, myVect)` produce an element-by-element output of `[ 1, 4, 9, 16]` when starting with an array of `[1, 2, 3, 4]`.

WARNING

Unfortunately, an element-by-element multiplication can produce incorrect results when working with algorithms. In many cases, what you really need is a *dot product,* which is the sum of the products of two number sequences. When working with vectors, the dot product is always the sum of the individual element-by-element multiplications and results in a single number. For example, `myVect.dot(myVect)` results in an output of `30`. If you sum the values from the element-by-element multiplication, you find that they do indeed add up to 30. The discussion at `https://www.mathsisfun.com/algebra/vectors-dot-product.html` tells you about dot products and helps you understand where they might fit in with algorithms. You can learn more about the linear algebra manipulation functions for `numpy` at `https://numpy.org/doc/stable/reference/routines.linalg.html`.

Creating a matrix is the right way to start

Many of the same techniques you use with vectors also work with matrixes. To create a basic matrix, you simply use the `array()` function as you would with a vector, but you define additional dimensions. A *dimension* is a direction in the matrix. For example, a two-dimensional matrix contains rows (one direction) and columns (a second direction). The array call `myMatrix = np.array([[1,2,3], [4,5,6], [7,8,9]])` produces a matrix containing three rows and three columns, like this:

```
[[1 2 3]
 [4 5 6]
 [7 8 9]]
```

Note how you embed three lists within a container list to create the two dimensions. To access a particular array element, you provide a row and column index value, such as `myMatrix[0, 0]` to access the first value of `1`. You can find a full listing of vector and matrix array-creation functions at `https://numpy.org/doc/stable/reference/routines.array-creation.html`.

REMEMBER

The NumPy package supports an actual matrix class. The matrix class supports special features that make it easier to perform matrix-specific tasks. You discover these features later in the chapter. For now, all you really need to know is how to create a matrix of the matrix data type. The easiest method is to make a call similar to the one you use for the array function, but using the mat function instead, such as myMatrix = np.mat([[1,2,3], [4,5,6], [7,8,9]]), which produces the following matrix:

```
[[1 2 3]
 [4 5 6]
 [7 8 9]]
```

To determine that this actually is a matrix, try print(type(myMatrix)), which outputs <class 'numpy.matrix'>. You can also convert an existing array to a matrix using the asmatrix() function. Use the asarray() function to convert a matrix object back to an array form.

WARNING

The only problem with the matrix class is that it works on only two-dimensional matrixes. If you attempt to convert a three-dimensional matrix to the matrix class, you see an error message telling you that the shape is too large to be a matrix.

Multiplying matrixes

Multiplying two matrixes involves the same concerns as multiplying two vectors (as discussed in the "Performing vector multiplication" section, earlier in this chapter). The following code produces an element-by-element multiplication of two matrixes:

```
a = np.array([[1,2,3],[4,5,6]])
b = np.array([[1,2,3],[4,5,6]])

print(a*b)
```

The output looks like this:

```
[[ 1  4  9]
 [16 25 36]]
```

WARNING

Note that a and b are the same shape: two rows and three columns. To perform an element-by-element multiplication, the two matrixes must be the same shape. Otherwise, you see an error message telling you that the shapes are wrong. As with vectors, the multiply() function also produces an element-by-element result.

Dot products work completely differently with matrixes. In this case, the number of columns in matrix a must match the number of rows in matrix b. However, the number of rows in matrix a can be any number, and the number of columns in matrix b can be any number as long as you multiply a by b. For example, the following code produces a correct dot product:

```
a = np.array([[1,2,3],[4,5,6]])
b = np.array([[1,2,3],[3,4,5],[5,6,7]])

print(a.dot(b))
```

with an output of:

```
[[22 28 34]
 [49 64 79]]
```

Note that the output contains the number of rows found in matrix a and the number of columns found in matrix b. So how does this all work? To obtain the value found in the output array at index [0,0] of 22, you sum the values of a[0,0] * b[0,0] (which is 1), a[0,1] * b[1,0] (which is 6), and a[0,2] * b[2,0] (which is 15) to obtain the value of 22. The other entries work precisely the same way.

TIP

To perform an element-by-element multiplication using two matrix objects, you must use the numpy multiply() function.

Defining advanced matrix operations

This book takes you through all sorts of interesting matrix operations, but you use some of them commonly, which is why they appear in this chapter. When working with arrays, you sometimes get data in a shape that doesn't work with the algorithm. Fortunately, numpy comes with a special reshape() function that lets you put the data into any shape needed. In fact, you can use it to reshape a vector into a matrix, as shown in the following code:

```
changeIt = np.array([1,2,3,4,5,6,7,8])
print(changeIt)

changeIt = changeIt.reshape(2,4)
print(changeIt)

changeIt = changeIt.reshape(2,2,2)
print(changeIt)
```

When you run this code, you see these outputs (spaces added for clarity):

```
[1 2 3 4 5 6 7 8]

[[1 2 3 4]
 [5 6 7 8]]

[[[1 2]
  [3 4]]

 [[5 6]
  [7 8]]]
```

REMEMBER

The starting shape of changeIt is a vector, but using the reshape() function turns it into a matrix. In addition, you can shape the matrix into any number of dimensions that work with the data. However, you must provide a shape that fits with the required number of elements. For example, calling changeIt.reshape(2,3,2) will fail because there aren't enough elements to provide a matrix of that size.

You may encounter two important matrix operations in some algorithm formulations. They are the transposition and inverse of a matrix. *Transposition* occurs when a matrix of shape n x m is transformed into a matrix m x n by exchanging the rows with the columns. Most texts indicate this operation by using the superscript *T*, as in A^T. You see this operation used most often for multiplication in order to obtain the right dimensions. When working with numpy, you use the transpose function to perform the required work. For example, when starting with a matrix that has two rows and four columns, you can transpose it to contain four rows with two columns each, as shown in this example:

```
changeIt = np.array([[1, 2, 3, 4], [5, 6, 7, 8]])
print(changeIt)

changeIt = np.transpose(changeIt)
print(changeIt)
```

The outputs look like this:

```
[[1 2 3 4]
 [5 6 7 8]]

[[1 5]
 [2 6]
 [3 7]
 [4 8]]
```

You apply *matrix inversion* to matrixes of shape m x m, which are square matrixes that have the same number of rows and columns. This operation is quite important because it allows the immediate resolution of equations involving matrix multiplication, such as `y = bX`, where you know vector y and matrix X, and you have to discover the values in the vector b. Because most scalar numbers (exceptions include zero) have a number whose multiplication results in a value of 1, the idea is to find a matrix inverse whose multiplication will result in a special matrix called the *identity matrix.* To see an identity matrix in `numpy`, use the `identity` function, like this:

```
print(np.identity(4))
```

which produces an output of:

```
[[1. 0. 0. 0.]
 [0. 1. 0. 0.]
 [0. 0. 1. 0.]
 [0. 0. 0. 1.]]
```

Note that an identity matrix contains all ones on the diagonal. Finding the inverse of a scalar is quite easy (the scalar number n has an inverse of n^{-1} that is 1/n). It's a different story for a matrix. Matrix inversion involves quite a large number of computations. The inverse of a matrix A is indicated as A^{-1}. When working with `numpy`, you use the `linalg.inv()` function to create an inverse. The following example shows how to create an inverse, use it to obtain a dot product, and then compare that dot product to the identity matrix by using the `allclose()` function.

```
a = np.array([[1,2], [3,4]])
b = np.linalg.inv(a)

print(np.allclose(np.dot(a,b), np.identity(2)))
```

REMEMBER

The output of `True` tells you `b` is the inverse of `a`. Sometimes, finding the inverse of a matrix is impossible. When a matrix cannot be inverted, it is referred to as a *singular matrix* or a *degenerate matrix.* Singular matrixes aren't the norm; they're quite rare.

Creating Combinations the Right Way

Shaping data often involves viewing the data in multiple ways. Data isn't simply a sequence of numbers — it presents a meaningful sequence that, when ordered the proper way, conveys information to the viewer. Creating the right data combinations by manipulating data sequences is an essential part of making algorithms do what you want them to do. The following sections look at three data-shaping techniques: permutations, combinations, and repetitions.

Distinguishing permutations

When you receive raw data, it appears in a specific order. The order can represent just about anything, such as the log of a data input device that monitors something like a production line. Perhaps the data is a series of numbers representing the number of products made at any particular moment in time. The reason that you receive the data in a particular order is important, but that order might not lend itself to obtaining the output you need from an algorithm. Creating a data *permutation,* a reordering of the data so that it presents a different view, might help to achieve a desired result.

You can view permutations in a number of ways. One method of viewing a permutation is as a random presentation of the sequence order. In this case, you can use the `numpy` `random.permutation()` function, as shown here:

```
a = np.array([1,2,3])
print(np.random.permutation(a))
```

What you see is a randomized version of the original data, such as `[2 1 3]`. Each time you run this code, you receive a different random ordering of the data sequence, which comes in handy with algorithms that require you to randomize the dataset to obtain the desired results. For example, sampling is an essential part of data analytics, and the technique shown is an efficient way to perform this task.

Another way to view the issue is the need to obtain all the permutations for a dataset so that you can try each one in turn. To perform this task, you need to import the `itertools` package. The following code shows a technique you can use to obtain a list of all the permutations of a particular vector:

```
from itertools import permutations

a = np.array([1,2,3])

for p in permutations(a):
    print(p)
```

The output you see looks like this:

```
(1, 2, 3)
(1, 3, 2)
(2, 1, 3)
(2, 3, 1)
(3, 1, 2)
(3, 2, 1)
```

If you want to use the *list comprehension* (`https://www.w3schools.com/python/python_lists_comprehension.asp`) approach, which is a shorter method of performing repetitive tasks, you can use `[print(p) for p in permutations(a)]` instead. You can read more about `itertools` at `https://docs.python.org/3/library/itertools.html`.

Shuffling combinations

In some cases, you don't need an entire dataset; all you really need are a few of the members in combinations of a specific length. For example, you might have a dataset containing four numbers and want only two-number combinations from it. (The ability to obtain parts of a dataset is a key function for generating a fully connected graph, which is described in Part 3 of the book.) The following code shows how to obtain such combinations:

```
from itertools import combinations

a = np.array([1,2,3,4])

for comb in combinations(a, 2):
    print(comb)
```

which produces this output:

```
(1, 2)
(1, 3)
(1, 4)
(2, 3)
(2, 4)
(3, 4)
```

The output contains all the possible two-number combinations of `a`. Note that this example uses the `itertools combinations()` function (the `permutations()` function appears in the previous section). Of course, you might not need all those combinations; perhaps a random subset of them would work better. In this case, you can rely on the random.sample() function to come to your aid, as shown here:

```
import random

pool = []

for comb in combinations(a, 2):
    pool.append(comb)

print(random.sample(pool, 3))
```

The precise combinations you see as output will vary, such as [(1, 2), (2, 3), (1, 4)]. However, the idea is that you've limited your dataset in two ways. First, you're not using all the data elements all the time, and second, you're not using all the possible combinations of those data elements. The effect is to create a relatively random-looking set of data elements that you can use as input to an algorithm. Python provides a whole host of randomizing methods that you can see at https://docs.python.org/3/library/random.html. Many of the later examples in this book also rely on randomization to help obtain the correct output from algorithms.

Facing repetitions

Repeated data can unfairly weight the output of an algorithm so that you get inaccurate results. Sometimes you need unique values to determine the outcome of a data manipulation. Fortunately, Python makes it easy to remove certain types of repeated data. Consider this example:

```
a = np.array([1,2,3,4,5,6,6,7,7,1,2,3])
b = np.array(list(set(a)))

print(b)
```

The output contains only the unique elements:

```
 [1, 2, 3, 4, 5, 6, 7]
```

REMEMBER

In this case, a begins with an assortment of numbers in no particular order and with plenty of repetitions. In Python, a set never contains repeated data. Consequently, by converting the list in a to a set and then back to a list, and then placing that list in an array, you obtain a vector that has no repeats.

Getting the Desired Results Using Recursion

Recursion, an elegant method of solving many computer problems, relies on the capability of a function to continue calling itself until it satisfies a particular condition. The term *recursion* actually comes from the Latin verb *recurrere,* which means to run back.

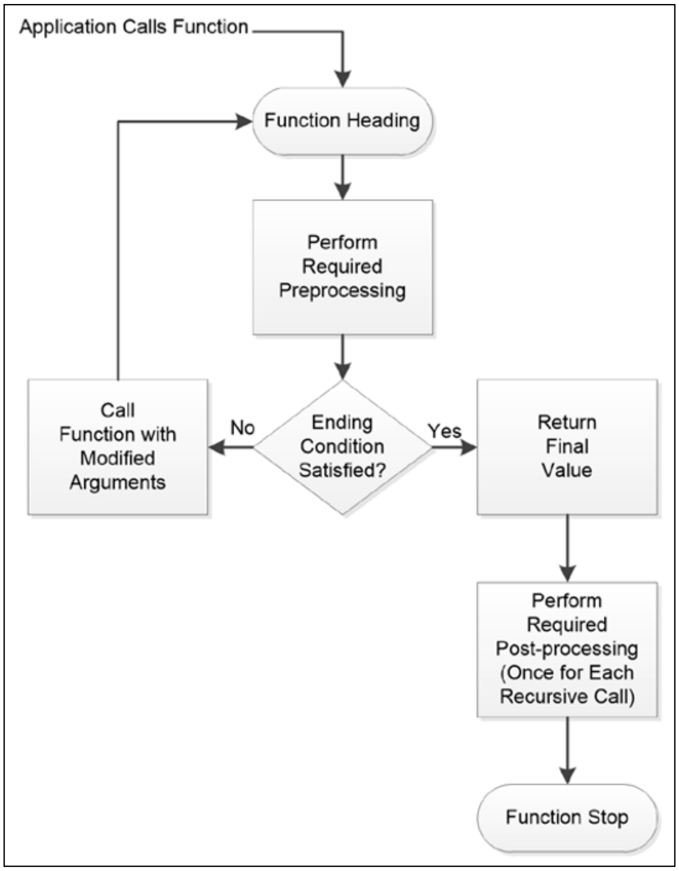
When you use recursion, you solve a problem by calling the same function multiple times but modifying the terms under which you call it. The main reason for using recursion is that it provides an easier way to solve problems when working with some algorithms because it mimics the way a human would solve it. Unfortunately, recursion is not an easy tool because it requires some effort to understand how to build a recursive routine, and it can cause out-of-memory problems on your computer if you don't set some memory settings. The following sections detail how recursion works and give you an example of how recursion works in Python.

Explaining recursion

Many people have a problem using recursion because they can't easily visualize how it works. In most cases, you call a Python function, it does something, and then it stops. However, in recursion, you call a Python function, it does something, and then it calls itself repeatedly until the task reaches a specific condition — but all those previous calls are still active. The calls unwind themselves one at a time until the first call finally ends with the correct answer, and this unwinding process is where most people encounter a problem. Figure 4-1 shows how recursion looks when using a flow chart.

Notice the conditional in the center. To make recursion work, the function must have such a conditional or it could become an endless loop. The conditional determines one of two things:

- The conditions for ending recursion haven't been met, so the function must call itself again.
- The conditions for ending recursion have been met, so the function returns a final value that is used to calculate the ending result.



Application Calls Function
Function Heading
Perform Required Preprocessing
Call Function with Modified Arguments
No
Ending Condition Satisfied?
Yes
Return Final Value
Perform Required Post-processing (Once for Each Recursive Call)
Function Stop

FIGURE 4-1: In the recursion process, a function continuously calls itself until it meets a condition.

REMEMBER

When a function calls itself, it doesn't use the same arguments that were passed to it. If it continuously used the same arguments, the condition would never change and the recursion would never end. Consequently, recursion requires that subsequent calls to the function must change the call arguments in order to bring the function closer to an ending solution.

One of the most common examples of recursion for all programming languages is the calculation of a factorial. A *factorial* is the multiplication of a series of numbers between a starting point and an ending point in which each number in the series is one less than the number before it. For example, to calculate 5! (read as five factorial), you multiple 5 * 4 * 3 * 2 * 1. The calculation represents a perfect and simple example of recursion. Here's the Python code you can use to perform the calculation.

```
def factorial(n):
    print("factorial called with n = ", str(n))
    if n == 1 or n == 0:
        print("Ending condition met.")
        return 1
    else:
        return n * factorial(n-1)

print(factorial(5))
```

Here is the output you see when running this example:

```
factorial called with n =  5
factorial called with n =  4
factorial called with n =  3
factorial called with n =  2
factorial called with n =  1
Ending condition met.
120
```

The code meets the ending condition when `n == 1`. Each successive call to `factorial()` uses `factorial(n-1)`, which reduces the starting argument by `1`. The output shows each successive call to factorial and the meeting of the final condition. The result, `120`, equals 5! (five factorial).

It's important to realize that there isn't just one method for using recursion to solve a problem. As with any other programming technique, you can find all sorts of ways to accomplish the same thing. For example, here's another version of the factorial recursion that uses fewer lines of code but effectively performs the same task:

```
def factorial(n):
    print("factorial called with n = ", str(n))
    if n > 1:
        return n * factorial(n-1)
    print("Ending condition met.")
    return 1

print(factorial(5))
```

REMEMBER

Note the difference. Instead of checking the ending condition, this version checks the continuation condition. As long as `n` is greater than `1`, the code will continue to make recursive calls. Even though this code is shorter than the previous version, it's also less clear because now you must think about what condition will end the recursion.

Eliminating tail call recursion

Many forms of recursion rely on a tail call. In fact, the first example in the previous section does. A *tail call* occurs any time the recursion makes a call to the function as the last thing before it returns. In the previous section, the line `return n * factorial(n-1)` is the tail call.

Tail calls aren't necessarily bad, and they represent the manner in which most people write recursive routines. However, using a tail call forces Python to keep track of the individual call values until the recursion rewinds. Each call consumes memory. At some point, the system will run out of memory and the call will fail, causing your algorithm to fail as well. Given the complexity and huge datasets used by some algorithms today, tail calls can cause considerable woe to anyone using them.

With a little fancy programming, you can potentially eliminate tail calls from your recursive routines. You can find a host of truly amazing techniques online, such as the use of a trampoline, as explained at `https://blog.moertel.com/posts/2013-06-12-recursion-to-iteration-4-trampolines.html`. (Mind you, this isn't the sort of trampoline you jump on at home!) However, the simplest approach to take when you want to eliminate recursion is to create an iterative alternative that performs the same task. For example, here is a `factorial()` function that uses iteration instead of recursion to eliminate the potential for memory issues:

```
def factorial(n):
    print("factorial called with n = ", str(n))
    result = 1
    while n > 1:
        result = result * n
        n = n - 1
        print("Current value of n is ", str(n))
    print("Ending condition met.")
    return result

print(factorial(5))
```

The output looks very similar to before:

```
factorial called with n =  5
Current value of n is  4
Current value of n is  3
Current value of n is  2
Current value of n is  1
Ending condition met.
120
```

The basic flow of this function is the same as the recursive function. A `while` loop replaces the recursive call, but you still need to check for the same condition and continue looping until the data meets the condition. The result is the same. However, replacing recursion with iteration is nontrivial in some cases, as explored in the example at `https://blog.moertel.com/posts/2013-06-03-recursion-to-iteration-3.html`.

Performing Tasks More Quickly

Obviously, getting tasks done as quickly as possible is always ideal. However, you always need to carefully weigh the techniques you use to achieve this efficiency. Trading a little memory to perform a task faster is great as long as you have the memory to spare. Later chapters in the book explore all sorts of ways to perform tasks faster, but you can try some essential techniques no matter what sort of algorithm you're working with at any given time. The following sections explore some of these techniques.

Considering divide and conquer

Some problems look overwhelming when you start them. Take, for example, writing a book. If you consider the entire book, writing it is an overwhelming task. However, if you break the book into chapters and consider just one chapter, the problem seems a little more doable. Of course, an entire chapter can seem a bit daunting, too, so you break the task down into first-level headings, which seems even more doable, but still not quite doable enough. The first-level headings could contain second-level headings and so on until you have broken down the problem of writing about a topic into short articles as much as you can. This is how divide and conquer works. You break a problem down into smaller problems until you find a problem that you can solve without too much trouble.

Computers can use the divide-and-conquer approach as well. Trying to solve a huge problem with an enormous dataset could take days — assuming that the task is even doable. However, by breaking the big problem down into smaller pieces, you can solve the problem much faster and with fewer resources. For example, when searching for an entry in a database, searching the entire database isn't necessary if you use a sorted database. Say that you're looking for the word *Hello* in the database. You can begin by splitting the database in half (letters *A* through *M* and letters *N* through *Z*). The letter *H* in *Hello* is less than *M* in the alphabet, so you look at the first half of the database rather than the second. Splitting the remaining half again (letters *A* through *G* and letters *H* through *M*), you now find that you need the second half of the remainder, which is now only a quarter of the database. Further splits eventually help you find precisely what you want by searching only a small fraction of the entire database. You call this search approach a *binary search.* The problem becomes one of following these steps:

1. Split the content in question in half.
2. Compare the keys for the content with the search term.
3. Choose the half that contains the key.
4. Repeat Steps 1 through 3 until you find the key.

REMEMBER

Most divide-and-conquer problems follow a similar approach, even though some of these approaches become quite convoluted. For example, instead of just splitting the database in half, you might split it into thirds in some cases. However, the goal is the same in all cases: Divide the problem into a smaller piece and determine whether you can solve the problem using just that piece as a generalized case. After you find the generalized case that you know how to solve, you can use that piece to solve any other piece as well. The following code shows an extremely simple version of a binary search that assumes that you have the list sorted.

```
def search(searchList, key):
    mid = int(len(searchList) / 2)
    print("Searching midpoint at ", str(searchList[mid]))

    if mid == 0:
        print("Key Not Found!")
        return key

    elif key == searchList[mid]:
        print("Key Found!")
        return searchList[mid]

    elif key > searchList[mid]:
        print("searchList now contains ",
              searchList[mid:len(searchList)])
        search(searchList[mid:len(searchList)], key)
    else:
        print("searchList now contains ",
              searchList[0:mid])
        search(searchList[0:mid], key)

aList = list(range(1, 21))
search(aList, 5)
```

When you run this code, you see this output:

```
Searching midpoint at  11
searchList now contains  [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
Searching midpoint at  6
searchList now contains  [1, 2, 3, 4, 5]
Searching midpoint at  3
searchList now contains  [3, 4, 5]
Searching midpoint at  4
searchList now contains  [4, 5]
Searching midpoint at  5
Key Found!
```

This recursive approach to the binary search begins with `aList` containing the numbers 1 through 20. It searches for a value of `5` in `aList`. Each iteration of the recursion begins by looking for the list's midpoint, `mid`, and then using that midpoint to determine the next step. When the `key` matches the midpoint, the value is found in the list and the recursion ends.

REMEMBER

Note that this example makes one of two recursive calls. When `key` is greater than the midpoint value of the existing list, `searchList[mid]`, the code calls `search` again with just the right side of the remaining list. In other words, every call to `search` uses just half the list found in the previous call. When `key` is less than or equal to `searchList[mid]`, search receives the left half of the existing list.

WARNING

The list may not contain a search value, so you must always provide an escape method for the recursion or the *stack* (a special area of memory used to store the call information; see `https://www.geeksforgeeks.org/stack-vs-heap-memory-allocation/` for details) will fill, resulting in an error message. In this case, the escape occurs when `mid == 0`, which means that there is no more `searchList` to search. For example, if you change `search(aList, 5)` to `search(aList, 22)`, you obtain the following output instead:

```
Searching midpoint at  11
searchList now contains  [11, 12, 13, 14, 15, 16, 17, 18,
 19, 20]
Searching midpoint at  16
searchList now contains  [16, 17, 18, 19, 20]
Searching midpoint at  18
searchList now contains  [18, 19, 20]
Searching midpoint at  19
searchList now contains  [19, 20]
Searching midpoint at  20
```

```
searchList now contains  [20]
Searching midpoint at  20
Key Not Found!
```

Note also that the code looks for the escape condition before performing any other work to ensure that the code doesn't inadvertently cause an error because of the lack of `searchList` content. When working with recursion, you must remain pro-active or endure the consequences later.

Distinguishing between different possible solutions

Recursion is part of many different algorithmic programming solutions, as you see in the upcoming chapters. In fact, it's hard to get away from recursion in many cases because an iterative approach proves nonintuitive, cumbersome, and time consuming. However, you can create a number of different versions of the same solution, each of which has its own characteristics, flaws, and virtues.

The solution that this chapter doesn't consider is sequential search, because a sequential search generally takes longer than any other solution you can employ. In a best-case scenario, a sequential search requires just one comparison to complete the search, but in a worst-case scenario, you find the item you want as the last check. As an average, sequential search requires `(n+1)/2` checks or `O(n)` time to complete. (The "Working with functions" section of Chapter 2 tells you more about big-O notation.)

The binary search in the previous section does a much better job than a sequential search does. It works on logarithmic time or `O(log n)`. In a best-case scenario, it takes only one check, as with a sequential search, but the output from the example shows that even a worst-case scenario, where the value doesn't even appear in the list, takes only six checks rather than the 21 checks that a sequential search would require.

WARNING

If you look at performance times alone, however, the data you receive can mislead you into thinking that a particular solution will work incredibly well for your application when in fact it won't. You must also consider the kind of data you work with, the complexity of creating the solution, and a host of other factors. That's why later examples in this book also consider the pros and cons of each approach — the hidden dangers of choosing a solution that seems to have potential and then fails to produce the desired result.

IN THIS CHAPTER

» Defining why you want to create your own class

» Putting the basic class together

» Performing some standard matrix computations

» Using the resulting class

Chapter 5 Developing a Matrix Computation Class

The use of Python libraries undoubtedly makes the developer's life easier because these libraries perform much of the coding work. And if the code is properly vetted, developers have fewer bugs to worry about in their code. So it might be hard to imagine a scenario in which you wouldn't want to use a library like NumPy (`https://numpy.org/`) to perform matrix manipulations. After all, it usually ranks in the top ten of Python libraries (see `https://towardsdatascience.com/best-python-libraries-for-every-python-developer-77daab4fa40e`). But even though using NumPy in most situations is beneficial, the first part of this chapter discusses why you might not want to use NumPy, and it tells you about some benefits of creating your own class to perform at least basic matrix manipulation tasks.

The next section of the chapter takes you through the process of creating a basic class for working with matrixes, which includes essentials like multiplying one matrix by another. This isn't going to be a commercial-quality class. Rather, the idea is to help you understand what's involved in creating such a class. A real class will likely need to provide more functionality, but this class serves well for demonstration purposes.

After you have a basic class to use, you start adding features to it to manipulate the matrixes that the class creates. For example, you may need to know how to flatten your matrix for certain types of calculation — and that's the purpose of the third section of the chapter. Again, it doesn't give you anything even approaching commercial quality, but you can get a good idea of what you might need to do to create your own extensions to the basic class.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `\A4D2E\A4D2E; 05; Matrix Class.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Avoiding the Use of NumPy

NumPy is a phenomenal Python library with a great deal of flexibility that provides robust performance and reliability. Of course, these are all reasons to use NumPy and discard any thoughts you might have about building your own class. However, there is no free lunch: Just as with any other developer aid, using NumPy comes with a price. If the cost of using NumPy in your organization is too high, you might want to review other libraries or simply build your own. Here are some issues to consider when working with NumPy.

- NumPy is used by a great many people, not just your organization. So a breaking change to the NumPy package that benefits the majority more than it harms the minority will always take place, according to `https://numpy.org/neps/nep-0023-backwards-compatibility.html`. In other words, something as simple as a NumPy update could cause your application to fail.
- Working with NumPy is a complex undertaking. The User Guide is 486 pages long (`https://numpy.org/doc/1.20/numpy-user.pdf`) and it doesn't cover every aspect of using NumPy (or even close to it). Consequently, developers using NumPy face a rather steep learning curve for features that they may not even need.
- Making the changes you need to NumPy might be difficult when you consider the guidelines at `https://numpy.org/doc/stable/dev/`. That is, to get the kind of NumPy your organization needs, you may end up jumping through hoops that you'd never face when creating your own class.
- The underlying implementation details for NumPy require that you know C/C++ in addition to Python. For example, NumPy structures like matrixes rely on C++ arrays, rather than Python's doubly linked lists. The advantage of this approach is that NumPy gives you a significant speed boost, but at the cost of using multiple programming languages. Using a native approach to working with matrixes is slower, but easier to understand.

- Using NumPy differs from using Python, which could be a problem even if the trade-off is simpler. For example, if you have two row matrixes and want to add them, NumPy allows you to do so using a single addition like this: `A + B`. The same code in Python produces a concatenation, which means that the two row matrixes are joined together. To add two matrixes together using Python, you could use a list comprehension solution, such as `[a + b for a, b in zip(A, B)]`. Yes, the Python approach is more complicated, but it's also pure Python.
- NumPy uses values that Python doesn't understand. The most common complaint provides a value called `NaN`, or Not-a-Number, to represent missing values. A lack of support for `NaN` in Python makes it hard to compare values, so now you're stuck with finding a NumPy solution to what should be a Python problem (see `https://medium.com/nerd-for-tech/a-z-with-numpy-library-6269de9c5413` for details).
- Using a contiguous range of memory to store data in NumPy could mean that NumPy will actually prove slower if the Python code performs a lot of insertions and deletions because the data will need to be shifted. The very thing that makes NumPy such a speed demon can also prove to be its undoing in the right circumstances (see `https://towardsdatascience.com/python-lists-are-sometimes-much-faster-than-numpy-heres-a-proof-4b3dad4653ad` for additional information).

TIP

There are other considerations to make with regard to using native Python over NumPy, but this list provides a good overview of what you should think about. However, it would also be less than useful to make a generalization and say that you should always use Python or always create your own matrix class. When making development decisions, you need to consider the application as a whole and determine which trade-offs make sense in a given situation.

Understanding Why Using a Class is Important

There are a great many reasons to use classes in Python. Many of these reasons focus on Object-Oriented Programming (OOP) techniques, such as:

- Encapsulation
- Inheritance
- Polymorphism

You can read about these reasons in articles like `https://www.programiz.com/python-programming/object-oriented-programming` and `https://realpython.com/python3-object-oriented-programming/`. However, these reasons don't really cover why you'd want to create classes for your matrix library; especially if you use functional programming techniques (see `https://www.geeksforgeeks.org/functional-programming-in-python/` as an example). The need for a class goes beyond using a particular programming paradigm or the usual "it seems like a good idea" excuse that people use without quite having any idea of what they mean by that phrase. So here are some reasons to use a class (or classes) to hold your matrix routines:

- **Organization:** Matrix routines can become quite complex in their own right without your having to remember where you put them. Using classes helps you organize the routines no matter what paradigm you employ to create them.
- **Ease of access:** Placing your matrix routines in a single file means that you can access all of them with a single import. However, if that import is immense, you've now dedicated substantial resources to potentially use just one or two features. By using classes to hold your matrix routines, you can divide your package into manageable parts and just import the part you need.
- **Easier development:** Creating your own matrix routines will require advanced programming skills. You could easily become overwhelmed with the complexity of the problem. By using the divide-and-conquer approach, you can divide the problems you need to solve into smaller pieces, making the entire package easier to develop because you need to deal with only one piece at a time.
- **Collision elimination:** Using a class brings everything together under one roof. More important, you access the methods within the class using the same class name, so you're less likely to encounter any sort of name-collision problem when working with other packages.
- **Cohesiveness:** Bringing all the code together in a single class tends to promote a cohesive (united) approach to coding so that you don't use one approach for one part of the package and a different approach for other parts of the package.

Building the Basic Class

A class or group of classes that deal with matrix manipulation will become quite complicated at some point if you want to create a fully functional and somewhat generic package. The level of complexity will depend greatly on how you plan to use the package. NumPy is so complex because it must address the needs of a large group of people in a generic way. Your class can be simpler because you know your specific needs. Even so, the following sections help you address the basic elements that will likely appear in any matrix class.

WARNING

The `Matrix` class is written with simplicity in mind so that you can more easily see the operations taking place. Consequently, it doesn't include type checking code, checks for matrix size, or any error trapping. A class used in the real world would contain all these elements (and more) to ensure that the class works with few errors. Keep the lack of these features in mind when working with the `Matrix` class by verifying that the input is correct.

Creating a matrix

The example `Matrix` class begins simply by providing code to create a two-dimensional matrix. You build onto this class as the chapter progresses, but starting with a good foundation is important. The following code helps you create two-dimensional matrixes (the most common used) that don't replicate the NumPy way of doing things. (In fact, the `Matrix` class shows alternative methods to the NumPy way of doing things throughout the chapter.)

```
class Matrix:
    rows = 0
    columns = 0
    matrix = []
    matrixRow = []
    dataCount = 0
    matrixList = []
    tempProduct = 0

    def __init__(self, Rows, Columns, Data = []):
        if Data == []:
            Data = [None] * (Rows * Columns)
        self.matrix = []
        self.rows = Rows
        self.columns = Columns
        for i in range(Rows):
            self.matrixRow = []
            for j in range(Columns):
                self.matrixRow.append(
                    Data[self.dataCount])
                self.dataCount += 1
            self.matrix.append(self.matrixRow)
```

The example makes a number of the variables used in the construction, maintenance, and manipulation of the matrixes available for viewing and use within the supporting code. These variables appear at the top of the class definition so that they're easy to find. The `__init__()` function (the class constructor) used to create a matrix won't use all of these variables, but you see them used with later functions.

REMEMBER

The `Matrix` constructor allows the creation of blank matrixes of a certain size, or matrixes that already have values initialized using a Python list. When creating a blank matrix, the code fills the values with `None` so that it's easy to check whether the matrix is initialized.

To create a matrix, the code defines individual rows and then appends those rows to the resulting matrix. Each column within a row contains one value from the `Data` list. The `dataCount` variable tracks the current location within the `Data` list.

Printing the resulting matrix

This section shows you how the `Matrix` class works by creating and then printing a matrix. The following code creates and prints a 2-x-3 matrix that isn't initialized:

```
myMatrix = Matrix(2, 3)
print(myMatrix.rows)
print(myMatrix.columns)
print(myMatrix.matrix)
```

The output shows that the `rows` property contains `2` and the `columns` property contains `3` as expected. The resulting matrix contains the value `None` for each value in the two-dimensional output:

```
2
3
[[None, None, None], [None, None, None]]
```

The following code creates an initialized 2-x-3 `Matrix` containing the values `0` through `5`. Using the `range()` function makes it easy to generate values for testing:

```
z = list(range(6))
print(z)
myMatrix2 = Matrix(2, 3, z)
print(myMatrix2.matrix)
```

The output that follows shows how the `__init__()` function works. The row-oriented function takes each member of the input list in turn and creates a matrix row from it. You could create a column-oriented class instead, based on your particular needs. To create this same matrix using NumPy, you'd need to import NumPy and then specify the matrix using code like this: `myMatrix = np.array([[1, 2, 3], [4, 5, 6]])`, which has the shape already in place.

```
 [0, 1, 2, 3, 4, 5]
[[0, 1, 2], [3, 4, 5]]
```

TIP

Even though NumPy doesn't provide a direct method of specifying the matrix shape during initialization, it does provide the `reshape()` function to modify the matrix shape after initialization. The `Matrix` class provides matrixes of a fixed size. There is no one best way to accomplish tasks, simply the way that works best in a particular situation, so assuming that the method used by a particular Python library is always best is usually a bad idea.

Accessing specific matrix elements

It's important to provide a method for accessing specific matrix elements in your class. The best way to accomplish this task is to create a `__getitem__()` function similar to the one shown here:

```
def __getitem__(self, index):
    return self.matrix[index]
```

REMEMBER

The `__getitem__()` function is just one of a long list of special method names available for use in your class. (Make sure that you add `__getitem__()` and the functions that follow in upcoming sections directly to the `Matrix` class and not at a top level.) You can read about more of these special methods at `https://docs.python.org/3/reference/datamodel.html#special-method-names`. These special methods provide a Python-specific method for performing tasks like operator overloading, so you should use them whenever possible in the creation of your class.

In the case of `__getitem__()` (`https://docs.python.org/3/reference/datamodel.html#object.__getitem__`), the code provides a method of slicing the matrix. All you need to do is return the part of the matrix referenced by `index`. The `index` can be any acceptable Python slice, as shown in the following code:

```
print(myMatrix2[1])
print(myMatrix2[1][2])
```

The output demonstrates that Python interprets the index appropriately depending on what the user provides as input (the first index is a row, and the second provides both row and column):

```
[3, 4, 5]
5
```

Performing scalar and matrix addition

Beyond the basic need to create, print, and slice the matrix, it's also important to perform some essential manipulations, such as addition. It shouldn't be too surprising that you use the `__add__()` special method to perform this task, as shown here.

```
def __add__(self, Value):
    self.matrixList = []
    if type(Value) == list:
        for i in range(self.rows):
            for j in range(self.columns):
                self.matrixList.append(
                    self.matrix[i][j] + Value[i][j])

    else:
        for i in range(self.rows):
            for j in range(self.columns):
                self.matrixList.append(
                    self.matrix[i][j] + Value)
    return Matrix(self.rows, self.columns,
                  self.matrixList)
```

The code covers two cases. The first case is that `Value` contains a matrix, so the code needs to add one matrix to another matrix. The second case is that `Value` contains an integer that is added to every member of the matrix. No matter which form of input the user provides, the values are added together using `matrixList`, which is an internal list variable.

At some point, `matrixList` contains a list of the correct values. The code then creates a new `Matrix` of the correct size and returns it to the caller. This approach ensures that the returned object is of type `Matrix`, and not of type `list`, which would be the case if the function didn't perform this last step.

The `__add__()` function works for both scalar and matrix addition, as demonstrated in the following code.

```
myMatrix2 += 2
print(myMatrix2.matrix)

myMatrix2 += [[2, 4, 6], [8, 10, 12]]
print(myMatrix2.matrix)
```

The output shows the correct addition values. (You can verify the outputs using NumPy, which uses the same addition technique as the `Matrix` class does.)

```
[[2, 3, 4], [5, 6, 7]]
[[4, 7, 10], [13, 16, 19]]
```

Performing multiplication

Any usable matrix manipulation class will also need to support two kinds of multiplication. The first is the element-wise product, which simply performs the multiplication on an element-by-element basis. The second is a dot product, which is often used for linear algebra. The following sections show how to perform both types of multiplication using the `Matrix` class.

Element-wise product

The element-wise product approach is used when you want to combine two matrixes through multiplication, rather than through some other operation such as addition. For example, you might have one matrix that shows the number of hours worked each day and a second matrix that shows the hourly wage for each worked day. Using the element-wise product would create a third matrix containing the total wage for each worked day. To create this result, you use the `__mul__()` function, shown here:

```
def __mul__(self, MatrixIn):
    self.matrixList = []
    for i in range(self.rows):
        for j in range(self.columns):
            self.matrixList.append(
                self.matrix[i][j] * MatrixIn[i][j])
    return Matrix(self.rows, self.columns,
                  self.matrixList)
```

The code simply multiplies the elements in one matrix by the same elements in the second matrix. To do this, both matrixes have to be the same size for the `Matrix` class. When working with NumPy, you have the option of performing a scalar or vector multiplication. Obviously, you could add more code to make this possible in the `Matrix` class as well. Here's the `Matrix` class version in use:

```
A = Matrix(2, 3, [1, 2, 3, 4, 5, 6])
B = Matrix(2, 3, [1, 2, 3, 4, 5, 6])
print(A.matrix)
print(B.matrix)
print((A * B).matrix)
```

REMEMBER

Notice that you use the `*` operator when obtaining an inner product with the `Matrix` class. The same holds true for NumPy: You use the `*` to obtain an inner product. Here's the output of the multiplication:

```
[[1, 2, 3], [4, 5, 6]]
[[1, 2, 3], [4, 5, 6]]
[[1, 4, 9], [16, 25, 36]]
```

As shown, the multiplication is straightforward in this case. For example, `A[0][1] * B[0][1]` equates to 2 * 2, which appears as 4 in the output.

Dot product

A lot of people have a hard time understanding why the dot product is useful, much less how to make it happen. The dot product comes in handy when performing tasks such as trying to compute total sales. Begin with a vector named `Price` that contains the prices for three kinds of fruit:

Apples	Cherries	Pears
1	2	1

A matrix, `Sales`, has the number of pounds of each item sold each day, as shown here:

	Monday	Tuesday	Wednesday	Thursday	Friday
Apples	5	3	4	3	2
Cherries	2	3	3	4	4
Pears	1	2	4	2	3

REMEMBER

The different orientations of the vector to the matrix is important in computing the dot product. To obtain total sales, you multiply the vector by the columns of the table. For example, to find the Monday total, you perform the math like this: (1 * 5) + (2 * 2) + (1 * 1), or $10. The output for all the days would look something like this.

```
[[10, 11, 14, 13, 13]]
```

Working with a matrix is a little more complex. Let's say you have matrix `Prices` that contains the prices for three kinds of fruit for each day of a week like this.

	Apples	**Cherries**	**Pears**
Monday	1	2	1
Tuesday	1	3	2
Wednesday	2	2	1
Thursday	2	3	2
Friday	1	2	2

So, on Monday, apples sold for $1 a pound, cherries $2 a pound, and pears $1 a pound. The sales amount changes by day of week, so you can't say that the value of each product is constant. The output from such a calculation would look something like this:

```
[[10, 11, 14, 13, 13],
 [13, 16, 21, 19, 20],
 [15, 14, 18, 16, 15],
 [18, 19, 25, 22, 22],
 [11, 13, 18, 15, 16]]
```

The output values now appear on a diagonal, so the second output would appear as the value 16, or (1 * 3) + (3 * 3) + (2 * 2), which are the Tuesday values in each matrix. Wednesday's total is 18, Thursday's is 22, and Friday's is 16. This is the how NumPy does things. Your custom class might just output the diagonal values, so no one has to interpret anything.

The code for performing this computation has to be generalized to accept a vector or a matrix as input, so it looks like this:

```
def dot(self, MatrixIn):
    self.matrixList = []
    for i in range(self.rows):
        for j in range(MatrixIn.columns):
            tempProduct = 0
            for k in range(self.columns):
                tempProduct += self.matrix[i][k] * \
                    MatrixIn[k][j]
            self.matrixList.append(tempProduct)
    return Matrix(self.rows, MatrixIn.columns,
                  self.matrixList)
```

The slicing functionality provided by Python automatically handles the differences between vector and matrix multiplication for you. However, the number of columns of the first entity (vector or matrix) must always match the number of rows of the second entity. The testing code for this example looks like this for a vector:

```
Price = Matrix(1, 3, [1, 2, 1])
Sales = Matrix(3, 5,
    [5, 3, 4, 3, 2, 2, 3, 3, 4, 4, 1, 2, 4, 2, 3])
print(Price.matrix)
print(Sales.matrix)
print(Price.dot(Sales).matrix)
```

The matrix testing code looks like this:

```
Prices = Matrix(5, 3,
    [1, 2, 1, 1, 3, 2, 2, 2, 1, 2, 3, 2, 1, 2, 2])
print(Prices.matrix)
print(Prices.dot(Sales).matrix)
```

In both cases, the output is precisely the same as you'd receive from NumPy.

Manipulating the Matrix

Many ways are available to manipulate a matrix, depending on the outcome you need. In fact, quite a few of these methods appear throughout this book. Some manipulations are more common than others, though. The following sections review three of these manipulations: transposition, calculating a determinant, and flattening.

Transposing a matrix

The "Dot product" section, earlier in this chapter, reviews how to obtain the dot product of two matrixes. That section looks at how to obtain total fruit sales, but it would be hard to overestimate the uses for dot product. To obtain the dot product, the two matrixes have to be oriented in a specific way. However, you might find that your matrix isn't oriented in the correct way, which is where transposition comes into play. This section looks at a simple transposition in which rows become columns. To perform this task, you use the following code:

```
def transpose(self):
    self.matrixList = []
    for i in range(self.columns):
        for j in range(self.rows):
            self.matrixList.append(self.matrix[j][i])
    return Matrix(self.columns, self.rows,
                  self.matrixList)
```

Essentially, the process involves copying the matrix, but in a manner that reverses rows and columns. The `matrixList` now contains the values in column order rather than row order (row order is normal). To create the correct output, the call to `Matrix()` must also reverse columns and rows so that the shape of the resulting matrix reflects the new order. The test code for this example looks like this:

```
print(A.matrix)
print(A.transpose().matrix)
```

The output reflects the change in orientation:

```
[[1, 2, 3], [4, 5, 6]]
[[1, 4], [2, 5], [3, 6]]
```

Calculating the determinant

The following sections discuss how to create code to calculate a determinant (which only applies to square matrices). Of course, you may also need a few insights into what a determinant is and why you'd want to calculate it, so the next section covers those details, too.

Why is the matrix so determined?

The determinant of a matrix is a special number that sees use in all sorts of applications, such as calculating the inverse of a matrix (`https://www.mathsisfun.com/algebra/matrix-inverse-minors-cofactors-adjugate.html`). The inverse of a matrix is the set of values that, when multiplied by the original matrix, results in an identity matrix. Wow, that sounds like a lot of babble, so here's a simplified version: If you have the value 10 and you calculate the inverse of 10, which is 1/10, then multiplying 10 * 1/10 results in an output of 1. The identity matrix is like the value 1 for matrixes. If you're really enthusiastic about learning more about inverses and the identity matrix, you can find an outstanding write-up at `https://www.mathsisfun.com/algebra/matrix-inverse.html`. The point is that you sometimes need the inverse of a matrix to perform specific tasks, which means finding the determinant.

TECHNICAL STUFF

You have many ways to find the determinant of a matrix. This example uses the Laplace expansion, which was originally created by Pierre-Simon Laplace (`https://www.britannica.com/biography/Pierre-Simon-marquis-de-Laplace`), because this approach lends itself quite easily to the use of recursion. This is not the fastest way to perform the calculation, but it's the most easily understood. If you want to see one of the alternatives, check out the shortcut method explained at `https://www.studypug.com/algebra-help/the-determinant-of-a-3-x-3-matrix-general-and-shortcut-method`.

TIP

This is one of those situations when you want to have a special calculator on hand to verify the output of your code. The Matrix Reshish site at `https://matrix.reshish.com/determinant.php` provides calculators for calculating the determinant of a matrix, along with all sorts of other helpful things like a matrix transposition and rank. The Symbolab calculator at `https://www.symbolab.com/solver/matrix-determinant-calculator` is helpful because it shows how to solve the determinant problem step by step, which can assist you when writing your code. It also shows many other methods of working with matrixes and the solutions to problems you might encounter.

Creating some prerequisite code

The code for this example begins with a `copyMatrix()` function that enables you to copy part of a matrix into a new matrix using slicing techniques. The reason you need to copy parts of a matrix is that the Laplace expansion reduces the task of calculating the determinant to one simple case; a 2-x-2 matrix. Consequently, the code requires some method of obtaining the required 2-x-2 matrix, which is the purpose of the `copyMatrix()` code, shown here:

```
def copyMatrix(self):
    for i in range(self.rows):
        for j in range(self.columns):
            self.matrixList.append(self.matrix[i][j])
    return Matrix(self.rows, self.columns,
                  self.matrixList)
```

REMEMBER

As shown, the code simply creates a new matrix that is precisely the same as the input matrix. The reason you must take this approach is that copying the matrix any other way could result in two variables that point to the same memory. Modifying one variable would necessarily modify the content of the other variable as well. The `copyMatrix()` function ensures that the new matrix actually does point to new memory.

Performing the calculation

To calculate the determinant of a 2-x-2 matrix, you multiply the diagonals and then subtract the first multiplication from the second. For example, you might start with a matrix that looks like this:

```
[[1, 2],
 [3, 4]]
```

In this case, the determinant is (1 * 4) – (3 * 2) or 4 – 6 for an output of –2. Keep recursion in mind now as you look at the calculation for the following 3-x-3 matrix:

```
 [[ 2, 5, 1],
 [ 5, 6, 7],
 [10, 9, 8]]
```

What you really see here are three 2-x-2 matrixes that can break down like this:

1. 2 * ((6 * 8) – (9 * 7)) = 2 * (48 – 63) = –30
2. 5 * ((5 * 8) – (10 * 7)) = 5 * (40 – 70) = –150
3. 1 * ((5 * 9) – (10 * 6)) = 1 * (45 – 60) = –15

To obtain the final result, you perform the math like this:

```
-30 - -150 + -15 = 105
```

The last part may look a bit tricky because it isn't readily apparent whether you add or subtract the 2-x-2 submatrix results. Actually, you just alternate between addition and subtraction, always beginning with subtraction, as shown. The most important concept to take away in this case is that you always multiply the top row by the 2-x-2 submatrix. Working with a 4-x-4 matrix is simply an extension of this principle. To perform this task, the class contains the following code:

```
def determinant(self, Result=0):
    # Address the simplest case first, the 2 X 2 matrix.
    if len(self.matrix) == 2:
        twoOut = self.matrix[0][0] * self.matrix[1][1] - \
            self.matrix[1][0] * self.matrix[0][1]
        return twoOut

    # Determine the number of rows in a matrix larger
    # than 2 X 2.
    rows = list(range(len(self.matrix)))

    # Process each focus column in turn.
    for focus in rows:

        # Create a copy of the matrix.
        submatrix = self.copyMatrix()

        # Remove the first row of the submatrix.
        submatrix.matrix = submatrix.matrix[1:]

        # Obtain the number of remamining rows to
        # process.
        subrows = len(submatrix.matrix)

        # Create the next smaller size matrix by slicing
        # out the focus rows.
        for i in range(subrows):
            submatrix.matrix[i] = \
                submatrix.matrix[i][0:focus] + \
                submatrix.matrix[i][focus+1:]

        # Determine the sign to use when performing the
        # multiplication.
        sign = (-1) ** (focus % 2)

        # Call the determinant() function recursively
        # with each smaller matrix.
        subdeterminant = submatrix.determinant()

        # Total the returns from the recursive calls.
        Result += sign * self.matrix[0][focus] * \
            subdeterminant

    return Result
```

The code has two parts. The first is the simple 2-x-2 matrix case that follows the process outlined earlier.

The second part begins by creating a copy of the current matrix into `submatrix`. The code then obtains just the top row in `submatrix`. Next, it slices out the next smaller size matrix. So if you're currently working with a 3-x-3 matrix, the code creates three 2-x-2 matrixes as described earlier. The code then determines whether to add or subtract each of the `submatrix` calculations and calls `determinant()` recursively. The final step is to add or subtract each of the recursive call results.

Flattening the matrix

Numerous algorithms require that you flatten a matrix (essentially turn it into a list) to obtain a desired result. You may also want to flatten a matrix to see the result of an algorithm more clearly or to use it in a specific way. Oddly enough, this particular task also sees a lot of activity for job interviews. No matter what reason you have for flattening a matrix, you have many ways to accomplish this task, and you can see discussions about them online. Here's the technique used for the `Matrix` class:

```
def flatten(self):
    self.matrixList = []
    for i in range(self.rows):
        for j in range(self.columns):
            self.matrixList.append(self.matrix[i][j])
    nestedResult = Matrix(1, self.rows * self.columns,
                          self.matrixList)
    nestedResult.matrix = nestedResult.matrix[0]
    return nestedResult
```

As with other elements of the class, this technique isn't guaranteed to provide the fastest result, but it does provide a straightforward method of accomplishing the problem. The code simply creates a `matrixList` that appends each of the elements in the matrix one after another. However, the result of this nested loop is a list, not a `Matrix`, so the next step is to create a `Matrix` containing a one-dimensional list.

The problem with the output at this point is that the resulting `Matrix` actually contains a list nested within another list. To correct the result, the code makes `nestedResult.matrix` equal to `nestedResult.matrix[0]`. The result is now a truly flattened matrix of type `Matrix`. Here's the test code for this example:

```
A = Matrix(3, 3, [1, 2, 3, 4, 5, 6, 7, 8, 9])
print(A.matrix)
print(A.flatten().matrix)
```

The output shows that the original matrix is indeed flattened in the output:

```
[[1, 2, 3], [4, 5, 6], [7, 8, 9]]
[1, 2, 3, 4, 5, 6, 7, 8, 9]
```

2 Understanding the Need to Sort and Search

IN THIS PART . . .

Stacking and piling data

Interacting with trees and graphs

Using merge sort and quick sort

Relying on search trees and the heap

Hashing data

IN THIS CHAPTER

» Defining why data requires structure

» Working with stacks, queues, lists, and dictionaries

» Using trees to organize data

» Using graphs to represent data with relations

Chapter 6 Structuring Data

Raw data is just that: raw. It's not structured or cleaned in any way. Before you can do anything with most data, you must structure it in some manner so that you can begin to see what the data contains (and, sometimes, what it doesn't). The first part of this chapter discusses the need for turning raw data into structured data.

Python provides access to a number of organizational structures for data. The book uses these structures, especially stacks, queues, and dictionaries, for many of the examples. Each data structure provides a different means of working with the data and a different set of tools for performing tasks such as sorting the data into a particular order. This chapter presents you with the most common organizational methods, including both trees and graphs (both of which are so important that they appear in their own sections).

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 06; Graphs.ipynb`, `A4D2E; 06; Remediation.ipynb`, `A4D2E; 06; Stacks, Queues, and Dictionaries.ipynb`, and `A4D2E; 06; Trees.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Determining the Need for Structure

Structuring data entails organizing it in some way so that all the data has the same attributes, appearance, and components. For example, you might get data from one source that contains dates in string form and another source that uses date objects. To use the information, you must make the kinds of data match. Data sources might also structure the data differently. One source might have the last and first name in a single field; another source might use individual fields for the same information. An important part of structuring data is organization. You aren't changing the data in any way — simply making the data more useful. (Structuring data contrasts with remediating or shaping the data, in which you sometimes do change values to convert one data type to another, or experience a loss of accuracy, such as with dates, when moving between data sources.)

Structure is an essential element in making algorithms work. As shown in the binary search example in Chapter 4, implementing an algorithm using structured data is much easier than trying to figure out how to interpret the data in code. For example, the binary search example relies on having the data in sorted order. Trying to perform the required comparisons with unsorted data would require a lot more effort and might even prove impossible to implement. With all this in mind, you need to consider the structural requirements for the data you use with your algorithms, as discussed in the following sections.

Making it easier to see the content

To work with data, it's essential to understand the data content. A search algorithm works only when you understand the dataset so that you know what to search for using the algorithm. Looking for words when the dataset contains numbers is an impossible task that always results in errors. Yet, search errors that result from not understanding the dataset content happen often, even with the best search engines. Humans make assumptions about dataset content that cause algorithms to fail. Consequently, the better you can see and understand the content through structured formatting, the easier it becomes to perform algorithm-based tasks successfully.

However, even looking at the content is often error prone when dealing with humans and computers. For example, if you attempt to search for a number formatted as a string when the dataset contains the numbers formatted as integers, the search will fail. Computers don't automatically translate between strings and integers as humans do. In fact, computers see everything as numbers, and strings are only an interpretation imposed on the numbers by a programmer. Therefore, when searching for "1" (the string), the computer sees it as a request for the number 49 when using ASCII characters. To find the numeric value 1, you must search for a 1 as an integer value.

REMEMBER

Structure also enables you to discover nuanced data details. For example, a telephone number can appear in the form (555)555-1212. If you perform a search or other algorithm task using the form 555-555-1212, the search might fail because of the handling of the area code at the beginning of the search term, using 555- instead of (555). These sorts of issues cause significant problems because most people see the two forms as equal, but the computer doesn't. Trying to impose form on humans rarely works and generally results in frustration that makes using the algorithm even harder, so structure imposed through data manipulation becomes even more important.

Matching data from various sources

Interacting with data from a single source is one problem; interacting with data from several sources is quite another. However, datasets today generally come from more than one source, so you need to understand the complications that using multiple data sources can cause. When working with multiple data sources, you must do the following:

- **Determine whether both datasets contain all the required data.** Two designers are unlikely to create datasets that contain precisely the same data, in the same format, of the same type, and in the same order. Consequently, you need to consider whether the datasets provide the data you need, or whether you need to remediate the data in some way to obtain the desired result, as discussed in the next section.
- **Check both datasets for data type issues.** One dataset could have dates input as strings, and another could have the dates input as actual date objects. Inconsistencies between data types will cause problems for an algorithm that expects data in one form and receives it in another.
- **Ensure that all datasets place the same meaning on data elements.** Data created by one source might have a different meaning than data created by another source. For example, the size of an integer can vary across sources, so you might see a 16-bit integer from one source and a 32-bit integer from another. Lower values have the same meaning, but the 32-bit integer can contain larger values, which can cause problems with the algorithm.
- **Verify the data attributes.** Data items have specific attributes (see `https://www.w3schools.com/python/python_datatypes.asp` for details). Chapter 4 points out that this interpretation can change when using `numpy`. In fact, you find that data attributes change between environments, and developers can change them even more by creating custom data types. To combine data from various sources, you must understand these attributes to ensure that you interpret the data correctly.

REMEMBER

The more time you spend verifying the compatibility of data from each of the sources you want to use for a dataset, the less likely you are to encounter problems when working with an algorithm. Data incompatibility issues don't always appear as outright errors. In some cases, an incompatibility can cause other issues, such as errant results that look correct but provide misleading information.

Combining data from multiple sources may not always mean creating a new dataset that looks precisely like the source datasets, either. In some cases, you create data aggregates or perform other forms of manipulation to create new data from the existing data. Analysis takes all sorts of forms, and some of the more exotic forms can produce terrible errors when used incorrectly. As an extreme example, consider what would happen when combining patient information from several sources and then creating combined patient entries in a new data source with all sorts of mismatches. A patient without a history of a particular disease could end up with records showing diagnosis and care of the disease.

Considering the need for remediation

After you find problems with your dataset, you need to remediate it so that the dataset works properly with the algorithms you use. For example, when working with conflicting data types, you must change the data types of each data source so that they match, and then create the single data source used with the algorithm. Most of this remediation, although time consuming, is straightforward. You simply need to ensure that you understand the data before making changes, which means being able to see the content in the context of what you plan to do with it. However, you need to consider what to do in two special cases: data duplication and missing data. The following sections show how to deal with these issues.

Dealing with data duplication

Duplicated data occurs for a number of reasons. Some of them are obvious. A user could enter the same data more than once. Distractions cause people to lose their place in a list, and sometimes two users enter the same record. Some of the sources of duplication are less obvious. Combining two or more datasets could create multiple records when the data appears in more than one location. You could also create data duplications when using various data-shaping techniques to create new data from existing data sources. Fortunately, packages such as Pandas let you remove duplicate data, as shown in the following example.

```
import pandas as pd

df = pd.DataFrame({'A': [0,0,0,0,0,1,0],
                   'B': [0,2,3,5,0,2,0],
                   'C': [0,3,4,1,0,2,0]})
```

```
print(df, "\n")

df = df.drop_duplicates()
print(df)
```

When you run this code, you see the following output, which shows the original data first and then the data with duplicates dropped:

```
   A  B  C
0  0  0  0
1  0  2  3
2  0  3  4
3  0  5  1
4  0  0  0
5  1  2  2
6  0  0  0

   A  B  C
0  0  0  0
1  0  2  3
2  0  3  4
3  0  5  1
5  1  2  2
```

The `drop_duplicates()` function removes the duplicate records found in rows 4 and 6 in this example. By reading your data from a source into a `pandas` `DataFrame`, you can quickly remove the extra entries so that the duplicates don't unfairly weight the output of any algorithms you use.

Dealing with missing values

Missing values can also skew the results of an algorithm's output. In fact, they can cause some algorithms to react oddly or even raise an error. You have many options when working with missing values. For example, you could set them to a standard value, such as 0 for integers. Of course, using a standard setting could also skew the results. Another approach is to use the mean of all the values, which tends to make the missing values not count. Using a mean is the approach taken in the following example:

```
import pandas as pd
import numpy as np
```

```
df = pd.DataFrame({'A': [0,0,1,None],
                   'B': [1,2,3,4],
                   'C': [np.NAN,3,4,1]},
                 dtype=int)
print(df, "\n")

values = pd.Series(df.mean(), dtype=int)
print(values, "\n")

df = df.fillna(values)
print(df)
```

When you run this code, you see the original data that includes both a `NaN` and a `None` entry first, and then the data with missing values filled in:

```
      A  B    C
0     0  1  NaN
1     0  2    3
2     1  3    4
3  None  4    1

A    0
B    2
C    2
dtype: int32

   A  B  C
0  0  1  2
1  0  2  3
2  1  3  4
3  0  4  1
```

The `fillna()` function enables you to get rid of the missing values whether they're not a number (`NaN`) or simply missing (`None`). You can supply the missing data values in a number of forms. This example relies on a series that contains the mean for each separate column of data (much as you would do when working with a database).

REMEMBER

Note that the code has been carefully created to not introduce errors into the output by ensuring that `values` is of the right data type. Normally, the `mean()` function outputs floating-point values, but you can force the series it fills into the right type. Consequently, the output not only lacks missing values but also contains values of the correct type.

Understanding other remediation issues

Remediation can take a number of other forms. Applications don't always enforce data input rules, so users can enter incorrect state or region names. Users can also misspell. Also, values are sometimes out of range or are simply impossible in a given situation.

You may not always be able to clean your data completely on the first try. Often you become aware of a problem by running the algorithm and noting that the results are skewed in some way or that the algorithm doesn't work at all (even if it did work on a subset of the data). When in doubt, check your data for potential remediation needs.

Stacking and Piling Data in Order

Python provides a number of storage methodologies (see `https://www.w3schools.com/python/python_lists.asp` as an example). As you've already seen in this chapter, packages often offer additional storage methods. Both NumPy and Pandas provide storage alternatives that you might consider when working through various data structuring problems.

REMEMBER

A common problem of data storage isn't just the fact that you need to store the data, but that you must store it in a particular order so that you can access it when necessary. For example, you may want to ensure that the first item you place on a stack of items to process is also the first item you actually do process. With this data-ordering issue in mind, the following sections describe the standard Python methods for ensuring orderly data storage that let you have a specific processing arrangement.

Ordering in stacks

A stack provides last in/first out (LIFO) data storage. The NumPy package provides an actual stack implementation. In addition, Pandas associates stacks with objects such as the `DataFrame`. However, both packages hide the stack implementation details, and seeing how a stack works really does help. Consequently, the following example implements a stack using a standard Python `list`.

```
MyStack = []
StackSize = 3
```

```
def DisplayStack():
   print("Stack currently contains:")
   for Item in MyStack:
      print(Item)

def Push(Value):
   if len(MyStack) < StackSize:
      MyStack.append(Value)
   else:
      print("Stack is full!")

def Pop():
   if len(MyStack) > 0:
      print("Popping: ", MyStack.pop())
   else:
      print("Stack is empty.")

# Test the stack functionality.

Push(1)
Push(2)
Push(3)
DisplayStack()

Push(4)

Pop()
DisplayStack()

Pop()
Pop()
Pop()
```

This code comes in two parts. The first part provides the stack implementation. The second part provides code to test the implementation. When you run this code, you see the following output:

```
Stack currently contains:
1
2
3
Stack is full!
Popping:  3
```

```
Stack currently contains:
1
2
Popping:  2
Popping:  1
Stack is empty.
```

The example ensures that the stack maintains the integrity of the data and works with it in the order you expect. The code relies on simple `list` manipulation, but it's effective in providing a stack representation that you can use for any need.

Using queues

Unlike stacks, queues are first in/first out (FIFO) data structures. As with stacks, you can find predefined implementations in many packages, including both NumPy and Pandas. Fortunately, you can also find a specific `queue` implementation in Python, which you find demonstrated in the following code:

```
import queue

MyQueue = queue.Queue(3)

print("Queue empty: ", MyQueue.empty())

MyQueue.put(1)
MyQueue.put(2)
MyQueue.put(3)
print("Queue full: ", MyQueue.full())

print("Popping: ", MyQueue.get())
print("Queue full: ", MyQueue.full())

print("Popping: ", MyQueue.get())
print("Popping: ", MyQueue.get())
print("Queue empty: ", MyQueue.empty())
```

You see the following output when you run this example:

```
Queue empty:  True
Queue full:  True
Popping:  1
```

```
Queue full:  False
Popping:  2
Popping:  3
Queue empty:  True
```

Using the built-in `queue` requires a lot less code than building a stack from scratch using a `list`, but notice how the two differ in output. The stack example pushes 1, 2, and 3 onto the stack, so the first value popped from the stack is 3. However, in this example, pushing 1, 2, and 3 onto the `queue` results in a first popped value of 1.

Finding data using dictionaries

Creating and using a `dictionary` is much like working with a `list` except that you must now define a key and value pair. The great advantage of this data structure is that dictionaries can quickly provide access to specific data items using the key. There are limits to the kinds of keys you can use. Here are the special rules for creating a key:

- **The key must be unique.** When you enter a duplicate key, the information found in the second entry wins; the first entry replaces the second.
- **The key must be immutable.** This rule means that you can use strings, numbers, or tuples for the key. You can't, however, use a `list` for a key.

REMEMBER

The difference between mutable and immutable values is that immutable values can't change. To change the value of a string, for example, Python actually creates a new string that contains the new value and gives the new string the same name as the old one. It then destroys the old string.

TIP

Python dictionaries are the software implementation of a data structure called a *hash table*, an array that maps keys to values. Chapter 7 explains hashes in detail and how using hashes can help dictionaries perform faster. You have no restrictions on the values you provide. A value can be any Python object, so you can use a dictionary to access an employee record or other complex data. The following example helps you understand how to use dictionaries better:

```
Colors = {"Sam": "Blue", "Amy": "Red", "Sarah": "Yellow"}

print(Colors["Sarah"])
print(Colors.keys())

for Item in Colors.keys():
   print("{0} likes the color {1}."
      .format(Item, Colors[Item]))
```

```
Colors["Sarah"] = "Purple"
Colors.update({"Harry": "Orange"})
del Colors["Sam"]

print(Colors)
```

When you run this code, you see the following output:

```
Yellow
dict_keys(['Sarah', 'Amy', 'Sam'])
Sarah likes the color Yellow.
Amy likes the color Red.
Sam likes the color Blue.
{'Harry': 'Orange', 'Sarah': 'Purple', 'Amy': 'Red'}
```

As you can see, a dictionary always has a key and value pair separated from each other by a colon (:). Instead of using an index to access individual values, you use the key. The special `keys()` function lets you obtain a list of keys that you can manipulate in various ways. For example, you can use the keys to perform iterative processing of the data values that the dictionary contains.

TIP

Dictionaries are a bit like individual tables within a database. You can update, add, and delete records to a dictionary as shown. The `update()` function can overwrite or add new entries to the dictionary.

Working with Trees

A tree structure looks much like the physical object in the natural world. Using trees helps you organize data quickly and find it in a shorter time than using many other data-storage techniques. You commonly find trees used for search and sort routines, but they have many other purposes as well. The following sections help you understand trees at a basic level. You find trees used in many of the examples in upcoming chapters.

Understanding the basics of trees

Building a tree works much like building a tree would work in the physical world, if anyone could do that. Each item you add to the tree is a *node.* Nodes connect to each other using *links.* The combination of nodes and links forms a structure that looks much like an upside-down tree, as shown in Figure 6-1.

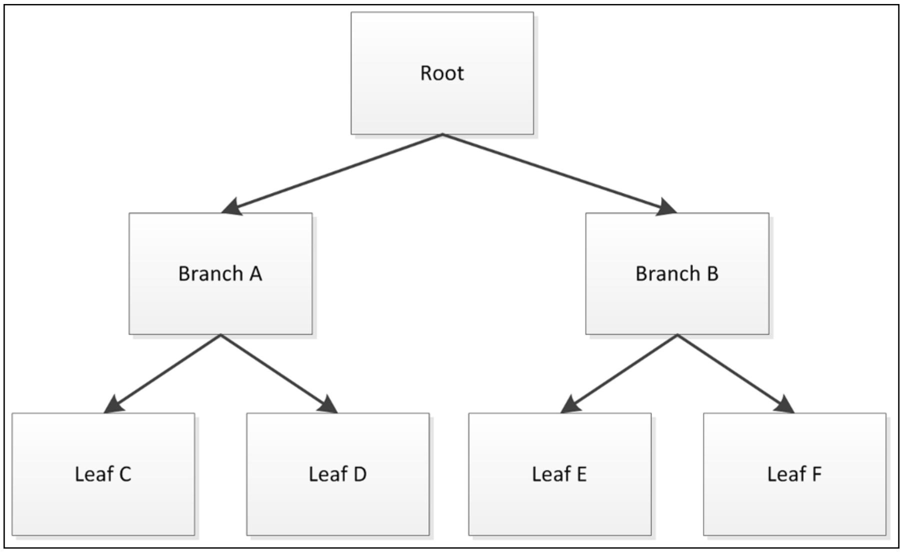


FIGURE 6-1: A tree in Python looks much like the physical alternative.

REMEMBER

Note that the tree has just one root node — just as with a physical tree. The *root node* provides the starting point for the various kinds of processing you perform. Connected to the root node are either branches or leaves. A *leaf node* is always an ending point for the tree. *Branch nodes* support either other branches or leaves. The type of tree shown in Figure 6-1 is a binary tree because each node has, at most, two connections.

In looking at the tree, Branch B is the child of the Root node. That's because the Root node appears first in the list. Leaf E and Leaf F are both children of Branch B, making Branch B the parent of Leaf E and Leaf F. The relationship between nodes is important because discussions about trees often consider the child/parent relationship between nodes. Without these terms, discussions of trees could become quite confusing.

Building a tree

Python doesn't come with a built-in tree object. A basic tree implementation requires that you create a class to hold the tree data object. The following code shows how you can create a basic tree class.

```
class binaryTree:
    def __init__(self, nodeData, left=None, right=None):
        self.nodeData = nodeData
        self.left  = left
        self.right = right
    def __str__(self):
        return str(self.nodeData)
```

This code just creates a basic tree object that defines the three elements that a node must include: data storage, left connection, and right connection. Because leaf nodes have no connection, the default value for `left` and `right` is `None`. The class also includes a method for printing the content of `nodeData` so that you can see what data the node stores.

Using this simple tree requires that you not try to store anything in `left` or `right` other than a reference to another node. Otherwise, the code will fail because there isn't any error trapping. The `nodeData` entry can contain any value. The following code shows how to use the `binaryTree` class to build the tree shown in Figure 6-1:

```
tree = binaryTree("Root")
BranchA = binaryTree("Branch A")
BranchB = binaryTree("Branch B")
tree.left = BranchA
tree.right = BranchB

LeafC = binaryTree("Leaf C")
LeafD = binaryTree("Leaf D")
LeafE = binaryTree("Leaf E")
LeafF = binaryTree("Leaf F")
BranchA.left = LeafC
BranchA.right = LeafD
BranchB.left = LeafE
BranchB.right = LeafF
```

You have many options when building a tree, but building it from the top down (as shown in this code) or the bottom up (in which you build the leaves first) are two common methods. Of course, you don't know whether the tree actually works at this point. *Traversing the tree* means checking the links and verifying that they actually do connect as you think they should. The following code shows how to use recursion (as described in Chapter 4) to traverse the tree you just built:

```
def traverse(tree):
    if tree.left != None:
        traverse(tree.left)
    if tree.right != None:
        traverse(tree.right)
    print(tree.nodeData)

traverse(tree)
```

The recursive routine, `traverse()`, starts printing at the leaves and moves toward the root, so you see the following output:

```
Leaf C
Leaf D
Branch A
Leaf E
Leaf F
Branch B
Root
```

You can see that `traverse()` prints both leaves and the parent of those leaves. The traversal follows the left branch first, and then the right branch. The root node comes last.

TECHNICAL STUFF

There are different kinds of data storage structures. Here is a quick list of the kinds of structures you commonly find:

- **Balanced trees:** A kind of tree that maintains a balanced structure through reorganization so that it can provide reduced access times.
- **Unbalanced trees:** A tree that places new data items wherever necessary in the tree without regard to balance. This method of adding items makes building the tree faster but reduces access speed when searching or sorting.
- **Heaps:** A sophisticated tree that allows data insertions into the tree structure. The use of data insertion makes sorting faster.

Later in the book, you find algorithms that use balanced trees, unbalanced trees, and heaps. For instance, Chapter 9 discusses the Dijkstra algorithm, and Chapter 14 discusses Huffman encoding.

Representing Relations in a Graph

Graphs are another form of common data structure used in algorithms. You see graphs used in places like maps for GPS and all sorts of other places where the top-down approach of a tree won't work. The following sections describe graphs in more detail.

Going beyond trees

A graph is a sort of a tree extension. As with trees, you have nodes that connect to each other to create relationships. However, unlike binary trees, a graph can have more than one or two connections. In fact, graph nodes often have a multitude of connections. To keep things simple, though, consider the graph shown in Figure 6-2.

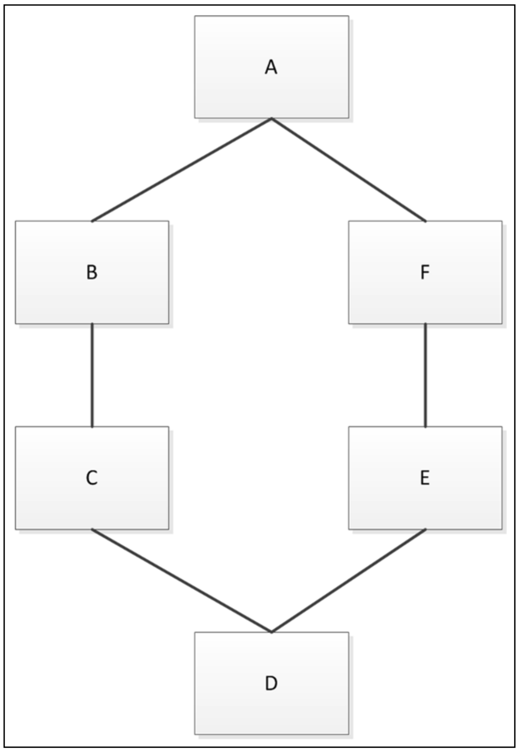


FIGURE 6-2: Graph nodes can connect to each other in myriad ways.

In this case, the graph creates a ring where A connects to both B and F. However, it need not be that way. Node A could be a disconnected node or could also connect to C. A graph shows connectivity between nodes in a way that is useful for defining complex relationships.

Graphs also add a few new twists that you might not have thought about before. For example, a graph can include the concept of directionality. Unlike a tree, which has parent/child relationships, a graph node can connect to any other node with a specific direction in mind. Think about streets in a city. Most streets are bidirectional, but some are one-way streets that allow movement in only one direction.

The presentation of a graph connection might not actually reflect the realities of the graph. A graph can designate a weight to a particular connection. The weight could define the distance between two points, define the time required to traverse the route, or provide other sorts of information.

Building graphs

Most developers use dictionaries (or sometimes lists) to build graphs. Using a dictionary makes building the graph easy because the key is the node name and the values are the connections for that node. For example, here is a dictionary that creates the graph shown in Figure 6-2.

```
graph = {'A': ['B', 'F'],
         'B': ['A', 'C'],
         'C': ['B', 'D'],
         'D': ['C', 'E'],
         'E': ['D', 'F'],
         'F': ['E', 'A']}
```

This dictionary reflects the bidirectional nature of the graph in Figure 6-2. It could just as easily define unidirectional connections, or provide nodes without any connections at all. However, the dictionary works quite well for this purpose, and you see it used in other areas of the book. Now it's time to traverse the graph using the following code:

```
def find_path(graph, start, end, path=[]):
        path = path + [start]

        if start == end:
            print("Ending")
            return path

        for node in graph[start]:
            print("Checking Node ", node)

            if node not in path:
                print("Path so far ", path)

                newp = find_path(graph, node, end, path)
                if newp:
                    return newp

find_path(graph, 'B', 'E')
```

When you run this code, the example begins with node 'A' and moves through all the graph connections to produce the following output:

```
Checking Node  A
Path so far  ['B']
Checking Node  B
Checking Node  F
Path so far  ['B', 'A']
Checking Node  E
Path so far  ['B', 'A', 'F']
Ending

['B', 'A', 'F', 'E']
```

Later chapters discuss how to find the shortest path. For now, the code finds only a path. It begins by building the path node by node. As with all recursive routines, this one requires an exit strategy, which is that when the start value matches the end value, the path ends.

Because each node in the graph can connect to multiple nodes, you need a for loop to check each of the potential connections. When the node in question already appears in the path, the code skips it (which can prevent the code from entering an infinite loop — a risk with graph algorithms). Otherwise, the code tracks the current path and recursively calls find_path() to locate the next node in the path.

IN THIS CHAPTER

- » **Performing sorts using merge sort and quick sort**
- » **Conducting searches using trees and the heap**
- » **Considering the uses for hashing and dictionaries**

Chapter 7 Arranging and Searching Data

This chapter is about using the four data operations — create, read, update, and delete (CRUD) — to manage data. The first section of this chapter focuses on sorting data. Placing data in an order that makes it easy to perform CRUD operations is important because the less code you need to make data access work, the better. In addition, even though sorting data might not seem particularly important, sorted data makes searches considerably faster, as long as the sort matches the search. Sorting and searching go together: You sort the data in a way that makes searching faster.

The second section of the chapter discusses searching. You won't be surprised to learn that many different ways are available to search for data. Some of these techniques are slower than others; some have attributes that make them attractive to developers. The fact is that no perfect search strategy exists, but the exploration for such a method continues.

The final section of the chapter looks at hashing and dictionaries. The use of indexing makes sorting and searching significantly faster but also comes with trade-offs that you need to consider (such as the use of additional resources). An *index* is a kind of pointer or an address. It's not the data, but it points to the data, much as your address points to your home. A block-by-block manual search for your home in the city would be time consuming because the person looking for you would need to ask each person at each address whether you're there, but finding your address in the phone book and then using that address to locate your home is much faster.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 07; Hashing.ipynb`, `A4D2E; 07; Search Techniques.ipynb`, and `A4D2E; 07; Sorting Techniques.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Sorting Data Using Merge Sort and Quick Sort

Sorting is one of the essentials of working with data. Consequently, a lot of people have come up with a lot of different ways to sort data over the years. All these techniques result in ordered data, but some work better than others, and some work exceptionally well for specific tasks. The following sections help you understand the need for searching as well as consider the various search options.

Understanding why sorting data is important

A case can be made for not sorting data. After all, the data is still accessible, even if you don't sort it — and sorting takes time. Of course, the problem with unsorted data is the same problem as that junk drawer in your kitchen (or wherever you have your junk drawer — assuming that you can find it at all). Looking for anything in the junk drawer is time consuming because you can't even begin to guess where to find something. Rather than just reach in and take what you want, you must take out myriad other items that you don't want in an effort to find the one item you need. Unfortunately, the item you need might not be in the junk drawer in the first place; you might have thrown it out or put it in a different drawer.

The junk drawer in your home is just like unsorted data on your system. When the data is unsorted, you need to search one item at a time, and you don't even know whether you'll find what you need without searching every item in the dataset first. It's a frustrating way to work with data. The binary search example in the "Considering divide and conquer" section of Chapter 4 points out the need for sorting quite well. Imagine trying to find an item in a list without sorting it first. Every search becomes a time-consuming sequential search.

REMEMBER

Simply sorting the data isn't enough. If you have an employee database sorted by last name, yet need to look up an employee by birth date, the sorting isn't useful. Say you want to find all the employees who have a birthday on a certain day. To find the birth date you need, you must still search the entire dataset one item at a time. Consequently, sorting must focus on a particular need. Yes, you needed the employee database sorted by department at one point and by last name at another time, but now you need it sorted by birth date in order to use the dataset effectively.

The need to maintain several sorted orders for the same data is the reason developers created indexes. Sorting a small index is faster than sorting the entire dataset. The index maintains a specific data order and points to the full dataset so that you can find what you need extremely fast. By maintaining an index for each sort requirement, you can effectively cut data access time and allow several people to access the data at the same time in the order in which they need to access it. The "Relying on Hashing" section, later in this chapter, gives you an idea of how indexing works and why you really need it in some cases, despite the additional time and resources needed to maintain the indexes.

TECHNICAL STUFF

Many ways are available to categorize sorting algorithms. One of these ways is the speed of the sort. When considering how effective a particular sort algorithm is at arranging the data, timing benchmarks typically look at two factors:

- **Comparisons:** To move data from one location in a dataset to another, you need to know where to move it, which means comparing the target data to other data in the dataset. Having fewer comparisons means better performance.
- **Exchanges:** Depending on how you write an algorithm, the data may not get to its final location in the dataset on the first try. The data might actually move several times. The number of exchanges affects speed considerably because now you're actually moving data from one location to another in memory. Fewer and smaller exchanges (such as when using indexes) means better performance.

Ordering data naïvely Ordering data naïvely for the purpose of making searching (and other tasks) easier means to order it using brute-force methods — without any regard whatsoever to making any kind of guess as to where the data should appear in the list. In addition, these techniques tend to work with the entire dataset instead of applying approaches that would likely reduce sorting time (such as the divide and conquer technique described in Chapter 4). However, these searches are also relatively easy to understand, and they use resources efficiently, so you shouldn't rule them out completely. Even though many searches fall into this category, the following sections look at the two most popular approaches.

Using a selection sort

The selection sort replaced a predecessor, the bubble sort, because it tends to provide better performance than the bubble sort. Even though both sorts have a worst-case sort speed of $O(n^2)$, the selection sort performs fewer exchanges. A selection sort works in one of two ways: It either looks for the smallest item in the list and places it in the front of the list (ensuring that the item is in its correct location) or looks for the largest item and places it in the back of the list. Either way, the sort is exceptionally easy to implement and guarantees that items immediately appear in the final location once moved (which is why some people call it an in-place comparison sort). Here's an example of a selection sort. (You can find this code in the `A4D2E; 07; Sorting Techniques.ipynb` downloadable source code file; see the Introduction for details.)

```
data = [9, 5, 7, 4, 2, 8, 1, 10, 6, 3]

for scanIndex in range(0, len(data)):
    minIndex = scanIndex

    for compIndex in range(scanIndex + 1, len(data)):
        if data[compIndex] < data[minIndex]:
            minIndex = compIndex

    if minIndex != scanIndex:
        data[scanIndex], data[minIndex] = \
            data[minIndex], data[scanIndex]
        print(data)
```

You see the following output as the code runs. Notice how each number arrives in the correct position as the sort progresses:

```
[1, 5, 7, 4, 2, 8, 9, 10, 6, 3]
[1, 2, 7, 4, 5, 8, 9, 10, 6, 3]
[1, 2, 3, 4, 5, 8, 9, 10, 6, 7]
[1, 2, 3, 4, 5, 6, 9, 10, 8, 7]
[1, 2, 3, 4, 5, 6, 7, 10, 8, 9]
[1, 2, 3, 4, 5, 6, 7, 8, 10, 9]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
```

Switching to an insertion sort

An insertion sort works by using a single item as a starting point and adding items to the left or right of it based on whether these items are less than or greater than the selected item. As the number of sorted items builds, the algorithm checks new items against the sorted items and inserts the new item into the right position in the list. An insertion sort has a best-case sort speed of O(n) and a worst case sort speed of O(n^2).

TECHNICAL STUFF

An example of best-case sort speed is when the entire dataset is already sorted because the insertion sort won't have to move any values. An example of the worst-case sort speed is when the entire dataset is sorted in reverse order because every insertion will require moving every value that already appears in the output. You can read more about the math involved in this sort at https://www.khanacademy.org/computing/computer-science/algorithms/insertion-sort/a/analysis-of-insertion-sort.

The insertion sort is still a brute-force method of sorting items, but it can require fewer comparisons than a selection sort. Here's an example of an insertion sort:

```
data = [9, 5, 7, 4, 2, 8, 1, 10, 6, 3]

for scanIndex in range(1, len(data)):
    temp = data[scanIndex]

    minIndex = scanIndex

    while minIndex > 0 and temp < data[minIndex - 1]:
        data[minIndex] = data[minIndex - 1]
        minIndex -= 1

    data[minIndex] = temp
    print(data)
```

The example output shows that it requires nine iterations for this example, in contrast to seven for the previous example. However, you find that the insertion sort performs better than the selection sort in other cases. It depends on the data you use as input.

```
 [5, 9, 7, 4, 2, 8, 1, 10, 6, 3]
[5, 7, 9, 4, 2, 8, 1, 10, 6, 3]
[4, 5, 7, 9, 2, 8, 1, 10, 6, 3]
[2, 4, 5, 7, 9, 8, 1, 10, 6, 3]
[2, 4, 5, 7, 8, 9, 1, 10, 6, 3]
[1, 2, 4, 5, 7, 8, 9, 10, 6, 3]
[1, 2, 4, 5, 7, 8, 9, 10, 6, 3]
[1, 2, 4, 5, 6, 7, 8, 9, 10, 3]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
```

Employing better sort techniques

As sort technology improves, the sort algorithms begin taking a more intelligent approach to getting data into the right order. The idea is to make the problem smaller and easier to manage. Rather than work with an entire dataset, smart sorting algorithms work with individual items, reducing the work required to perform the task. The following sections discuss two such smart sorting techniques.

Rearranging data with merge sort

A merge sort works by applying the divide-and-conquer approach. The sort begins by breaking the dataset into individual pieces and sorting the pieces. It then merges the pieces in a manner that ensures that it has sorted the merged piece. The sorting and merging continues until the entire dataset is again a single piece. The worst-case sort speed of the merge sort is `O(n log n)`, which makes it considerably faster than the techniques used in the previous section (because log n is always smaller than n). This sort actually requires the use of two functions. The first function works recursively to split the pieces apart and put them back together again.

```
data = [9, 5, 7, 4, 2, 8, 1, 10, 6, 3]

def mergeSort(list):
    # Determine whether the list is broken into
    # individual pieces.
    if len(list) < 2:
        return list

    # Find the middle of the list.
    middle = len(list)//2
    # Break the list into two pieces.
    left = mergeSort(list[:middle])
    right = mergeSort(list[middle:])

    # Merge the two sorted pieces into a larger piece.
    print("Left side: ", left)
    print("Right side: ", right)
    merged = merge(left, right)
    print("Merged ", merged)
    return merged
```

The second function performs the actual task of merging the two sides using an iterative process. Here’s the code used to merge the two pieces:

```
def merge(left, right):
    # When the left side or the right side is empty,
    # it means that this is an individual item and is
    # already sorted.
    if not len(left):
        return left
    if not len(right):
        return right

    # Define variables used to merge the two pieces.
    result = []
    leftIndex = 0
    rightIndex = 0
    totalLen = len(left) + len(right)

    # Keep working until all of the items are merged.
    while (len(result) < totalLen):

        # Perform the required comparisons and merge
        # the pieces according to value.
        if left[leftIndex] < right[rightIndex]:
            result.append(left[leftIndex])
            leftIndex+= 1
        else:
            result.append(right[rightIndex])
            rightIndex+= 1

        # When the left side or the right side is longer,
        # add the remaining elements to the result.
        if leftIndex == len(left) or \
            rightIndex == len(right):
                result.extend(left[leftIndex:]
                              or right[rightIndex:])
                break

    return result

mergeSort(data)
```

The `print` statements in the code help you see how the merging process works. Even though the process seems quite complex, it really is relatively straightforward when you work through the merging process shown here:

```
Left side:  [9]
Right side:  [5]
```

```
Merged  [5, 9]
Left side:  [4]
Right side:  [2]
Merged  [2, 4]
Left side:  [7]
Right side:  [2, 4]
Merged  [2, 4, 7]
Left side:  [5, 9]
Right side:  [2, 4, 7]
Merged  [2, 4, 5, 7, 9]
Left side:  [8]
Right side:  [1]
Merged  [1, 8]
Left side:  [6]
Right side:  [3]
Merged  [3, 6]
Left side:  [10]
Right side:  [3, 6]
Merged  [3, 6, 10]
Left side:  [1, 8]
Right side:  [3, 6, 10]
Merged  [1, 3, 6, 8, 10]
Left side:  [2, 4, 5, 7, 9]
Right side:  [1, 3, 6, 8, 10]
Merged  [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
```

Solving sorting issues the best way using quick sort

The quick sort is one of the fastest methods of sorting data. In reading about merge sort and quick sort online, you find that some people prefer to use one over the other in a given situation. For example, most people feel that a quick sort works best for sorting arrays, and merge sort works best for sorting linked lists (see the discussion at `https://www.geeksforgeeks.org/why-quick-sort-preferred-for-arrays-and-merge-sort-for-linked-lists/`). Tony Hoare wrote the first version of quick sort in 1959, but since that time, developers have written many other versions of quick sort. The average sort time of a quick sort is `O(n log n)`, but the worst-case sort time is $O(n^2)$.

UNDERSTANDING QUICK SORT WORST-CASE PERFORMANCE

Quick sort seldom incurs the worst-case sort time. However, even modified versions of the quick sort can have a worst-case sort time of $O(n^2)$ when one of these events occurs:

- The dataset is already sorted in the desired order.
- The dataset is sorted in reverse order.
- All the elements in the dataset are the same.

All these problems occur because of the pivot point that a less intelligent sort function uses (often, the choice made is a poor one). Fortunately, using the right programming technique can mitigate these problems by defining something other than the leftmost or rightmost index as the pivot point. The techniques that modern quick sort versions rely on include:

- Choosing a random index
- Choosing the middle index of the partition
- Choosing the median of the first, middle, and last element of the partition for the pivot (especially for longer partitions)

The first part of the task is to partition the data. The code chooses a pivot point that determines the left and right side of the sort. Here is the partitioning code for this example:

```
data = [9, 5, 7, 4, 2, 8, 1, 10, 6, 3]

def partition(data, left, right):
    pivot = data[left]
    lIndex = left + 1
    rIndex = right

    while True:
        while lIndex <= rIndex and data[lIndex] <= pivot:
            lIndex += 1
        while rIndex >= lIndex and data[rIndex] >= pivot:
            rIndex -= 1
        if rIndex <= lIndex:
            break
        data[lIndex], data[rIndex] = \
            data[rIndex], data[lIndex]
        print(data)

    data[left], data[rIndex] = data[rIndex], data[left]
    print(data)
    return rIndex
```

The inner loop of this example continuously searches for elements that are in the wrong place and swaps them. When the code can no longer swap items, it breaks out of the loop and sets a new pivot point, which it returns to the caller. This is the iterative part of the process. The recursive part of the process handles the left and right side of the dataset, as shown here:

```
def quickSort(data, left, right):
    if right <= left:
        return
    else:
        pivot = partition(data, left, right)
        quickSort(data, left, pivot-1)
        quickSort(data, pivot+1, right)

    return data

quickSort(data, 0, len(data)-1)
```

The amount of comparisons and exchanges for this example are relatively small compared to the other examples. Here is the output from this example:

```
[9, 5, 7, 4, 2, 8, 1, 3, 6, 10]
[6, 5, 7, 4, 2, 8, 1, 3, 9, 10]
[6, 5, 3, 4, 2, 8, 1, 7, 9, 10]
[6, 5, 3, 4, 2, 1, 8, 7, 9, 10]
[1, 5, 3, 4, 2, 6, 8, 7, 9, 10]
[1, 5, 3, 4, 2, 6, 8, 7, 9, 10]
[1, 2, 3, 4, 5, 6, 8, 7, 9, 10]
[1, 2, 3, 4, 5, 6, 8, 7, 9, 10]
[1, 2, 3, 4, 5, 6, 8, 7, 9, 10]
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
```

Using Search Trees and the Heap

Search trees enable you to look for data quickly. Chapter 4 introduces you to the idea of a binary search, and the "Working with Trees" section of Chapter 6 helps you understand trees to some extent. Obtaining data items, placing them in sorted order in a tree, and then searching that tree is one of the faster ways to find information.

A special kind of tree structure is the *binary heap,* which places each of the node elements in a special order. The root node always contains the smallest value. When viewing the branches, you see that upper-level branches are always a smaller value than lower-level branches and leaves. The effect is to keep the tree balanced and in a predictable order so that searching becomes extremely efficient. The cost is in keeping the tree balanced. The following sections describe how search trees and the heap work in detail.

Considering the need to search effectively

Of all the tasks that applications do, searching is the most time consuming as well as the one required the most. Even though adding data (and sorting it later) does require some amount of time, the benefit to creating and maintaining a dataset comes from using it to perform useful work, which means searching it for important information. Consequently, you can sometimes get by with less efficient CRUD functionality and even a less-than-optimal sort routine, but searches must proceed as efficiently as possible. The only problem is that no one search performs every task with absolute efficiency, so you must weigh your options based on what you expect to do as part of the search routines.

Two of the more efficient methods of searching involve the use of the binary search tree (BST) and binary heap. Both search techniques rely on a tree-like structure to hold the keys used to access data elements. However, the arrangement of the two methods is different, which is why one has advantages over the other when performing certain tasks. Figure 7-1 shows the arrangement for a BST.

Note how the keys follow an order in which lesser numbers appear to the left and greater numbers appear to the right. The root node contains a value that is in the middle of the range of keys, giving the BST an easily understood, well-adjusted approach to storing the keys. Contrast this arrangement to the binary heap shown in Figure 7-2.

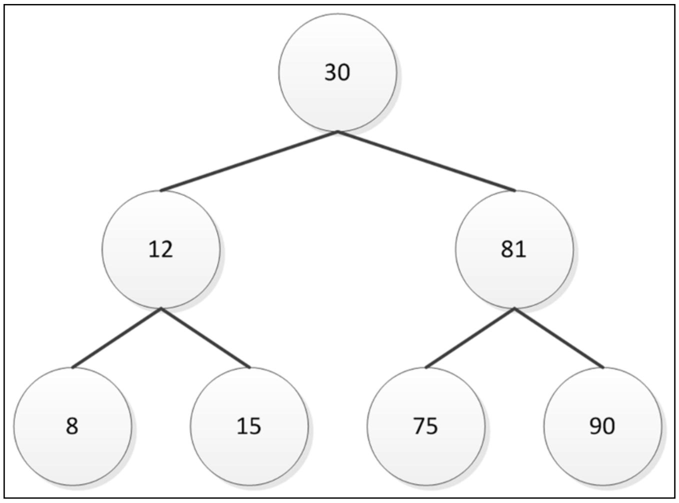


FIGURE 7-1: The arrangement of keys when using a BST.

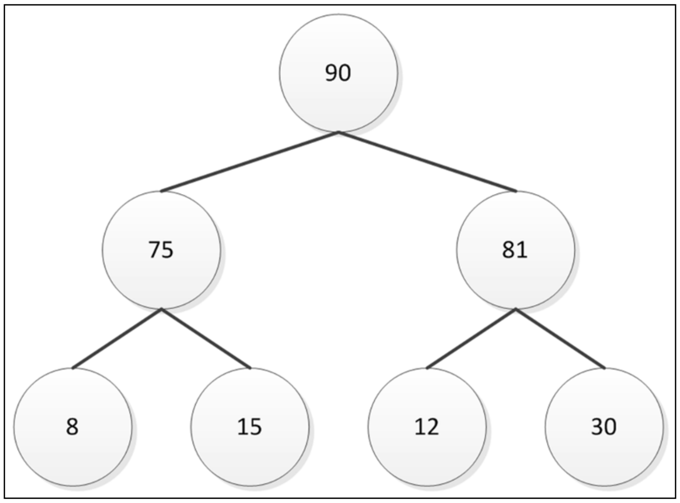


FIGURE 7-2: The arrangement of keys when using a binary heap.

Each level contains values that are less than the previous level, and the root contains the maximum key value for the tree. In addition, in this particular case, the lesser values appear on the left and the greater on the right (although this order isn't strictly enforced). The figure actually depicts a *binary max heap.* You can also create a *binary min heap* in which the root contains the lowest key value and each level builds to higher values, with the highest values appearing as part of the leaves.

REMEMBER

As previously noted, BST has some advantages over binary heap when used to perform a search. The following list provides some of the highlights of these advantages:

- Searching for an element requires `O(log n)` time when the tree is balanced, contrasted to `O(n)` time for a binary heap.
- Printing the elements in order requires only `O(log n)` time, contrasted to `O(n log n)` time for a binary heap.
- Finding the floor and ceiling requires `O(log n)` time.
- Locating Kth smallest/largest element requires `O(log n)` time when the tree is properly configured.

Whether these times are important depends on your application. BST tends to work best in situations in which you spend more time searching and less time building the tree. A binary heap tends to work best in dynamic situations in which keys change regularly. The binary heap also offers advantages, as described in the following list:

- Creating the required structures requires fewer resources because binary heaps rely on arrays, making them cache friendlier as well.
- Building a binary heap requires `O(n)` time, contrasted to BST, which requires `O(n log n)` time.
- Using pointers to implement the tree isn't necessary.
- Relying on binary heap variations (for example, the Fibonacci Heap) offers advantages such as increase and decrease key times of `O(1)` time (for performing tasks such as adding and removing items).

Building a binary search tree

You can build a BST using a variety of methods. Some people use a dictionary; others use custom code (see the articles at `https://interactivepython.org/courselib/static/pythonds/Trees/SearchTreeImplementation.html` and `https://code.activestate.com/recipes/577540-python-binary-search-tree/` for examples). However, most developers don't want to reinvent the wheel when it comes to BST. With this in mind, you need a package, such as `bintrees`, which provides all the required functionality to create and interact with BST using a minimum of code. To download and install `bintrees`, open a command prompt, type **pip install bintrees**, and press Enter. You see `bintrees` installed on your system. The documentation for this package appears at `https://pypi.org/project/bintrees/2.2.0/`.

You can use `bintrees` for all sorts of needs, but the example in this section looks specifically at a BST. In this case, the tree is unbalanced. The following code shows how to build and display a BST using `bintrees`. (You can find this code in the `A4D2E; 07; Search Techniques.ipynb` downloadable source code file; see the Introduction for details.)

```
from bintrees import BinaryTree

data = {3:'White', 2:'Red', 1:'Green', 5:'Orange',
        4:'Yellow', 7:'Purple', 0:'Magenta'}

tree = BinaryTree(data)
tree.update({6:'Teal'})

def displayKeyValue(key, value):
    print('Key: ', key, 'Value: ', value)

tree.foreach(displayKeyValue)
print('Item 3 contains: ', tree.get(3))
print('The maximum item is: ', tree.max_item())
```

You see this output when you run the code:

```
Key:  0 Value:  Magenta
Key:  1 Value:  Green
Key:  2 Value:  Red
Key:  3 Value:  White
Key:  4 Value:  Yellow
Key:  5 Value:  Orange
Key:  6 Value:  Teal
Key:  7 Value:  Purple
Item 3 contains:  White
The maximum item is:  (7, 'Purple')
```

To create a binary tree, you must supply key and value pairs. One way to perform this task is to create a dictionary as shown. After you create the tree, you can use the `update()` function to add new entries. The entries must include a key and value pair as shown.

TIP

This example uses a function to perform a task with the data in `tree`. In this case, the function merely prints the key and value pairs, but you could use the tree as input to an algorithm for analysis (among other tasks). The function, `displayKeyValue()`, acts as input to the `foreach()` function, which displays the key and value pairs as output. You also have access to myriad other features, such as using `get` to obtain a single item, or `max_item()` to obtain the maximum item stored in `tree`.

Performing specialized searches using a binary heap

As with BST, you have many ways to implement a binary heap. Writing one manually or using a dictionary does work well, but relying on a package makes things considerably faster and more reliable. The `heapq` package comes with Python, so you don't even need to install it. You can find the documentation for this package at `https://docs.python.org/3/library/heapq.html`. The following example shows how to build and search a binary heap using `heapq`:

```
import heapq

data = {3:'White', 2:'Red', 1:'Green', 5:'Orange',
        4:'Yellow', 7:'Purple', 0:'Magenta'}

heap = []
for key, value in data.items():
    heapq.heappush(heap, (key, value))
heapq.heappush(heap, (6, 'Teal'))
heap.sort()

for item in heap:
    print('Key: ', item[0], 'Value: ', item[1])
print('Item 3 contains: ', heap[3][1])
print('The maximum item is: ', heapq.nlargest(1, heap))
```

Running this code produces the following output:

```
Key:  0 Value:  Magenta
Key:  1 Value:  Green
Key:  2 Value:  Red
Key:  3 Value:  White
Key:  4 Value:  Yellow
Key:  5 Value:  Orange
Key:  6 Value:  Teal
Key:  7 Value:  Purple
Item 3 contains:  White
The maximum item is:  [(7, 'Purple')]
```

The example code performs the same tasks and provides the same output as the example in the previous section, except that it relies on a binary heap in this case. The dataset is the same as before. However, note the difference in the way you add the data to the heap using `heappush()`. In addition, after adding a new item, you must call `sort()` to ensure that the items appear in sorted order. Manipulating the data is much like manipulating a list, in contrast to the dictionary approach used for `bintrees`. Whichever approach you use, it pays to choose an option that works well with the application you want to create and provides the fastest possible search times for the tasks you perform.

Relying on Hashing

A major problem with most sort routines is that they sort all the data in a dataset. When the dataset is small, you hardly notice the amount of data that the sort routine attempts to move. However, as the dataset gets larger, the data movement becomes noticeable as you sit staring at the screen for hours on end. A way around this problem is to sort just the key information. A *key* is the identifying data for a particular data record. When you interact with an employee record, the employee name or number usually serves as a key for accessing all the other information you have about the employee. It's senseless to sort all the employee information when you really need only the keys sorted, which is what using hashing is all about. When working with these data structures, you gain a major speed advantage by sorting the smaller amount of data presented by the keys, rather than the records as a whole.

Putting everything into buckets

Until now, the search and sort routines in the book work by performing a series of comparisons until the algorithm finds the correct value. The act of performing comparisons slows the algorithms because each comparison takes some amount of time to complete.

A smarter way to perform the task involves predicting the location of a particular data item in the data structure (whatever that structure might be) before actually looking for it. That's what a *hash table* does — provides the means to create an index of keys that points to individual items in a data structure so that an algorithm can easily predict the location of the data. Placing keys into the index involves using a *hash function* that turns the key into a numeric value. The numeric value acts as an index into the hash table, and the hash table provides a pointer to the full record in the dataset. Because the hash function produces repeatable results, you can predict the location of the required data. In many cases, a hash table provides a search time of `O(1)`. In other words, you need only one comparison to find the data.

REMEMBER

A hash table contains a specific number of *slots* that you can view as buckets for holding data. Each slot can hold one data item. The number of filled slots when compared to the number of available slots is the *load factor*. When the load factor is high, the potential for *collisions* (where two data entries have the same hash value) becomes greater as well. The next section of the chapter discusses how to avoid collisions, but all you really need to know for now is that they can occur.

One of the more typical methods for calculating the hash value for an input is to obtain the modulus of the value divided by the number of slots. For example, if you want to store the number 54 into a hash table containing 15 slots, the hash value is 9. Consequently, the value 54 goes into slot 9 of the hash table when the slots are numbers from 0 through 14. A real hash table will contain a lot more slots, but 15 works fine for the purposes of this section. After placing the item into the hash slot, you can use the hash function a second time to find its location.

TIP

Theoretically, if you have a perfect hash function and an infinite number of slots, every value you present to the hash function will produce a unique value. In some cases, the hash calculation can become quite complex to ensure unique values most of the time. However, the more complex the hash calculation, the less benefit you receive from hashing, so keeping things simple is the best way to go.

Hashing can work with all sorts of data structures. However, for the purposes of demonstration, the following example uses a simple list to hold the original data and a second list to hold the resulting hash. (You can find this code in the `A4D2E; 07; Hashing.ipynb` downloadable source code file; see the Introduction for details.)

```
data = [22, 40, 102, 105, 23, 31, 6, 5]
hash_table = [None] * 15
tblLen = len(hash_table)

def hash_function(value, table_size):
    return value % table_size

for value in data:
    hash_table[hash_function(value, tblLen)] = value

print(hash_table)
```

Running this code produces the following hash values:

```
[105, 31, None, None, None, 5, 6, 22, 23, None, 40, None,
 102, None, None]
```

To find a particular value again, you just run it through `hash_function()`. For example, `print(hash_table[hash_function(102, tblLen)])` displays `102` as output after locating its entry in `hash_table`. Because the hash values are unique in this particular case, `hash_function()` can locate the needed data every time.

Avoiding collisions

A problem occurs when two data entries have the same hash value. If you simply write the value into the hash table, the second entry will overwrite the first, resulting in a loss of data. *Collisions*, the use of the same hash value by two values, require you to have some sort of strategy in mind for handling them. Of course, the best strategy is to avoid the collision in the first place.

One of the methods for avoiding collisions is to ensure that you have a large enough hash table. Keeping the load factor low is your first line of defense against having to become creative in the use of your hash table. However, even with a large table, you can't always avoid collisions. Sometimes the potential dataset is so large, but the used dataset so small, that avoiding the problem becomes impossible. For example, if you have a school with 400 children and rely on their social security number for identification, collisions are inevitable because no one is going to create a hash table with a billion entries for that many children. The waste of memory would be enormous. Consequently, a hash function may have to use more than just a simple modulus output to create the hash value. Here are some techniques you can use to avoid collisions:

- **Partial values:** When working with some types of information, part of that information repeats, which can create collisions. For example, the first three digits of a telephone number can repeat for a given area, so removing those numbers and using just the remaining four may help solve a collision problem.
- **Folding:** Creating a unique number might be as easy as dividing the original number into pieces, adding the pieces together, and using the result for the hash value. For example, using the telephone number 555-1234, the hash could begin by breaking it into pieces: 55 51 234, and then adding the result together to obtain 340 as the number used to generate the hash.
- **Mid-square:** The hash squares the value in question, uses some number of digits from the center of the resulting number, and discards the rest of those digits. For example, consider the value 120. When squared, you get 14,400. The hash could use 440 to generate the hash value and discard the 1 from the left and the 0 from the right.

Obviously, there are as many ways to generate the hash as someone has imagination to create them. Unfortunately, no amount of creativity is going to solve every collision problem, and collisions are still likely to occur. Therefore, you need another plan. When a collision does occur, you can use one of the following methods to address it:

- **Linear probing (a kind of open addressing):** The code stores the value in the next open slot by looking through the slots sequentially until it finds an open slot to use. The problem with this approach is that it assumes an open slot for each potential value, which may not be the case. In addition, open addressing means that the search slows considerably after the load factor increases. You can no longer find the needed value on the first comparison.
- **Rehashing:** The code hashes the hash value plus a constant. For example, consider the value 1,020 when working with a hash table containing 30 slots and a constant of 100. The hash value in this case is 22. However, if slot 22 already contains a value, rehashing `((22 + 100) % 30)` produces a new hash value of 2. In this case, you don't need to search the hash table sequentially for a value. When implemented correctly, a search might still include a low number of comparisons to find the target value.
- **Chaining:** Each slot in the hash table can hold multiple values. You can implement this approach by using a list within a list. Every time a collision occurs, the code simply appends the value to the list in the target slot. This approach offers the benefit of knowing that the hash will always produce the correct slot, but the list within that slot will still require some sort of sequential (or other) search to find the specific value.

Creating your own hash function

You may at times need to create custom hash functions in order to meet the needs of the algorithm you use or to improve its performance. Apart from cryptographic uses (which deserve a book alone), Chapter 12 presents common algorithms that leverage different hash functions, such as the Bloom Filter, the HyperLogLog, and the Count-Min Sketch, that leverage the properties of custom hash functions to extract information from huge amounts of data.

DISCOVERING UNEXPECTED USES OF HASHES

Apart from the algorithms detailed in this book, other important algorithms are based on hashes. For instance, the Locality-sensitive Hashing (LSH) algorithm relies on a large number of hash functions to stitch apparently separated information together. If you wonder how marketing companies and intelligence services put different chunks of information together based on names and addresses that aren't identical (for example, guessing that "Los Angels," "Los Angles," and "Los Angleles" all refer to Los Angeles) the answer is LSH. LSH chunks the information to check into parts and digests it using many hash functions, resulting in the production of a special hash result, which is an address for a bucket used to hold similar words. LSH is quite complex in its implementation, but check out this material from the Massachusetts Institute of Technology (MIT): `http://www.mit.edu/~andoni/LSH/`.

You can find many examples of different hash functions in the Python `hashlib` package. The `hashlib` package contains algorithms such as these:

- **Secure Hash Algorithms (SHA):** These algorithms include SHA1, SHA224, SHA256, SHA384, and SHA512. Released by the National Institute of Standards and Technology (NIST) as a U.S. Federal Information Processing Standard (FIPS), SHA algorithms provide support for security applications and protocols.
- **RSA's MD5 algorithm:** Initially designed for security applications, this hash turned into a popular way to checksum files. Checksums reduce files to a single number that enables you to determine whether the file was modified since hash creation (letting you determine whether the file you downloaded wasn't corrupted and hasn't been altered by a hacker). To ensure file integrity, just check whether the MD5 checksum of your copy corresponds to the original one communicated by the author of the file.

However, you can combine the output of multiple hash functions when working with complex applications that rely on a large dataset. Simply sum the results of the various outputs after having done a multiplication on one or more of them. The sum of two hash functions treated in this way retains the qualities of the original hash functions, even though the result is different and impossible to recover as the original elements of the sum. Using this approach means that you have a brand-new hash function to use as your secret hash recipe for algorithms and applications.

The following code snippet relies on the `hashlib` package and the `md5` and `sha1` hash algorithms. You just provide a number to use for the multiplication inside the hash sum. (Because numbers are infinite, you have a function that can produce infinite hashes.)

```
from hashlib import md5, sha1

def hash_f(element, i, length):
    """ Function to create many hash functions """
    h1 = int(md5(element.encode('ascii')).hexdigest(),16)
    h2 = int(sha1(element.encode('ascii')).hexdigest(),16)
    return (h1 + i*h2) % length
```

Here is some code to test the `hash_f()` function with its associated output:

```
print (hash_f("CAT", 1, 10**5))
64018

print (hash_f("CAT", 2, 10**5))
43738
```

REMEMBER

If you wonder where to find other uses of hash tables around you, check out Python's dictionaries. Dictionaries are, in fact, hash tables, even though they have a smart way to deal with collisions, and you won't lose your data because two hashed keys casually have the same result. The fact that the dictionary index uses a hash is also the reason for its speed in checking whether a key is present. Also, the use of a hash explains why you can't use every data type as a key. The key you choose must be something that Python can turn into a hash result. Lists, for instance, are unhashable because they are mutable; you can change them by adding or removing elements. Nevertheless, if you transform your list into a string, you can use it as a key for a dictionary in Python.

3

Exploring the World of Graphs

IN THIS PART . . .

Considering graphs and their uses

Interacting with graphs in various ways

Navigating graphs to meet specific needs

Searching and ranking web pages

IN THIS CHAPTER

» **Defining why networks are important**

» **Demonstrating graph drawing techniques**

» **Considering graph functionality**

» **Using numeric formats to represent graphs**

Chapter 8 Understanding Graph Basics

G*raphs* are structures that present a number of nodes (or vertexes) connected by a number of edges or arcs (depending on the representation). When you think about a graph, think about a structure like a map, where each location on the map is a node and the streets are the edges. This presentation differs from a tree where each path ends up in a leaf node. A tree could look like an organizational chart or a family hierarchy. Most important, tree structures actually do look like trees and have a definite start and end. This chapter begins by helping you understand the importance of networks, which are a kind of graph commonly used for all sorts of purposes.

REMEMBER

You can represent graphs in a variety of ways, most of them abstract. Unless you're really good at visualizing abstractions in your mind (most people aren't), you need to know how to draw a graph so that you can actually see it. People rely on their vision to understand how things work. The act of turning the numbers that represent a graph into a graphic visualization is *plotting.* Languages like Python excel at plotting because it's such an incredibly important feature. In fact, plotting is one of the reasons that this book uses Python rather than another language, such as C (which is good at performing a completely different set of tasks).

After you can visualize a graph, you need to know what to do with the graphic representation. This chapter starts you off by measuring graph functionality. You perform tasks like count the edges and vertexes to determine things like graph complexity. Seeing a graph also enables you to perform tasks like computing centrality with greater ease. You build on what you discover in this chapter in Chapter 9.

The numeric presentation of a graph is important, even if it makes understanding the graph hard. The plot is for you, but the computer doesn't really understand the plot (despite having drawn it for you). Think of the computer as more of an abstract thinker. With the need to present a graph in a form that the computer can manipulate, this chapter discusses three techniques for putting a graph into numeric format: matrixes, sparse representations, and lists. All these techniques have advantages and disadvantages, and you use them in specific ways in future chapters (beginning with Chapter 9). Other ways are also available to put a graph in numeric format, but these three methods will serve you well in communicating with the computer.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 08; Draw Graph.ipynb`, `A4D2E; 08; Graph Centrality.ipynb`, `A4D2E; 08; Graph Conversion.ipynb`, and `A4D2E; 08; Graph Measurements.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Explaining the Importance of Networks

A *network* is a kind of graph that associates names with the vertexes (nodes or points), edges (arcs or lines), or both. Associating names with the graph features reduces the level of abstraction and makes understanding the graph easier. The data that the graph models becomes real in the mind of the person viewing it, even though the graph truly is an abstraction of the real world put into a form that both humans and computers can understand in different ways. The following sections help you understand the importance of networks better so that you can see how their use in this book simplifies the task of discovering how algorithms work and how you can benefit from their use.

Considering the essence of a graph

Graphs appear as ordered pairs in the form G = (V, E), where G is the graph, V is a list of vertexes, and E is a list of edges that connect the vertexes. An edge is actually a numeric pair that expresses the two vertexes that it connects. Consequently, if you have two vertexes that represent cities, Houston (which equals 1) and Dallas (which equals 2), and you want to connect them with a road, you create an edge, `Highway`, that contains a pair of vertex references, `Highway = [Houston, Dallas]`. The graph would appear as `G = [(Houston, Dallas)]`, which simply says that there is a first vertex, Houston, with a connection to Dallas, the second vertex. Using the order of presentation of the vertexes, Houston is adjacent to Dallas; in other words, a car would leave Houston and enter Dallas.

Graphs come in several forms. An *undirected graph* (as shown in Figure 8-1) is one in which the order of the edge entries doesn't matter. A road map would represent an undirected graph in most cases because traffic can travel along the road in both directions.

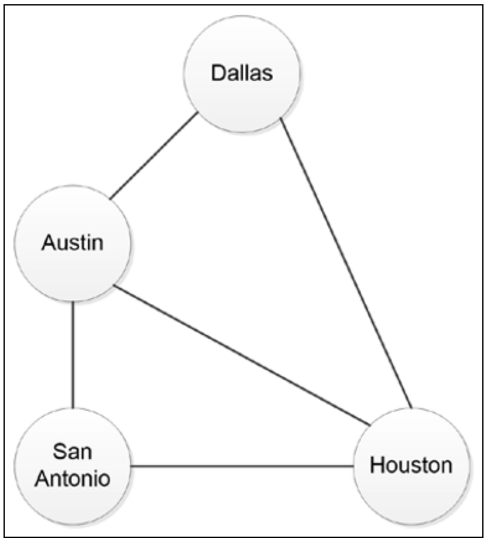


FIGURE 8-1: Presenting a simple undirected graph.

A *directed graph,* like the one shown in Figure 8-2, is one in which the order of the edge entries does matter because the flow is from the first entry to the second. In this case, most people call the edges *arcs* to differentiate them from undirected entries. Consider a graph representation of a traffic light sequence where Red equals 1, Yellow equals 2, and Green equals 3. The three arcs required to express the sequence are: `Go = [Red, Green]`, `Caution = [Green, Yellow]`, and `Stop = [Yellow, Red]`. The order of the entries is important because the flow from Go, to Caution, to Stop is important. Imagine the chaos that would result if the signal light chose to ignore the directed graph nature of the sequence.

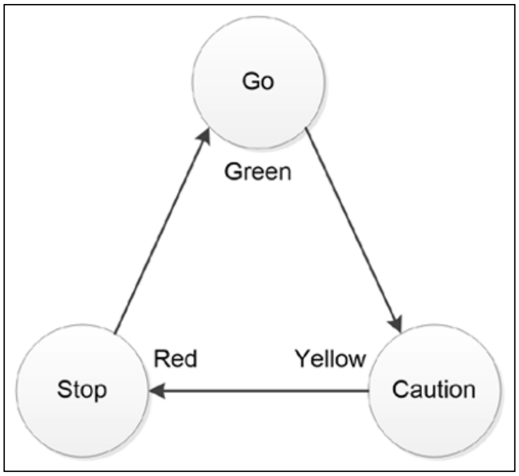


FIGURE 8-2: Creating the directed version of the same graph.

A third essential kind of graph that you must consider is the mixed graph. Think about the road map again. It isn't always true that traffic flows both ways on all roads. When creating some maps, you must consider the presence of one-way streets. In Figure 8-3, you see that you must go from Point D to get to Point A. However, you can go from Point E in any of four directions and from Points B, D, F, and H to get into Point E. Consequently, you need both undirected and directed subgraphs in the same graph, which is what you get with a *mixed graph.*

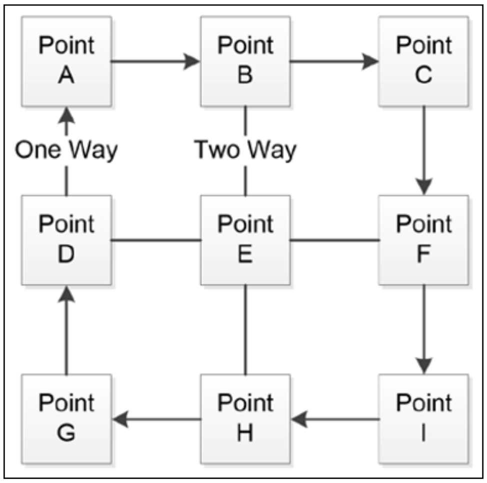


FIGURE 8-3: A mixed graph shows a mix of directed and undirected subgraphs.

Another graph type to consider is the *weighted graph* (shown in Figure 8-4), which has values assigned to each of the edges or arcs. Think about the road map again. People often want to know more than simply the direction to travel; they also want to know how far away the next destination is or how much time to allocate for getting there. A weighted graph provides this sort of information, and you use the weights in many different ways when performing calculations using graphs.

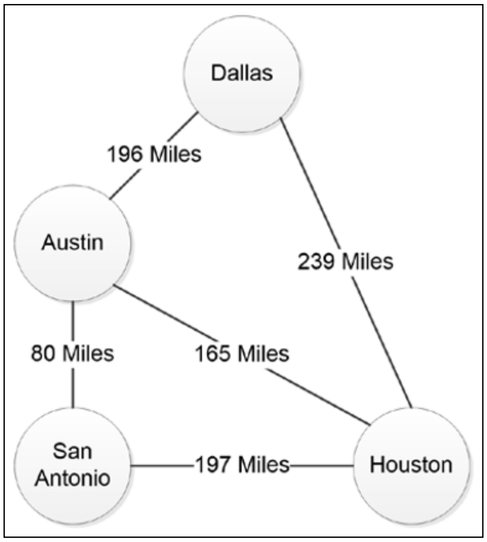


FIGURE 8-4: Using a weighted graph to make things more realistic.

Along with the weighted graph, you might also need a vertex-labeled graph when creating a road map. When working with a *vertex-labeled graph,* each vertex has a name associated with it. Consider looking at a road map where the mapmaker hasn't labeled the towns. Yes, you can see the towns, but you don't know which one is which without labels. You can find additional graph types described at `http://web.cecs.pdx.edu/~sheard/course/Cs163/Doc/Graphs.html`.

Finding graphs everywhere

Graphs might seem like one of those esoteric math features that you found boring in school, but graphs are actually quite exciting because you use them all the time without really thinking about it. Of course, it helps to know that you won't normally deal with the numbers behind the graphs. Think about a map. What you see is a graph, but you see it in graphic format, with cities, roads, and all sorts of other features. The thing is, when you see a map, you think about a map, not a graph (but your GPS does see a graph, which is why it can always suggest the shortest route to your destination). If you were to start looking around, you'd find many common items that are graphs but are called something else.

REMEMBER

Some graphs aren't visual in nature, but you still don't see them as graphs. For example, telephone menu systems are a form of directional graph. In fact, for all their seeming simplicity, telephone graphs are actually somewhat complex. They can include loops and all sorts of other interesting structures. Something you might try is to map the graph for a menu system at some point. You might be surprised at just how complex some of them can be.

Another form of menu system appears as part of applications. To perform tasks, most applications take you through a series of steps in a special kind of subapplication called a *wizard*. The use of wizards makes seemingly complex applications much easier to use, but to make the wizards work, the application developer must create a graph depicting the series of steps.

It may surprise you to find that even recipes in cookbooks are a kind of graph (and creating a pictorial representation of the relationships between ingredients can prove interesting). Each ingredient in the recipe is a node. The nodes connect using the edges created by the instructions for mixing the ingredients. Of course, a recipe is just a kind of chemistry, and chemical graphics show the relationship between elements in a molecule. (Yes, people actually are having this discussion; you can see one such thread at `https://stackoverflow.com/questions/7749073/representing-a-cooking-recipe-in-a-graph-database`, and you can even find an article about it at `https://medium.com/@condenastitaly/when-food-meets-ai-the-smart-recipe-project-eea259f53ed2`.)

REMEMBER

The point is that you see these graphs all the time, but you don't see them as graphs — you see them as something else, such as a recipe or a chemical formula. Graphs can represent many kinds of relationships between objects, implying an order sequence, time dependence, or causality.

Showing the social side of graphs

Graphs have social implications because they often reflect relationships between people in various settings. One of the most obvious uses of graphs is the organizational chart. Think about it: Each node is a different person in the organization, with edges connecting the nodes to show the various relationships between individuals. The same holds true for all sorts of graphs, such as those that show family history. However, in the first case, the graph is undirected because communication flows both ways between managers and subordinates (although the nature of the conversation differs based on direction). In the second case, the graph is directed because two parents bear children. The flow shows the direction of heredity from a founding member to the current children.

Social media benefits from the use of graphs as well. For example, a whole industry exists for analyzing the relationships between tweets on Twitter (`https://`

twittertoolsbook.com/10-awesome-twitter-analytics-visualization-tools/ talks about just some of these tools). The analysis relies on the use of graphs to discover the relationships between individual tweets.

However, you don't have to look at anything more arcane than email to see graphs used for social needs. The Enron corpus includes the 200,399 email messages of 158 senior executives, dumped onto the Internet by the Federal Energy Regulatory Commission (FERC). Scientists and scholars have used this corpus to create many social graphs to disclose how the seventh largest company in the United States needed to file bankruptcy in 2001 (see https://www.technologyreview.com/2013/07/02/177506/the-immortal-life-of-the-enron-e-mails/ and https://new.pythonforengineers.com/blog/analysing-the-enron-email-corpus/ to learn how this corpus has helped and is actually helping advance the analysis of complex graphs).

Even your computer has social graphs on it. No matter which email application you use, you can group emails in various ways, and these grouping methods normally rely on graphs to provide a structure. After all, trying to follow the flow of discussion without knowing which messages are responses to other messages is a lost cause. Yes, you could do it, but as the number of messages increases, the effort requires more and more time until it's wasted because of the time constraints most people have.

Understanding subgraphs

Relationships depicted by graphs can become quite complex. For example, when depicting city streets, most streets allow traffic in both directions, making an undirected graph perfect for representation purposes. However, some streets allow traffic in only one direction, which means that you need a directed graph in this case. The combination of two-way and one-way streets makes representation using a single graph type impossible (or at least inconvenient). Mixing undirected and directed graphs in a single graph means that you must create subgraphs to depict each graph type and then connect the subgraphs in a larger graph. Some graphs that contain subgraphs are so common that they have specific names, which is a mixed graph in this case.

Subgraphs are useful for other purposes as well. For example, you might want to analyze a loop within a graph, which means describing that loop as a subgraph. You don't need the entire graph, just the nodes and edges required to perform the analysis. All sorts of disciplines use this approach. Yes, developers use it to ensure that parts of an application work as expected, but city engineers also use it to understand the nature of traffic flow in a particularly busy section of the city. Medical professionals also use subgraphs to understand the flow of blood or other liquids between organs in the body. The organs are the nodes and the blood vessels are the edges. In fact, many of these graphs are weighted — it's essential to know how much blood is flowing, not just that it's flowing.

Complex graphs can also hide patterns that you need to know about. For example, the same cycle can appear in multiple parts of the graph, or you might see the same cycle within different graphs. By creating a subgraph from the cycle, you can easily perform comparisons within the same graph or between graphs to see how they compare. For example, a biologist might want to compare the cycle of mutation for one animal against the cycle of mutation for another animal. To make this comparison, the biologist would need to create the representation as a subgraph of the processes for the entire animal. (You can see an interesting view of this particular use of graphs at `https://www.sciencedirect.com/science/article/pii/S1359027896000569`.) The graph appears near the beginning of the article as Figure 1.

Defining How to Draw a Graph

A few people can visualize data directly in their minds. However, most people really do need a graphic presentation of the data to understand it. This point is made clear by the use of graphics in business presentations. You could tell others about last year's sales by presenting tables of numbers. After a while, most of your audience would nod off and you'd never get your point across. The reason is simple: The tables of numbers are precise and present a lot of information, but they don't do it in a way that people understand.

REMEMBER

Plotting the data and showing the sales numbers as a bar chart helps people see the relationships between the numbers with greater ease. If you want to point out that sales are increasing each year, a bar chart with bars of increasing length makes this point quickly. Interestingly enough, using the plot actually presents the data in a less accurate way. Trying to see that the company made $3,400,026.15 last year and $3,552,215.82 this year when looking at a bar chart is nearly impossible. Yes, the table would show this information, but people don't really need to know that level of detail — they simply need to see the annual increase — the contrast in earnings from year to year. However, your computer is interested in details, which is why plots are for humans and matrixes are for computers.

The following sections help you discover the wonders of plotting. You get a quick overview of how plots work with Python. (These principles appear in later chapters in a more detailed form.) The sections that follow offer a start so that you can more easily understand the plots presented later.

Distinguishing the key attributes

Before you can draw a graph, you need to know about graph attributes. As previously mentioned, graphs consist of nodes (or vertexes) and either edges (for undirected graphs) or arcs (for directed graphs). Any graph that you want to draw will contain these elements. However, how you represent these elements depends partly on the package you choose to use. For the sake of simplicity, the book relies on a combination of two packages:

- **NetworkX (**`https://networkx.org/`**):** Contains code for drawing graphs.
- **matplotlib (**`http://matplotlib.org/`**):** Provides access to all sorts of drawing routines, some of which can display graphs created by NetworkX.

REMEMBER

To use packages in Python, you must import them. When you need to use external packages, you must add special code, such as the following lines of code that provide access to `matplotlib` and `networkx`. (You can find this code in the `A4D2E; 08; Draw Graph.ipynb` downloadable source code file; see the Introduction for details.)

```
import networkx as nx
import matplotlib.pyplot as plt
```

Now that you have access to the packages, you create a graph. In this case, a graph is a sort of container that holds the key attributes that define the graph. Creating a container lets you draw the graph so that you can see it later. The following code creates a NetworkX `Graph` object:

```
AGraph = nx.Graph()
```

Adding the key attributes to `AGraph` comes next. You must add both nodes and edges using the following code:

```
Nodes = range(1,5)
Edges = [(1,2), (2,3), (3,4), (4,5), (1,3), (1,5)]
```

As previously mentioned, `Edges` describe connections between `Nodes`. In this case, `Nodes` contains values from 1 through 5, so `Edges` contains connections between those values.

WARNING

NETWORKX API

Sometimes a developer makes a major, code-breaking change to an Application Programming Interface (API) to make a product better. This book uses NetworkX extensively to reduce the work required to create graphs. However, the version of NetworkX used in this book is a newer version that is incompatible with older code. In order to work with the examples in this book, you must have NetworkX 2.5 or above installed. The examples were tested using NetworkX 2.6.2, but any version 2.5 or above will work. To verify your NetworkX version, use either the `pip list` or the `conda list networkx` command. You find NetworkX used in Chapters 8, 9, 10, 11, and 16.

Of course, the `Nodes` and `Edges` are just sitting there now and won't appear as part of `AGraph`. You must put them into the container to see them. Use the following code to add the `Nodes` and `Edges` to `AGraph`.

```
AGraph.add_nodes_from(Nodes)
AGraph.add_edges_from(Edges)
```

The NetworkX package contains all sorts of functions you can use to interact with individual nodes and edges, but the approach shown here is the fastest way to do things. Even so, you might find that you want to add additional edges later. For example, you might want to add an edge between 2 and 4, in which case you would call the `AGraph.add_edge(2, 4)` function.

Drawing the graph

You can interact in all sorts of ways with the `AGraph` container object that you create in the previous section, but many of those ways to interact are abstract and not very satisfying if you're a visually oriented person. Sometimes it's just nice to see what an object contains by looking at it. The following code displays the graph contained in `AGraph`:

```
draw_params = {
    'with_labels':True,
    'node_color':'skyblue',
    'node_size':700, 'width':2,
    'font_size':14,
    'pos': nx.layout.spring_layout(AGraph, seed=1)}

nx.draw(AGraph, **draw_params)
plt.show()
```

The drawing process begins by creating `draw_params`, which describes how to draw the graph. This example tells NetworkX to use labels, to set the node color to sky blue, and various other features.

The `draw()` function provides various arguments that you can use to dress up the display. However, you can supply these arguments separately using `draw_params`, as shown in the preceding code. Figure 8-5 shows the graph contained in `AGraph`.

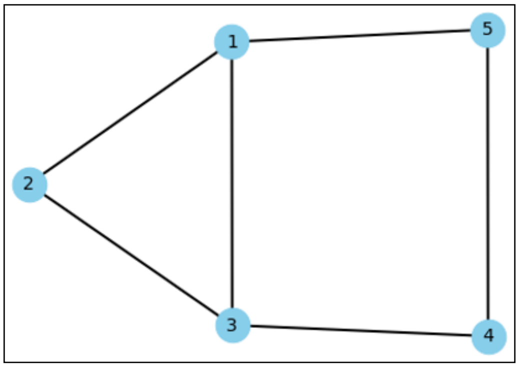


FIGURE 8-5: Seeing what a graph contains makes it easier to understand.

Measuring Graph Functionality

After you can visualize and understand a graph, you need to consider the question of which parts of the graph are important. After all, you don't want to spend your time performing analysis on data that doesn't really matter in the grand scheme of things. Think about someone who is analyzing traffic flow to improve the street system. The intersections represent vertexes and the streets represent edges along which the traffic flows. By knowing how the traffic flows, that is, which vertexes and edges see the most traffic, you can start thinking about which roads to widen and which need more repair because more traffic uses them.

However, just looking at individual streets isn't enough. A new skyscraper may bring with it a lot of traffic that affects an entire area. The skyscraper represents a central point around which traffic flow becomes more important. The most important vertexes are those central to the new skyscraper. Calculating *centrality,* the most important vertexes in a graph, can help you understand which parts of the graph require more attention. The following sections discuss the basic issues you must consider when measuring *graph functionality,* which is the capability of the graph to model a specific problem.

Counting edges and vertexes

As graphs become more complex, they convey more information, but they also become harder to understand and manipulate. The number of edges and vertexes in a graph determines graph complexity. However, you use the combination of edges and vertexes to tell the full story. For example, you can have a node that isn't connected to the other nodes in any way. It's legal to create such a node in a graph to represent a value that lacks connections to the others. Using the following code, you can easily determine that node 6 has no connections to the others because it lacks any edge information. (You can find this code in the `A4D2E; 08; Graph Measurements.ipynb` downloadable source code file; see the Introduction for details on how to find this file.)

```
import networkx as nx
import matplotlib.pyplot as plt

AGraph = nx.Graph()

Nodes = range(1,5)
Edges = [(1,2), (2,3), (3,4), (4,5), (1,3), (1,5)]

AGraph.add_nodes_from(Nodes)
AGraph.add_edges_from(Edges)

AGraph.add_node(6)
sorted(nx.connected_components(AGraph))
```

When you run this code, you see this output:

```
[{1, 2, 3, 4, 5}, {6}]
```

The output from this code shows that nodes 1 through 5 are connected and that node 6 lacks a connection. You can remedy this situation by adding another edge; use the following code and then check again:

```
AGraph.add_edge(1,6)
sorted(nx.connected_components(AGraph))
```

This time you see the desired output of

```
[{1, 2, 3, 4, 5, 6}]
```

The output now shows that every one of the nodes connects to at least one other node. However, you don't know which nodes have the most connections. The count of edges to a particular node is the *degree.* The higher the degree, the more complex the node becomes. By knowing the degree, you can develop an idea of which nodes are most important. The following code shows how to obtain the degree for the example graph:

```
print([val for (node, val) in AGraph.degree()])
```

When you run this code, you see the degrees for each node in order:

```
[4, 2, 3, 2, 2, 1]
```

The degree values appear in node order, so node 1 has four connections and node 6 has only one connection. Node 1 is therefore the most important, followed by node 3, which has three connections.

When modeling real-world data, such as the tweets about a particular topic, the nodes also tend to cluster. You might think of this tendency as a kind of trending — what people feel is important now. The fancy math term for this tendency is *clustering,* and measuring this tendency helps you understand which group of nodes is most important in a graph. Here is the code you use to measure clustering for the example graph:

```
nx.clustering(AGraph)
```

The output of this measurement proves interesting, as shown here:

```
{1: 0.16666666666666666, 2: 1.0, 3: 0.3333333333333333,
 4: 0.0, 5: 0.0, 6: 0.0}
```

The output shows that the nodes are most likely to cluster around node 2 even though node 1 has the highest degree. That's because both nodes 1 and 3 have high degrees and node 2 is between them.

REMEMBER

Clustering graphs aids in understanding data. The technique helps to show that some nodes in the graph are better connected and some nodes risk isolation. When you understand how elements connect in a graph, you can determine how to strengthen its structure or, on the contrary, destroy it. During the Cold war, military scientists from both the United States and the Soviet bloc studied graph clustering to better understand how to disrupt the other side's supply chain in case of a conflict.

USE OF WHITESPACE IN OUTPUT

The output for this example appears on two lines in the book, even though it appears on just one line in Jupyter Notebook. The addition of whitespace helps the output appear in a readable size on the page — it doesn't affect the actual information. Other examples in the book also show output on multiple lines, even when it appears on a single line in Jupyter Notebook.

Computing centrality

Centrality comes in a number of different forms because importance often depends on different factors. The important elements of a graph when analyzing tweets will differ from the important elements when analyzing traffic flow. Fortunately, NetworkX provides you with a number of methods for calculating centrality. For example, you can calculate centrality based on node degrees. The following code uses the modified graph from the previous section of the chapter. (You can find this code in the `A4D2E; 08; Graph Centrality.ipynb` downloadable source code file; see the Introduction for details on where to find this file.)

```
import networkx as nx
import matplotlib.pyplot as plt

AGraph = nx.Graph()

Nodes = range(1,6)
Edges = [(1,2), (2,3), (3,4), (4,5),
         (1,3), (1,5), (1,6)]

AGraph.add_nodes_from(Nodes)
AGraph.add_edges_from(Edges)

nx.degree_centrality(AGraph)
```

When you run this code, you see the following output:

```
{1: 0.8, 2: 0.4, 3: 0.6000000000000001, 4: 0.4, 5: 0.4,
 6: 0.2}
```

The values differ by the number of connections for each node. Because node 1 has four connections (it has the highest degree), it also has the highest centrality. You can see how this works by plotting the graph using this code:

```
draw_params = {
    'with_labels':True,
    'node_color':'skyblue',
    'node_size':700, 'width':2,
    'font_size':14,
    'pos': nx.layout.spring_layout(AGraph, seed=5)}

nx.draw(AGraph, **draw_params)
```

This code produces the output shown in Figure 8-6.

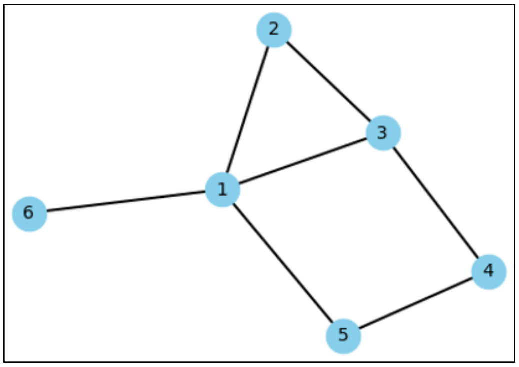


FIGURE 8-6: Plotting the graph can help you see degree centrality with greater ease.

Node 1 is indeed in the center of the graph with the most connections. The node 1 degree ensures that it's the most important based on the number of connections. When working with directed graphs, you can also use the `in_degree_centrality()` and `out_degree_centrality()` functions to determine degree centrality based on connection type rather than just the number of connections.

When working with traffic analysis, you might need to determine which locations are central based on their distance to other nodes. Even though a shopping center in the suburbs may have all sorts of connections to it, the fact that it is in the suburbs may reduce its impact on traffic. Yet, a supermarket in the center of the city with few connections might have a great impact on traffic because it's close to so many other nodes. To see how this works, add another node, 7, that is disconnected to the graph. The centrality of that node is infinite because no other node can reach it. The following code shows how to calculate the closeness centrality for the various nodes in the example graph:

```
AGraph.add_node(7)
nx.closeness_centrality(AGraph)
```

When you run this code, you see the following output:

```
{1: 0.6944444444444445,
 2: 0.5208333333333334,
 3: 0.5952380952380952,
 4: 0.462962962962963,
 5: 0.5208333333333334,
 6: 0.4166666666666667,
 7: 0.0}
```

The output shows the centrality of each node in the graph based on its closeness to every other node. Notice that node 7 has a value of 0, which means that it's an infinite distance to every other node. On the other hand, node 1 has a high value because it's close to every node to which it has a connection. By calculating the closeness centrality, you can determine which nodes are the most important based on their location.

Another form of distance centrality is betweenness. Say that you're running a company that transfers goods throughout the city. You'd like to know which nodes have the greatest effect on these transfers. Perhaps you can route some traffic around this node to make your operation more efficient. When calculating betweenness centrality, you determine the node that has the highest number of short paths coming to it. Here's the code used to perform this calculation (with the disconnected node 7 still in place):

```
nx.betweenness_centrality(AGraph)
```

The output of this check is

```
{1: 0.36666666666666664,
 2: 0.0,
 3: 0.13333333333333333,
 4: 0.03333333333333333,
 5: 0.06666666666666667,
 6: 0.0,
 7: 0.0}
```

As you might expect, node 7 has no effect on transfer between other nodes because it has no connections to the other nodes. Likewise, because node 6 is a leaf node with only one connection to another node, it has no effect on transfers. Look again at Figure 8-6. The subgraph consisting of nodes 1, 3, 4, and 5 have the greatest effect on the transfer of items in this case. No connection exists between nodes 1 and 4, so nodes 3 and 5 act as intermediaries. In this case, node 2 acts like a leaf node.

TIP

NetworkX gives you a number of other centrality functions. You can find a complete list of these functions at `https://networkx.org/documentation/stable/reference/algorithms/centrality.html`. The important consideration is to determine how you want to calculate importance. Considering centrality in light of the kind of importance you want to attach to the vertexes and edges in a graph is essential.

Putting a Graph in Numeric Format

Precision is an important part of using algorithms. Even though too much precision hides the overall pictures from humans, computers thrive on detail. Often, the more detail you can provide, the better the results you receive. However, the form of that detail is important. To use certain algorithms, the data you provide must appear in certain forms or the result you receive won't make sense (it will contain errors or have other issues).

Fortunately, NetworkX supplies a number of functions to convert your graph into forms that other packages and environments can use. These functions appear at `https://networkx.org/documentation/stable/reference/convert.html`. The following sections show how to present graph data as a NumPy (`https://numpy.org/`) matrix, SciPy (`https://scipy.org/`) sparse representation, and a standard Python list. You use these representations as the book progresses to work with the various algorithms. (The code in the following sections appears in the `A4D2E; 08; Graph Conversion.ipynb` file and relies on the graph you create in the "Counting edges and vertexes" section, earlier in this chapter.)

Adding a graph to a matrix

Using NetworkX, you can easily move your graph to a NumPy matrix and back again as needed to perform various tasks. You use NumPy to perform all sorts of data manipulation tasks. By analyzing the data in a graph, you might see patterns that wouldn't ordinarily be visible. Here's the code used to convert the graph into a matrix that NumPy can understand:

```
import networkx as nx
import matplotlib.pyplot as plt

AGraph = nx.Graph()
```

```
Nodes = range(1,6)
Edges = [(1,2), (2,3), (3,4), (4,5),
         (1,3), (1,5), (1,6)]

AGraph.add_nodes_from(Nodes)
AGraph.add_edges_from(Edges)

nx.to_numpy_matrix(AGraph)
```

The output of this code is the following matrix:

```
matrix([[ 0.,  1.,  1.,  0.,  1.,  1.],
        [ 1.,  0.,  1.,  0.,  0.,  0.],
        [ 1.,  1.,  0.,  1.,  0.,  0.],
        [ 0.,  0.,  1.,  0.,  1.,  0.],
        [ 1.,  0.,  0.,  1.,  0.,  0.],
        [ 1.,  0.,  0.,  0.,  0.,  0.]])
```

The resulting rows and columns show where connections exist. For example, there is no connection between node 1 and itself, so row 1, column 1, has a 0 in it. However, there is a connection between node 1 and node 2, so you see a 1 in row 1, column 2, and row 2, column 1 (which means that the connection goes both ways as an undirected connection).

The size of this matrix is affected by the number of nodes (the matrix has as many rows and columns as nodes), and when it grows huge, it has many nodes to represent because the total number of cells is the square of the number of nodes. For instance, you can't represent the Internet using such a matrix because a conservative estimate calculates that at 10^10 websites, you'd need a matrix with 10^20 cells to store its structure, something impossible with the present computing capacity.

In addition, the number of nodes affects its content. If *n* is number of nodes, you find a minimum of 0 ones and a maximum of n^2 ones. The fact that the number of ones is few or large makes the graph dense or sparse, and that's relevant because if the connections between nodes are few, such as in the case of websites, more efficient solutions exist for storing graph data.

Using sparse representations

The SciPy package also performs various math, scientific, and engineering tasks. When using this package, you can rely on a sparse matrix to hold the data. A sparse matrix is one in which only the actual connections appear in the matrix; all other entries don't exist. Using a sparse matrix saves resources because the memory requirements for a sparse matrix are small. Here is the code you use to create a SciPy sparse matrix from a NetworkX graph:

```
print(nx.to_scipy_sparse_matrix(AGraph))
```

This is the output you can expect to see from this code:

```
  (0, 1)	1
  (0, 2)	1
  (0, 4)	1
  (0, 5)	1
  (1, 0)	1
  (1, 2)	1
  (2, 0)	1
  (2, 1)	1
  (2, 3)	1
  (3, 2)	1
  (3, 4)	1
  (4, 0)	1
  (4, 3)	1
  (5, 0)	1
```

As you can see, the entries show the various edge coordinates. Each active coordinate has a 1 associated with it. The coordinates are 0 based. This means that `(0, 1)` actually refers to a connection between nodes 1 and 2.

Using a list to hold a graph

Depending on your needs, you might find that you also require the ability to create a dictionary of lists. Many developers use this approach to create code that performs various analysis tasks on graphs. You can see one such example at `https://www.geeksforgeeks.org/generate-graph-using-dictionary-python/`. The following code shows how to create a dictionary of lists for the example graph:

```
nx.to_dict_of_lists(AGraph)
```

Here is the dictionary of lists form of the graph (note that the order of the numbers you see might vary):

```
{1: [2, 3, 5, 6], 2: [1, 3], 3: [1, 2, 4], 4: [3, 5],
 5: [1, 4], 6: [1]}
```

Notice that each node represents a dictionary entry, followed by a list of the nodes to which it connects. For example, node 1 connects to nodes 2, 3, 5, and 6.

IN THIS CHAPTER

» **Working with graphs**

» **Performing sorting tasks**

» **Reducing the tree size**

» **Locating the shortest route between two points**

Chapter 9 Reconnecting the Dots

Global Positioning System (GPS) setups work because you can use algorithms to traverse the points on the map and the streets that connect them. In fact, by the time you finish this chapter, you understand the basis used to make a GPS navigator work (but not necessarily the mechanics of making it happen). Of course, the fundamental requirement for using a graph to create a GPS navigator is the capability to search for connections between points on the map, as discussed in the first section of the chapter.

To make sense of a graph, you need to sort the nodes, as described in the second section of the chapter, to create a specific organization. Without organization, making any sort of decision becomes impossible. An algorithm might end up going in circles or giving inconvenient output.

When you view a map, you don't look at the information in the lower-right corner when you actually need to work with locations and roads in the upper-left corner. A computer doesn't know that it needs to look in a specific place until you tell it to do so. To focus attention in a specific location, you need to reduce the graph size, as described in the third section of the chapter.

After the problem is simplified, an algorithm can find the shortest route between two points, as described in the fourth section of the chapter. After all, you don't want to spend any more time in traffic than necessary, fighting your way from home to your destination (and back again). The concept of finding the shortest route is a bit more convoluted than you might think, so the fourth section looks at some of the specific requirements for performing routing tasks in detail.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 09; Graph Traversing.ipynb`, `A4D2E; 09; Minimum Spanning Tree.ipynb`, and `A4D2E; 09; Shortest Path.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Traversing a Graph Efficiently

Traversing a graph means to search (visit) each vertex (node) in a specific order. The process of visiting a vertex can include both reading and updating it. As you traverse a graph, an unvisited vertex is *undiscovered.* After a visit, the vertex becomes *discovered* (because you just visited it) or *processed* (because the algorithm tried all the edges departing from it). The order of the search determines the kind of search performed, and many algorithms are available to perform this task. The following sections discuss two such algorithms.

CONSIDERING REDUNDANCY

When traversing a tree, every path ends in a leaf node so that you know that you have reached the end of that path. However, when working with a graph, the nodes interconnect such that you might have to traverse some nodes more than once to explore the entire graph. As the graph becomes denser, the possibility of visiting the same node more than once increases. Dense graphs can greatly increase both computational and storage requirements.

To reduce the negative effects of visiting a node more than once, it's common to mark each visited node in some manner to show that the algorithm has visited it. When the algorithm detects that it has visited a particular node, it can simply skip that node and move onto the next node. Marking visited nodes decreases the performance penalties inherent in redundancy.

Marking visited nodes also enables verification that the search is complete. Otherwise, an algorithm can end up in a loop and continue to make the rounds through the graph indefinitely.

Creating the graph

To see how traversing a graph might work, you need a graph. The examples in this section rely on a common graph so that you can see how the two techniques work. The following code shows the adjacency list found at the end of Chapter 8.

```
graph = {'A': ['B', 'C'],
         'B': ['A', 'C', 'D'],
         'C': ['A', 'B', 'D', 'E'],
         'D': ['B', 'C', 'E', 'F'],
         'E': ['C', 'D', 'F'],
         'F': ['D', 'E']}
```

The graph features a bidirectional path that goes from A, B, D, and F on one side (starting at node A) and A, C, E, and F along the second side (again, starting at node A). There are also connections (that act as possible shortcuts) going from B to C, from C to D, and from D to E. Using the NetworkX package presented in Chapter 8 lets you display the adjacency as a picture so that you can see how the vertexes and edges appear (see Figure 9-1) by using the following code:

```
import networkx as nx
import matplotlib.pyplot as plt

Graph = nx.Graph()
for node in graph:
    Graph.add_nodes_from(node)
    for edge in graph[node]:
        Graph.add_edge(node,edge)

pos = { 'A': [0.00, 0.50], 'B': [0.25, 0.75],
        'C': [0.25, 0.25], 'D': [0.75, 0.75],
        'E': [0.75, 0.25], 'F': [1.00, 0.50]}
draw_params = {'with_labels':True,
               'node_color':'skyblue',
               'node_size':700, 'width':2,
               'font_size':14}

nx.draw(Graph, pos, **draw_params)
plt.show()
```

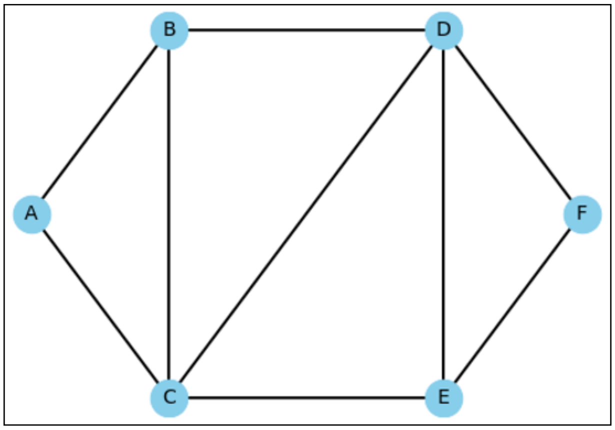


FIGURE 9-1: Representing the example graph by NetworkX.

Applying breadth-first search

A breadth-first search (BFS) begins at a start node and explores every node that attaches to the root. It then searches the next level — exploring each level in turn until it reaches the end. Consequently, in the example graph, the search explores from A to B and C before it moves on to explore D. BFS explores the graph in a systematic way, exploring vertexes all around the starting vertex in a circular fashion. It begins by visiting all the vertexes a single step from the starting vertex; it then moves two steps out, and then three steps out, and so on. The following code demonstrates how to perform a breadth-first search:

```
def bfs(graph, start):
    queue = [start]
    queued = [start]
    path = list()
    while queue:
        print('Queue is: %s' % queue)
        vertex = queue.pop(0)
        print('Processing %s' % vertex)
        for candidate in graph[vertex]:
            if candidate not in queued:
                queued.append(candidate)
                queue.append(candidate)
                path.append(vertex + '>' + candidate)
                print('Adding %s to the queue'
                       % candidate)
    return path

steps = bfs(graph, 'A')
print('\nBFS:', steps)
```

Here's the output that's printed when executing the code snippet:

```
Queue is: ['A']
Processing A
Adding B to the queue
Adding C to the queue
Queue is: ['B', 'C']
Processing B
Adding D to the queue
Queue is: ['C', 'D']
Processing C
Adding E to the queue
Queue is: ['D', 'E']
Processing D
Adding F to the queue
Queue is: ['E', 'F']
Processing E
Queue is: ['F']
Processing F

BFS: ['A>B', 'A>C', 'B>D', 'C>E', 'D>F']
```

REMEMBER

The output shows how the algorithm searches. It's in the order that you expect — one level at a time. The biggest advantage of using BFS is that it's guaranteed to return a shortest path between two points as the first output when used to find paths.

TIP

The example code uses a simple list as a queue. As described in the "Using queues" section of Chapter 6, a queue is a first in/first out (FIFO) data structure that works like a line at a bank, where the first item put into the queue is also the first item that comes out. Python provides an even better data structure called a deque (pronounced *deck*) that you can use as both a queue and a stack. You can discover more about the `deque` function at `https://pymotw.com/2/collections/deque.html`.

Applying depth-first search

In addition to BFS, you can use a depth-first search (DFS) to discover the vertexes in a graph. When performing a DFS, the algorithm begins at a start node and then explores every node from that point down a single path to the end. It then backtracks and begins exploring the paths not taken in the current search path until it reaches the start node again. At that point, if other paths to take from the start node are available, the algorithm chooses one and begins the same search again. The idea is to explore each path completely before exploring any other path. To make this search technique work, the algorithm must mark each vertex it visits. In this way, it knows which vertexes require a visit and can determine which path to take next. Using BFS or DFS can make a difference according to the way in which you need to traverse a graph. From a programming point of view, the difference between the two algorithms is how each one stores the vertexes to explore the following:

- **A queue for BFS,** a list that works according to the FIFO principle. Newly discovered vertexes don't wait long for processing.
- **A stack for DFS,** a list that works according to the last in/first out (LIFO) principle.

The following code shows how to create a DFS:

```
def dfs(graph, start):
    stack = [start]
    parents = {start: start}
    path = list()
    while stack:
        print('Stack is: %s' % stack)
        vertex = stack.pop(-1)
        print('Processing %s' % vertex)
        for candidate in graph[vertex]:
            if candidate not in parents:
                parents[candidate] = vertex
                stack.append(candidate)
                print('Adding %s to the stack'
                       % candidate)
        path.append(parents[vertex] + '>' + vertex)
    return path[1:]

steps = dfs(graph, 'A')
print('\nDFS:', steps)
```

Here is the output that's printed when executing the code snippet:

```
Stack is: ['A']
Processing A
Adding B to the stack
Adding C to the stack
Stack is: ['B', 'C']
Processing C
Adding D to the stack
Adding E to the stack
Stack is: ['B', 'D', 'E']
Processing E
Adding F to the stack
Stack is: ['B', 'D', 'F']
Processing F
Stack is: ['B', 'D']
Processing D
Stack is: ['B']
Processing B

DFS: ['A>C', 'C>E', 'E>F', 'C>D', 'A>B']
```

The last line of output shows the actual search order. Note that the search begins at the start node, as expected, but then follows down the left side of the graph around to the beginning. The final step is to search the only branch off the loop that creates the graph in this case, which is D.

Note that the output is not the same as for the BFS. The processing route begins with node A and moves to the opposite side of the graph, to node F. The code then retraces back to look for overlooked paths. This behavior depends on the use of a stack in place of a queue. Reliance on a stack means that you could also implement this kind of search using recursion. The use of recursion would make the algorithm faster, so you could obtain results faster than when using a BFS. The trade-off is that you use more memory when using recursion.

Determining which application to use

The choice between BFS and DFS depends on how you plan to apply the output from the search. Developers often employ BFS to locate the shortest route between two points as quickly as possible. This means that you commonly find BFS used in applications such as GPS, where finding the shortest route is paramount. For the purposes of this book, you also see BFS used for spanning tree, shortest path, and many other minimization algorithms.

A DFS finds an entire path before exploring any other path. You use it when you need to search in detail, rather than generally. You often see DFS used in games, where finding a complete path is important. It's also an optimal approach to perform tasks such as finding a solution to a maze.

REMEMBER

Decide between BFS and DFS based on the limitations of each technique. BFS needs lots of memory because it systematically stores all the paths before finding a solution. DFS needs less memory, but you have no guarantee that it'll find the shortest and most direct solution.

Sorting the Graph Elements

The ability to search graphs efficiently relies on sorting. After all, imagine going to a library and finding the books placed in any order the library felt like putting them in on the shelves. Locating a single book would take hours. A library works because the individual books appear in specific locations that make them easy to find.

Libraries also exhibit another property that's important when working with certain kinds of graphs. When performing a book search, you begin with a specific category, and then a row of books, and then a shelf in that row, and finally the book. You move from less specific to more specific when performing the search, which means that you don't revisit the previous levels. Therefore, you don't end up in odd parts of the library that have nothing to do with the topic at hand.

The following sections review *Directed Acyclic Graphs (DAGs)*, which are finite directed graphs that don't have any loops in them. In other words, you start from a particular location and follow a specific route to an ending location without ever going back to the starting location. This kind of graph has all sorts of practical uses, such as schedules, with each vertex representing a particular milestone.

GRAPHS WITH LOOPS

Sometimes you need to express a process in such a manner that a set of steps repeats. For example, when washing your car, you rinse, soap down, and then rinse again. However, if you find a dirty spot, an area that the soap didn't clean the first time, you soap it again and rinse it again to verify that the spot is gone. That's what a loop does; it creates a situation in which a set of steps repeats in one of two ways:

- **Meets a specific condition:** The spot on the car is gone.
- **Performs a specific number of times:** This is the maximum number of repetitions you perform to prevent damage to the car's paint job.

Working on Directed Acyclic Graphs (DAGs)

Directed acyclic graphs (DAGs) are among the most important kinds of graphs because they see so many practical uses. The basic principles of DAGs are that they

- Follow a particular order so that you can't get from one vertex to another and back to the beginning vertex using just any route.
- Provide a specific path from one vertex to another (even if multiple paths exist) so that you can create a predictable set of routes.

You see DAGs used for many organizational needs. For example, a family tree is an example of a DAG. Even when the activity doesn't follow a chronological or other overriding order, the DAG enables you to create predictable routes, which makes DAGs easier to process than many other kinds of graphs you work with.

However, DAGs can use optional routes. Imagine that you're building a burger. The menu system starts with a bun bottom. You can optionally add condiments to the bun bottom, or you can move directly to the burger on the bun. The route always ends up with a burger, but you have multiple paths for getting to the burger. After you have the burger in place, you can choose to add cheese or bacon before adding the bun top. You take a specific path, but each path can connect to the next level in several ways.

Relying on topological sorting

An important element of DAGs is that you can represent a myriad of activities using them. However, some activities require that you approach tasks in a specific order. This is where topological sorting comes into play. *Topological sorting* orders all the vertexes of a graph on a line with the direct edges pointing from left to right. Arranged in such a fashion, the code can easily traverse the graph and process the vertexes one after the other, in order.

When you use topological sorting, you organize the graph so that every graph vertex leads to a later vertex in the sequence. For example, when creating a schedule for building a skyscraper, you don't start at the top and work your way down. You begin with the foundation and work your way up. Each floor can represent a milestone. When you complete the second floor, you don't go to the third and then redo the second floor. Instead, you move on from the third floor to the fourth floor, and so on. Any sort of scheduling that requires you to move from a specific starting point to a specific ending point can rely on a DAG with topological sorting.

Topological sorting can help you determine that your graph has no cycles (because otherwise, you can't order the edges connecting the vertexes from left to right; at least one node will refer to a previous node). In addition, topological sorting also proves helpful in algorithms that process complex graphs because it shows the best order for processing them.

You can obtain topological sorting using the DFS traversal algorithm. Simply note the processing order of the vertexes by the algorithm. In the previous example, the output appears in this order: A, C, E, F, D, and B. Follow the sequence in Figure 9-1 and you notice that the topological sorting follows the edges on the external perimeter of graph. It then makes a complete tour: After reaching the last node of the topological sort, you're just a step away from A, the start of the sequence.

Reducing to a Minimum Spanning Tree

Many problems that algorithms solve rely on defining a minimum of resources to use, such as defining an economical way to reach all the points on a map. This problem was paramount in the late nineteenth and early twentieth centuries when railway and electricity networks started appearing in many countries, revolutionizing transportation and ways of living. Using private companies to build such networks was expensive (it took a lot of time and workers). Using less material and a smaller workforce offered savings by reducing redundant connections.

REMEMBER

Some redundancy is desirable in critical transportation or energy networks even when striving for economical solutions. If only one method connects the network, it's easily disrupted, interrupting services to many customers.

Getting the minimum spanning tree historical context

In Moravia, the eastern part of Czech Republic, the Czech mathematician Otakar Borůvka found a solution in 1926 that allows constructing an electrical network using the least amount of wire possible. His solution is quite efficient because it not only allowed for finding a way to connect all the towns in Moravia in the most economical way possible, but also had a time complexity of `O(m*log n)`, where m is the number of edges (the electrical cable) and n the number of vertexes (the towns). Others have improved Borůvka's solution since then. Even though the algorithms you find in books are better designed and easier to grasp (such as those from Prim and Kruskal), they don't achieve better results in terms of time complexity.

A minimal spanning tree defines the problem of finding the most economical way to accomplish a task. A *spanning tree* is the list of edges required to connect all the vertexes in an undirected graph. A single graph could contain multiple spanning trees, depending on the graph arrangement, and determining how many trees it contains is a complex issue. Each path you can take from start to completion in a graph is another spanning tree. The spanning tree visits each vertex only once; it doesn't loop or do anything to repeat path elements.

Working with unweighted versus weighted graphs

When you work on an unweighted graph, the spanning trees are the same length. In unweighted graphs, all edges have the same length, and the order you visit them in doesn't matter because the path is always the same. All possible spanning trees have the same number of edges, n-1 edges (n is the number of vertexes), of the same exact length. Moreover, any graph traversal algorithm, such as BFS or DFS, suffices to find one of the possible spanning trees.

Things become tricky when working with a weighted graph with edges of different lengths. In this case, of the many possible spanning trees, a few, or just one, have the minimum length possible. A *minimum spanning tree* is a spanning tree that guarantees a path with the least possible edge weight. An undirected graph generally contains just one minimum spanning tree, but, again, it depends on the configuration. Think about minimum spanning trees this way: When looking at a map, you see a number of paths to get from point A to point B. Each path has places where you must turn or change roads, and each of these junctions is a vertex. The distance between vertexes represents the edge weight. Generally, one path between point A and point B provides the shortest route.

Creating a minimum spanning tree example

Minimum spanning trees need not always consider the obvious. For example, when considering maps, you might not be interested in distance; you might instead want to consider time, fuel consumption, or myriad other needs. Each of these needs could have a completely different minimum spanning tree. With this in mind, the following example helps you understand minimum spanning trees better and demonstrates how to solve the problem of figuring out the smallest edge weight for any given problem. To demonstrate a minimum spanning tree solution using Python, the following code updates the previous graph by adding edge weights.

```
import networkx as nx
import matplotlib.pyplot as plt
```

```
graph = {'A': {'B':2, 'C':3},
         'B': {'A':2, 'C':2, 'D':2},
         'C': {'A':3, 'B':2, 'D':3, 'E':2},
         'D': {'B':2, 'C':3, 'E':1, 'F':3},
         'E': {'C':2, 'D':1, 'F':1},
         'F': {'D':3, 'E':1}}

Graph = nx.Graph()
for node in graph:
    Graph.add_nodes_from(node)
    for edge, weight in graph[node].items():
        Graph.add_edge(node,edge, weight=weight)

pos = { 'A': [0.00, 0.50], 'B': [0.25, 0.75],
        'C': [0.25, 0.25], 'D': [0.75, 0.75],
        'E': [0.75, 0.25], 'F': [1.00, 0.50]}

draw_params = {'with_labels':True,
               'arrows': True,
               'node_color':'skyblue',
               'node_size':700, 'width':2,
               'font_size':14}

labels = nx.get_edge_attributes(Graph,'weight')
nx.draw(Graph, pos, **draw_params)
nx.draw_networkx_edge_labels(Graph, pos,
                             font_size=14,
                             edge_labels=labels)
plt.show()
```

Figure 9-2 shows that all edges have a value now. This value can represent something like time, fuel, or money. Weighted graphs can represent many possible optimization problems that occur in geographical space (such as movement between cities) because they represent situations in which you can come and go from a vertex.

Interestingly, all edges have positive weights in this example. However, weighted graphs can have negative weights on some edges. Many situations take advantage of negative edges. For instance, they're useful when you can both gain and lose from moving between vertexes, such as gaining or losing money when transporting or trading goods, or releasing energy in a chemical process.

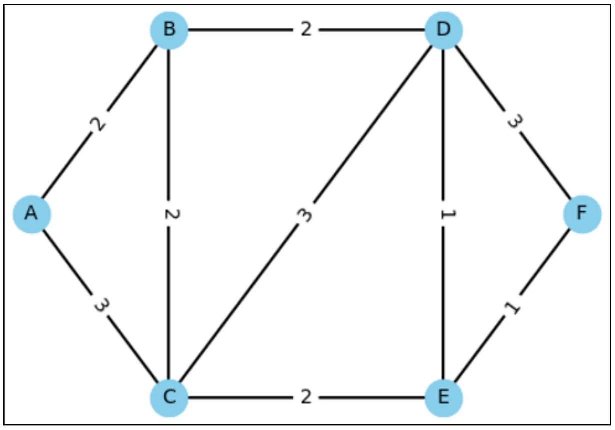


FIGURE 9-2: The example graph becomes weighted.

REMEMBER

Not all algorithms are well suited for handling negative edges. It's important to note those that can work with only positive weights.

Discovering the correct algorithms to use

You can find many different algorithms to use to create a minimum spanning tree. The most common are greedy algorithms, which run in polynomial time. *Polynomial time* is a power of the number of edges, such as `O(n²)` or `O(n³)` (see the "Considering NP complete problems" section of Chapter 15 for additional information about polynomial time). The major factors that affect the running speed of such algorithms involve the decision-making process — that is, whether a particular edge belongs in the minimum spanning tree or whether the minimum total weight of the resulting tree exceeds a certain value. With this in mind, here are some of the algorithms available for solving a minimum spanning tree:

- **Borůvka's:** Invented by Otakar Borůvka in 1926, this algorithm relies on a series of stages in which it identifies the edges with the smallest weight in each stage. The calculations begin by looking at individual vertexes, finding the smallest weight for that vertex, and then combining paths to form forests of individual trees until it creates a path that combines all the forests with the smallest weight.
- **Prim's:** Originally invented by Jarnik in 1930, Prim rediscovered it in 1957. This algorithm starts with an arbitrary vertex and grows the minimum spanning tree one edge at a time by always choosing the edge with the least weight that connects to a node that isn't already in the tree to the growing tree.
- **Kruskal's:** Developed by Joseph Kruskal in 1956, it uses an approach that combines Borůvka's algorithm (creating forests of individual trees) and Prim's

algorithm (looking for the minimum edge for each vertex and building the forests one edge at a time).

TIP

These algorithms use a greedy approach. Greedy algorithms appear in Chapter 2 among the families of algorithms, and you see them in detail in Chapter 15. In a *greedy approach*, the algorithm gradually arrives at a solution by taking, in an irreversible way, the best decision available at each step. For instance, if you need the shortest path between many vertexes, a greedy algorithm takes the shortest edges among those available between all vertexes.

Introducing priority queues

Later in this chapter, you see how to implement Prim's and Kruskal's algorithms for a minimum spanning tree, and Dijkstra's algorithm for the shortest path in a graph using Python. However, before you can do that, you need a method to find the edges with the minimum weight among a set of edges. Such an operation implies ordering, and ordering elements costs time. It's a complex operation, as described in Chapter 7. Because the examples repeatedly reorder edges, a data structure called the *priority queue* comes in handy.

The *priority queues* used here rely on heap tree-based data structures that allow fast element ordering when you insert them inside the heap. Like the magician's magic hat, priority heaps store edges with their weights and are immediately ready to provide you with the inserted edge whose weight is the minimum among those stored.

This example uses a class that allows it to perform priority-queue comparisons that determine whether the queue contains elements and when those elements contain a certain edge (avoiding double insertions). The priority queue has another useful characteristic (whose usefulness is explained when working on Dijkstra's algorithm): If you insert an edge with a different weight than previously stored, the code updates the edge weight and rearranges the edge position in the heap.

```
from heapq import heapify, heappop, heappush

class priority_queue():
    def __init__(self):
        self.queue = list()
        heapify(self.queue)
        self.index = dict()
    def push(self, priority, label):
        if label in self.index:
            self.queue = [(w,l)
```

```
                for w,l in self.queue if l != label]
            heapify(self.queue)
        heappush(self.queue, (priority, label))
        self.index[label] = priority
    def pop(self):
        if self.queue:
            return heappop(self.queue)
    def __contains__(self, label):
        return label in self.index
    def __len__(self):
        return len(self.queue)
```

Leveraging Prim's algorithm

Prim's algorithm generates the minimum spanning tree for a graph by traversing the graph vertex by vertex. Starting from any chosen vertex, the algorithm adds edges using a constraint in which, if one vertex is currently part of the spanning tree and the second vertex isn't part of it, the edge weight between the two must be the least possible among those available. By proceeding in this fashion, the chance of creating cycles in the spanning tree is less (it could happen if you add an edge whose vertexes are already in both spanning trees) and you're guaranteed to obtain a minimal tree because you add the edges with the least weight. In terms of steps, the algorithm includes these three phases, with the last one being iterative:

1. Track both the edges of the minimum spanning tree and the used vertexes as they become part of the solution.
2. Start from any vertex in the graph and place it into the solution.
3. Determine whether there are still vertexes that aren't part of the solution:
   a. Enumerate the edges that touch the vertexes in the solution.
   b. Insert the edge with the minimum weight into the spanning tree. (This is the greedy principle at work in the algorithm: Always choose the minimum at each step to obtain an overall minimum result.)

By translating these steps into Python code, you can test the algorithm on the example weighted graph using the following code:

```
def prim(graph, start):
    treepath = {}
    total = 0
    queue = priority_queue()
    queue.push(0, (start, start))
    while queue:
        weight, (node_start, node_end) = queue.pop()
        if node_end not in treepath:
            treepath[node_end] = node_start
            if weight:
                print("Added edge from %s" \
                      " to %s weighting %i"
                      % (node_start, node_end, weight))
                total += weight
            for next_node, weight \
            in graph[node_end].items():
                queue.push(weight , (node_end, next_node))
    print("Total spanning tree length: %i" % total)
    return treepath

treepath = prim(graph, 'A')
```

The code execution prints the following output:

```
Added edge from A to B weighting 2
Added edge from B to C weighting 2
Added edge from B to D weighting 2
Added edge from D to E weighting 1
Added edge from E to F weighting 1
Total spanning tree length: 8
```

The algorithm prints the processing steps, showing the edge it adds at each stage and the weight the edge adds to the total. The example displays the total sum of weights and the algorithm returns a Python dictionary containing the ending vertex as key and the starting vertex as value for each edge of the resulting spanning tree. Another function, `represent_tree()`, turns the key and value pairs of the dictionary into a tuple and then sorts each of the resulting tuples for better readability of the tree path:

```
def represent_tree(treepath):
    progression = list()
    for node in treepath:
        if node != treepath[node]:
            progression.append((treepath[node], node))
    return sorted(progression, key=lambda x:x[0])

print(represent_tree(treepath))
```

This version of the output is a little more readable.

```
[('A','B'), ('B','C'), ('B','D'), ('D','E'), ('E','F')]
```

REMEMBER

The `represent_tree()` function reorders the output of Prim's algorithm for better readability. However, the algorithm works on an undirected graph, which means that you can traverse the edges in both directions. The algorithm incorporates this assumption because there is no edge directionality check to add to the priority queue for later processing.

Testing Kruskal's algorithm

Kruskal's algorithm uses a greedy strategy, just as Prim's does, but it picks the shortest edges from a global pool containing all the edges. To determine whether an edge is a suitable part of the solution, the algorithm relies on an aggregative process in which it gathers vertexes together. When an edge involves vertexes already in the solution, the algorithm discards it to avoid creating a cycle. The algorithm proceeds in the following fashion:

1. Put all the edges into a heap and sort them so that the shortest edges are on top.
2. Create a set of trees, each one containing only one vertex (so that the number of trees is the same number as the vertexes). You connect trees as an aggregate until the trees converge into a tree of minimal length that spans all the vertexes.
3. Repeat the following operations until the solution doesn't contain as many edges as the number of vertexes in the graph:
   a. Choose the shortest edge from the heap.
   b. Determine whether the two vertexes connected by the edge appear in different trees from among the set of connected trees.
   c. When the trees differ, connect the trees using the edge (defining an aggregation).
   d. When the vertexes appear in the same tree, discard the edge.
   e. Repeat steps a through d for the remaining edges on the heap.

The following example demonstrates how to turn these steps into Python code:

```
def kruskal(graph):
    priority = priority_queue()
    print("Pushing all edges into the priority queue")
    treepath = list()
    connected = dict()
    for node in graph:
        connected[node] = [node]
        for dest, weight in graph[node].items():
            priority.push(weight, (node,dest))
    print("Totally %i edges" % len(priority))
    print("Connected components: %s"
           % connected.values())

    total = 0
    while len(treepath) < (len(graph)-1):
        (weight, (start, end)) = priority.pop()
        if end not in connected[start]:
            treepath.append((start, end))
            print("Summing %s and %s components:"
                   % (connected[start],connected[end]))
            print("\tadded edge from %s " \
                   "to %s weighting %i"
                   % (start, end, weight))
            total += weight
            connected[start] += connected[end][:]
            for element in connected[end]:
                connected[element]= connected[start]
    print("Total spanning tree length: %i" % total)
    return sorted(treepath, key=lambda x:x[0])

print('\nMinimum spanning tree: %s' % kruskal(graph))
```

Kruskal's algorithm, when running, returns the following output:

```
Pushing all edges into the priority queue
Totally 9 edges
Connected components: dict_values([['A'], ['E'], ['F'],
                                  ['B'], ['D'], ['C']])
Summing ['E'] and ['D'] components:
        added edge from E to D weighting 1
Summing ['E', 'D'] and ['F'] components:
        added edge from E to F weighting 1
Summing ['A'] and ['B'] components:
        added edge from A to B weighting 2
Summing ['A', 'B'] and ['C'] components:
        added edge from B to C weighting 2
Summing ['A', 'B', 'C'] and ['E', 'D', 'F'] components:
        added edge from B to D weighting 2
Total spanning tree length: 8

Minimum spanning tree:
[('A','B'), ('B','C'), ('B','D'), ('E','D'), ('E','F')]
```

TIP

Kruskal's algorithm offers a solution that's similar to the one proposed by Prim's algorithm. However, different graphs may provide different solutions for the minimum spanning tree when using Prim's and Kruskal's algorithms because each algorithm proceeds in different ways to reach its conclusions.

Determining which algorithm works best

Both Prim's and Kruskal's algorithms output a single connected component, joining all the vertexes in the graph by using one of the least long sequences of edges (a minimum spanning tree). By summing the edge weights, the algorithms determine the length of the resulting spanning tree. Because both algorithms provide a working solution, you must rely on running time and the type of weighted graph to determine which is best.

As for running time, both algorithms provide similar results with Big-O complexity rating of `O(E*log(V))`, where `E` is the number of edges and `V` the number of vertexes. However, you must account for how they solve the problem because there are differences in the average expected running time.

Prim's algorithm incrementally builds a single solution by adding edges, whereas Kruskal's algorithm creates an ensemble of partial solutions and aggregates them. In creating its solution, Prim's algorithm relies on data structures that are more complex than Kruskal's because it continuously adds potential edges as candidates and keeps picking the shortest edge to proceed toward its solution. When operating on a dense graph, Prim's algorithm is preferred over Kruskal's because its priority queue based on heaps does all the sorting jobs quickly and efficiently.

REMEMBER

The example uses a priority queue based on a binary heap for picking up the shortest edges, but there are even faster data structures, such as the *Fibonacci heap*, which can produce faster results when the heap contains many edges. Using a Fibonacci heap, the running complexity of Prim's algorithm can mutate to `O(E +V*log(V))`, which is clearly advantageous if you have a lot of edges (the `E` component is now summed instead of multiplied) compared to the previous reported running time `O(E*log(V))`.

Kruskal's algorithm doesn't much need a priority queue (even though one of the examples uses one) because the enumeration and sorting of edges happens just once at the beginning of the process. Being based on simpler data structures that work through the sorted edges, it's the ideal candidate for regular, sparse graphs with fewer edges.

Finding the Shortest Route

The shortest route between two points isn't necessarily a straight line, especially when a straight line doesn't exist in your graph. Say that you need to run electrical lines in a community. The shortest route would involve running the lines as needed between each location without regard to where those lines go. However, real life tends not to allow a simple solution. You may need to run the cables beside roads and not across private property, which means finding routes that reduce the distances as much as possible.

Defining what it means to find the shortest path

Many applications exist for shortest-route algorithms. The idea is to find the path that offers the smallest distance between point A and point B. Finding the shortest path is useful for both transportation (how to arrive at a destination consuming the least fuel) and communication (how to route information to allow it to arrive earlier). Unexpected applications of the shortest-path problem may also arise in image processing (for separating contours of images), gaming (how to achieve certain game goals using the fewest moves), and many other fields in which you can reduce the problem to an undirected or directed weighted graph.

The Dijkstra algorithm has found the most uses in solving the shortest-path problem. Edsger W. Dijkstra, a Dutch computer scientist, devised the algorithm to demonstrate the processing power of the ARMAC computer (`http://www-set.win.tue.nl/UnsungHeroes/machines/armac.html`) in 1959. The algorithm initially solved the shortest distance between 64 cities in the Netherlands based on a simple graph map.

REMEMBER

Other algorithms can solve the shortest-path problem. The Bellman-Ford and Floyd-Warshall are more complex but can handle graphs with negative weights. (Negative weights can present some problems for the Dijkstra algorithm.) Though it is not immediately intuitive, negative weights have a meaningful representation in the real world. If you're measuring energy consumption when moving between points in space and you're using an electric engine, consider that when going downhill, an electric car produces energy, so its energy consumption will be negative in a graph for that arc. Other examples of negative weights could be in a social network when you consider dislikes together with likes, or when you map financial transactions into a graph.

Because the shortest-path problem involves graphs that are both weighted and directed, the example graph requires another update before proceeding (you can see the result in Figure 9-3).

```
import networkx as nx
import matplotlib.pyplot as plt

graph = {'A': {'B':2, 'C':3},
         'B': {'C':2, 'D':2},
         'C': {'D':3, 'E':2},
         'D': {'F':3},
         'E': {'D':1,'F':1},
         'F': {}}

Graph = nx.DiGraph()
for node in graph:
    Graph.add_nodes_from(node)
    for edge, weight in graph[node].items():
        Graph.add_edge(node,edge, weight=weight)

pos = { 'A': [0.00, 0.50], 'B': [0.25, 0.75],
        'C': [0.25, 0.25], 'D': [0.75, 0.75],
        'E': [0.75, 0.25], 'F': [1.00, 0.50]}

draw_params = {'with_labels':True,
               'arrows': True,
               'node_color':'skyblue',
               'node_size':700, 'width':2,
               'font_size':14}

nx.draw(Graph, pos, **draw_params)
nx.draw_networkx_edge_labels(Graph, pos,
                             font_size=14,
                             edge_labels=labels)

plt.show()
```

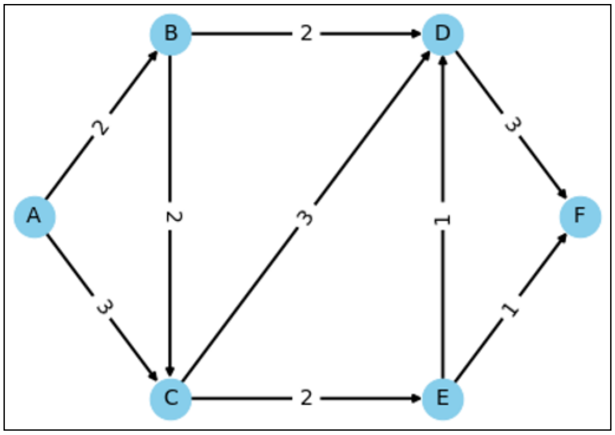


FIGURE 9-3: The example graph becomes weighted and directed.

Adding a negative edge

The example can apply some simple modifications to the graph in the previous section to insert a negative edge between nodes B and C (Figure 9-4 shows the placement of the negative edges):

```
ngraph = {'A': {'B':2, 'C':3},
          'B': {'C':-1, 'D':2},
          'C': {'D':3, 'E':2},
          'D': {'F':3},
          'E': {'D':-1,'F':1},
          'F': {}}

nGraph = nx.DiGraph()
for node in ngraph:
    nGraph.add_nodes_from(node)
    for edge, weight in ngraph[node].items():
        nGraph.add_edge(node, edge, weight=weight)
labels = nx.get_edge_attributes(nGraph,'weight')

nx.draw(nGraph, pos, **draw_params)
nx.draw_networkx_edge_labels(nGraph, pos,
                             font_size=14,
                             edge_labels=labels)
plt.title("negative edges")
plt.show()
```

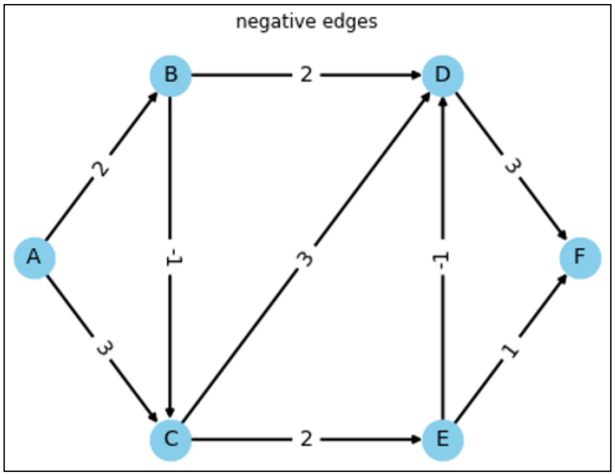


FIGURE 9-4: Negative edges are added to the example graph.

A special case is when there are negative cycles in a graph. Having negative cycles poses problems to all algorithms computing the shortest route. A necessary condition to include a negative-weight cycle in a graph is to use negative weights for the edges, but that's not enough. You also need to have a cycle, that is, a series of circularly connected nodes, whose weights sum to a negative number. Because the sum of the cycle is negative, a greedy algorithm trying to minimize the total cost of the edges it transits may never escape it and ends up being trapped there (as shown in Figure 9-5 between A and C).

```
ncgraph = {'A': {'B':1},
           'B': {'C':1, 'D':2},
           'C': {'A':-3, 'D':3, 'E':2},
           'D': {'F':3},
           'E': {'D':1,'F':1},
           'F': {}}

ncGraph = nx.DiGraph()
for node in ncgraph:
    ncGraph.add_nodes_from(node)
    for edge, weight in ncgraph[node].items():
        ncGraph.add_edge(node, edge, weight=weight)

labels = nx.get_edge_attributes(ncGraph,'weight')

nx.draw(ncGraph, pos, **draw_params)
nx.draw_networkx_edge_labels(ncGraph, pos,
                             font_size=14,
                             edge_labels=labels)
plt.title("negative cycle")
plt.show()
```

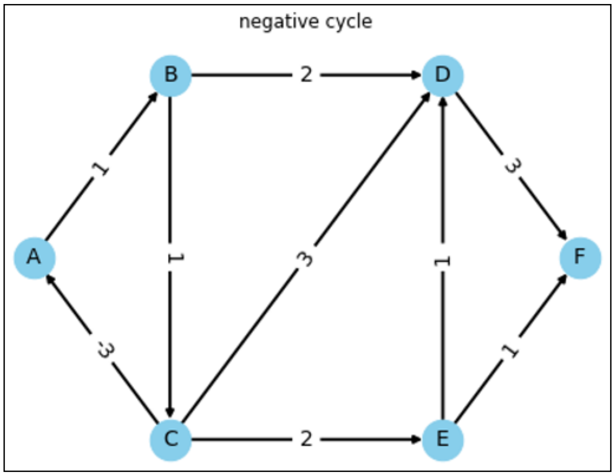


FIGURE 9-5: A negative cycle in a graph can create problems for some algorithms.

This variation of the original graph uses modifications to create a negative cycle around the nodes A, B, and C: When arriving at the C node, the algorithm can't get back to A because it's the less costly move and because the cycle can lower the overall path cost.

Explaining Dijkstra's algorithm

Dijkstra's algorithm requires a starting and (optionally) ending vertex as input. If you don't provide an ending vertex, the algorithm computes the shortest distance between the starting vertex and every other vertex in the graph. When you define an ending vertex, the algorithm stops upon reading that vertex and returns the result up to that point, no matter how much of the graph remains unexplored.

The algorithm starts by estimating the distance of the other vertexes from the starting point. This is the starting belief it records in the priority queue and is set to infinity by convention. Then the algorithm proceeds to explore the neighboring nodes, similar to a breadth-first search (BFS). This allows the algorithm to determine which nodes are near and that their distance is the weight of the connecting edges. It stores this information in the priority queue by an appropriate weight update.

REMEMBER

Naturally, the algorithm explores the neighbors because a directed edge connects them with the starting vertex. Dijkstra's algorithm accounts for the edge direction.

At this point, the algorithm moves to the nearest vertex on the graph based on the shortest edge in the priority queue. Technically, the algorithm *visits* a new vertex. It starts exploring the neighboring vertexes, excluding the vertexes that it has already visited, determines how much it costs to visit each of the unvisited vertexes, and evaluates whether the distance to visit them is less than the distance it recorded in the priority queue.

When the distance in the priority queue is infinite, this means that it's the algorithm's first visit to that vertex, and the algorithm records the shorter distance. When the distance recorded in the priority queue isn't infinite, but it's more than the distance that the algorithm has just calculated, it means that the algorithm has found a *shortcut,* a shorter way to reach that vertex from the starting point, and it stores the information in the priority queue. Of course, if the distance recorded in the priority queue is shorter than the one just evaluated by the algorithm, the algorithm discards the information because the new route is longer. After updating all the distances to the neighboring vertexes, the algorithm determines whether it has reached the end vertex. If not, it picks the shortest edge present in the priority queue, visits it, and starts evaluating the distance to the new neighboring vertexes.

REMEMBER

As the narrative of the algorithm explained, Dijikstra's algorithm keeps a precise accounting of the cost to reach every vertex that it encounters, and it updates its information only when it finds a shorter way. The running complexity of the algorithm using a binary heap in Big-O notation is `O((E + V)*log(V))`, where `E` is the number of edges and `V` the number of nodes (vertexes) in the graph. Using a Fibonacci heap, the complexity can lower to `O(E + V*log(V))`. The following code shows how to implement Dijikstra's algorithm using Python:

```
def dijkstra(graph, start, end):
    inf = float('inf')
    known = set()
    priority = priority_queue()
    path = {start: start}

    for vertex in graph:
        if vertex == start:
            priority.push(0, vertex)
        else:
            priority.push(inf, vertex)

    last = start
    while last != end:
        (weight, actual_node) = priority.pop()
        if actual_node not in known:
            for next_node in graph[actual_node]:
                upto_actual = priority.index[actual_node]
                upto_next = priority.index[next_node]
                to_next = upto_actual + \
                graph[actual_node][next_node]
                if to_next < upto_next:
                    priority.push(to_next, next_node)
                    print("Found shortcut from %s to %s"
                          % (actual_node, next_node))
                    print("\tTotal length up so far: %i"
                           % to_next)
                    path[next_node] = actual_node
            last = actual_node
            known.add(actual_node)

    return priority.index, path

dist, path = dijkstra(graph, 'A', 'F')
```

After running the code, you receive the following output:

```
Found shortcut from A to C
   Total length up so far: 3
Found shortcut from A to B
   Total length up so far: 2
Found shortcut from B to D
   Total length up so far: 4
Found shortcut from C to E
   Total length up so far: 5
Found shortcut from D to F
   Total length up so far: 7
Found shortcut from E to F
   Total length up so far: 6
```

The algorithm returns a couple of useful pieces of information: the shortest path to destination and the minimum recorded distances for the visited vertexes. To visualize the shortest path, you need a `reverse_path()` function that rearranges the path to make it readable:

```
def reverse_path(path, start, end):
    progression = [end]
    while progression[-1] != start:
        progression.append(path[progression[-1]])
    return progression[::-1]

print(reverse_path(path, 'A', 'F'))
```

Here is the output you see after running the code.

```
['A', 'C', 'E', 'F']
```

You can also know the shortest distance to every node encountered by querying the `dist` dictionary:

```
print(dist)
```

The output shows the correlation between node and distance, as shown here:

```
{'D': 4, 'A': 0, 'B': 2, 'F': 6, 'C': 3, 'E': 5}
```

Explaining the Bellman-Ford algorithm

The Bellman-Ford algorithm is probably one of the most studied algorithms in computer science courses at universities all around the world because it has many important real-world applications. This algorithm is used to find the shortest path to reach each router in a server network, and it's particularly apt in doing so because, contrary to other algorithms, it can be distributed; that is the computations necessary for the algorithm to complete can be shared among multiple computers, making the task speedier and easier,

The Bellman-Ford algorithm, devised to solve the same problem as Dijkstra's, takes a different approach to solve the problem, which makes it more suitable for a world of networked computers. Although the Dijkstra algorithm takes a greedy approach by exploring only the nearest edges before deciding on a particular path, Bellman-Ford's algorithm instead checks and proceeds on them all.

This choice affects the running complexity of the algorithm in Big-O notation, which is now `O(E*V)`, where `E` is the number of edges and `V` the number of nodes (vertexes) in the graph. However, this choice also makes it easier to split the algorithm's computations into separate tasks because each computer can explore a different set of consecutive edges.

Routing information more efficiently

This section's implementation of the Bellman-Ford algorithm requires the graph and a starting point as input because it considers all the other nodes of the graph as ending points. Starting at the beginning, it traces two pieces of information: the distance of each terminal node (which initially is set to infinite) and the last node that made the algorithm update the distance information about each other node. Both pieces of information are recorded using a Python dictionary.

The algorithm then iterates through each node and then through each edge of the graph (based on the node being explored). This is an exhaustive search through the structure of the edges of the graph. At each iteration step, the algorithm computes the actual distance from the starting node to the node being evaluated, adding the edge being explored. If the sum of the two represents a shorter path than presently known, the information is updated both in the distance dictionary and in the last node dictionary (because this dictionary represents the previous node in the shorter path).

```
def bellman_ford(graph, start):
    inf = float('inf')
    distance = {node: inf if node!=start else 0.0 for node in
           graph}
    previous = {node: None for node in graph}

    for actual_node in graph:
        for next_node in graph[actual_node]:
            edge_weight = graph[actual_node][next_node]
            tempDistance = (distance[actual_node] +
                            edge_weight)
            if tempDistance < distance[next_node]:
                distance[next_node] = tempDistance
                previous[next_node] = actual_node
    return distance, previous
```

When all the iterations are completed, the function returns the distance and the previous node dictionaries for further computations.

Proving algorithm versatility

The Bellman-Ford algorithm is more versatile than other algorithms. Even if you can't use the distances it returns immediately, further data manipulations provide more usable information. First, by reiterating the graph edges, you can spot when there are discrepancies. Summing the shortest distance to a node with the edge cost to reach another destination node and comparing it to the shortest distance to that destination node provides a hint about a negative cycle when there is a discrepancy, because the sum should always be equal to or greater than the shortest distance. When there is a negative cycle, distance estimates using the Bellman-Ford algorithm are not exact. Second, using the previous node information, you can rebuild the shortest path from the source node to every other node.

```
def detect_negative_cycle(graph, distance, previous):
    for actual_node in graph:
        for next_node in graph[actual_node]:
            edge_weight = graph[actual_node][next_node]
            if distance[actual_node] + edge_weight <
            distance[next_node]:
                return True
    return False

def retrace_shortest_path(previous, end):
    path = [end]
    while path[0] != 'A':
        path = [previous[end]] + path
        end = previous[end]
    return path
```

Using the following code, you can see the two previous functions `detect_negative_cycle()` and `retrace_shortest_path()` working on the original graph data:

```
distance, previous = bellman_ford(graph, 'A')
print(distance)
print("path:", retrace_shortest_path(previous, 'F'))
neg_cycle = detect_negative_cycle(graph, distance, previous)
print(f"There are negative cycles in the graph: {neg_cycle}")
```

The output returns the exact distances to each destination node and the path to reach node F from node A. More important, you know that there are no negative cycles in the graph and can trust the results.

```
{'A': 0.0, 'B': 2.0, 'C': 3.0, 'D': 4.0, 'E': 5.0, 'F': 6.0}
path: ['A', 'C', 'E', 'F']
There are negative cycles in the graph: False
```

The following code tests the algorithm using a graph containing a negative edge:

```
distance, previous = bellman_ford(ngraph, 'A')
print(distance)
print("path:", retrace_shortest_path(previous, 'F'))
neg_cycle = detect_negative_cycle(ngraph, distance, previous)
print(f"There are negative cycles in the graph: {neg_cycle}")
```

The following result points out a new shortest path to reach node F from node A, this time leveraging the presence of the negative edge. The absence of negative cycles ensures the validity of the computations.

```
{'A': 0.0, 'B': 2.0, 'C': 1.0, 'D': 2.0, 'E': 3.0, 'F': 4.0}
path: ['A', 'B', 'C', 'E', 'F']
There are negative cycles in the graph: False
```

Finally, you can test the algorithm using a graph that has a negative cycle.

```
distance, previous = bellman_ford(ncgraph, 'A')
print(distance)
print("path:", retrace_shortest_path(previous, 'F'))
neg_cycle = detect_negative_cycle(ncgraph, distance, previous)
print(f"There are negative cycles in the graph: {neg_cycle}")
```

The output is similar to the other outputs but for two significant details: one of the shortest distances is negative (reaching the start node from the start node) and the function detecting negative cycles has raised an alarm.

```
{'A': -1.0, 'B': 1.0, 'C': 2.0, 'D': 3.0, 'E': 4.0, 'F': 5.0}
path: ['A', 'B', 'C', 'E', 'F']
There are negative cycles in the graph: True
```

In the end, you can't trust the results provided for this graph because it has a negative cycle. By examining a few nodes and edges, you can easily spot a negative edge, but on larger graphs, you can rely only on the Bellman-Ford algorithm for the fastest check.

Explaining the Floyd-Warshall algorithm

Robert W. Floyd, a computer scientist and recipient of the Turing award in 1978, devised the Floyd-Warshall algorithm in its present form. You can find other forms of this algorithm formulated by other computer scientists in the past:

- Bernard Roy in 1959
- Stephen Warshall in 1962
- It is also similar to the Kleene's algorithm published in 1956

Floyd-Warshall is a dynamic programming algorithm because it solves overlapping subproblems (so you can avoid recomputing duplicate calculations) and its solution is obtained by using the solutions of its subproblems (a property called *optimal substructure*).

The Floyd-Warshall algorithm, as well as other algorithms seen so far in this book, can compute distances between nodes in a graph, and it works fine with edges showing a negative cost. It outputs a square matrix relating all the nodes in a graph with their relative distances (technically called a distance matrix). Because the algorithm iterates three times across the nodes of the graph in a nested way, its time complexity depends uniquely on the number of nodes present and is `O(V³)`, where `V` stands for vertexes, that is nodes.

Comparing with other algorithms

Even though the Floyd-Warshall algorithm performance resembles Dijkstra and Bellman-Ford, there are a few important differences:

- The Dijkstra algorithm works the best (it has the lower complexity) when finding the distance between two nodes in a graph, though it cannot perform properly if some edges in the graph have a negative cost.
- The Bellman-Ford algorithm returns the distance of a node with respect to all the nodes present in the graph. It performs properly even when there are negative weights, but it's slower than Dijkstra.
- The Floyd-Warshall algorithm returns the distance of every node with respect to all the other nodes present in the graph and is relatively efficient in doing so, but it's the slowest of the three because it returns much more information. However, in some cases, Dijkstra's and Bellman-Ford's algorithms can produce the same result as the Floyd-Warshall algorithm, but require longer execution times and more computations.

Both Bellman-Ford and Floyd-Warshall's algorithms can handle negative weights if there are no negative cycles. Instead, in case of negative edge weights, Dijkstra algorithm exploits the situation to avoid visiting every node. In such an occurrence, the results provided by a Dijkstra algorithm are unreliable.

A different situation occurs when there are negative cycles in the graph. In such a case, the Bellman-Ford will fail and won't return a solution, but the Floyd-Warshall will complete its execution nevertheless. You can also detect the negative cycle because, in the returned matrix, you find that some node has a negative distance to itself (distances to itself are on the diagonal of the matrix).

Using three passes is better

This implementation of the Floyd-Warshall algorithm uses two functions. The first one, given a graph, obtains the distance between two nodes if they are adjacent; otherwise, the function returns zero distance if the two nodes are the same one, or infinite distance if the nodes are different.

```
def dist(graph, start, end):
    if end in graph[start]:
        return float(graph[start][end])
    elif start == end:
        return 0.0
    else:
        return float('inf')
```

Using the dist() function, it's easy to create the initial distance matrix of the Floyd-Warshall algorithm as a dictionary of dictionaries, a way to represent a square distance matrix with which you can determine the shortest distance between a starting node (represented on rows) and an ending node (represented in columns). The core idea of the algorithm is, in fact, to start from a square matrix whose known distances are just the distances of adjacent nodes and expand it to contain the shortest path between nodes (when they are reachable; otherwise the distance remains infinite).

```
def floyd_warshall(graph):

    mat = {row: {col: dist(graph, row, col)
                 for col in graph} for row in graph}
    for k in mat:
        for i in mat:
            for j in mat:
                if mat[i][j] > mat[i][k] + mat[k][j]:
                    mat[i][j] = mat[i][k] + mat[k][j]
    return mat
```

The algorithm operates using three nested cycles. In all the cycles, it iterates through nodes. During the iterations, the algorithm checks the distances between the pivot node (from the first iteration, k in the code), the starting node (from the second iteration, i in the code) and the destination node (from the third iteration, j in the code). Because this is a triangulation, it updates the distance between the starting node and the destination node if it is greater than the distance of reaching the destination node from the starting node and passing by the pivot node. By going through all the passes of the algorithm, you can be sure that the algorithm computes the exact distance matrix if the graph has no negative cycles.

The function returns the distance matrix as an output. Because a dictionary of dictionaries expresses the result, you need a code snippet to unfold it into a list of lists, a data structure that contains the row and column labels for easier reading. Naturally, you could also use other data structures like a Pandas DataFrame (https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.DataFrame.html) in which you could represent the row and column labels better, but this example uses a lower level of sophistication to demonstrate its workings better:

```
def print_mat(mat):
    els = [item for item in mat]
    labels = [' '] + [item for item in els]
    printable = [labels]
    for k, row in enumerate(els):
        printable.append([labels[k+1]] + [mat[row][col] for col
   in els])
    return printable
```

To determine whether there are negative cycles, you need to consider what happens to nodes whose initial distance is zero under such circumstances. Usually, such a situation occurs when you compute the distance of a node to itself. In this case, because the Floyd-Warshall algorithm looks for alternative shorter paths passing by another node, you won't ever find an alternative node unless the node is part of a negative cycle. Hence, observing the diagonal of the distance matrix produced by the algorithm, where the distance paths to the same nodes lie, if you spot any negative value, it signifies the presence of negative cycles in the graph. The following code just extracts the diagonal of the distance matrix:

```
def extract_diagonal(mat):
    return [mat[item][item] for item in mat]
```

Now that the code is complete, you can run the algorithm on the example graph:

```
print_mat(floyd_warshall(graph))
```

You see the following distance matrix and read it looking for the starting node on the row labels (on the leftmost column) and the ending node on the column labels (to be found on the first row). The diagonal, representing the distance of a node to itself, should be filled by zero values. If on a cell of the matrix you find an infinite value (inf), it implies that there is no way in the graph to reach that node given that starting point. (It happens normally on directed graphs.)

```
[[' ', 'A', 'B', 'C', 'D', 'E', 'F'],
 ['A', 0.0, 2.0, 3.0, 4.0, 5.0, 6.0],
 ['B', inf, 0.0, 2.0, 2.0, 4.0, 5.0],
 ['C', inf, inf, 0.0, 3.0, 2.0, 3.0],
 ['D', inf, inf, inf, 0.0, inf, 3.0],
 ['E', inf, inf, inf, 1.0, 0.0, 1.0],
 ['F', inf, inf, inf, inf, inf, 0.0]]
```

You can also inspect the distance matrix of the graph with the negative edge:

```
print_mat(floyd_warshall(ngraph))
```

The output reveals that some paths have negative values:

```
[[' ', 'A', 'B', 'C', 'D', 'E', 'F'],
['A', 0.0, 2.0, 1.0, 2.0, 3.0, 4.0],
['B', inf, 0.0, -1.0, 0.0, 1.0, 2.0],
['C', inf, inf, 0.0, 1.0, 2.0, 3.0],
['D', inf, inf, inf, 0.0, inf, 3.0],
['E', inf, inf, inf, -1.0, 0.0, 1.0],
['F', inf, inf, inf, inf, inf, 0.0]
```

Finally you can produce the distance matrix for the graph with the negative cycle and extract its diagonal.

```
mat = floyd_warshall(ncgraph)
extract_diagonal(mat)
```

The outputted diagonal contains negative values:

```
[-1.0, -1.0, -2.0, 0.0, 0.0, 0.0]
```

REMEMBER

There are no shortest paths between any pair of edges that are part of a negative cycle. This is because the length produced by any such paths will be arbitrarily negative depending on the passes of the algorithm.

IN THIS CHAPTER

» Seeing social networks in graph form

» Interacting with graph content

Chapter 10 Discovering Graph Secrets

Chapter 8 helps you understand the foundations of graphs as they apply to mathematics. Chapter 9 increases your knowledge by helping you see the relationship of graphs to algorithms. This chapter helps you focus on applying the theories of these previous two chapters to interact with graphs in practical ways.

The first section conveys the character of social networks by using graphs. It considers the importance of connections created by social networks. For example, conversation analysis can reveal patterns that help you understand the underlying topic better than simply reading the conversations would do. A particular conversation branch might attract greater attention because it's more important than another conversation branch. Of course, you must perform this analysis while dealing with issues such as spam. Analysis of this sort can lead to all sorts of interesting conclusions, such as where to spend more advertising money to attract the most attention and, therefore, sales.

The second section looks at navigating graphs to achieve specific results. For example, when driving, you might need to know the best route to take between two points given that, even though one route is shorter, it also has construction that makes a second route better. Sometimes you need to randomize your search to discover a best route or a best conclusion. This section of the chapter also discusses that issue.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 10; Graph Secrets.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Envisioning Social Networks as Graphs

Every social interaction necessarily connects with every other social interaction of the same type. For example, consider a social network such as Facebook. The links on your page connect with family members, but they also connect with outside sources that in turn connect with other outside sources. Each of your family members also has external links. Direct and indirect connections between various pages eventually link every other page together, even though the process of getting from one page to another may require the use of myriad links. Connectivity occurs in all sorts of other ways as well. The point is that studying social networks simply by viewing a Facebook page or other source of information is hard. *Social Network Analysis (SNA)* is the process of studying the interactions in social networks using graphs called *sociograms,* in which nodes (such as a Facebook page) appear as points, and ties (such as external page links) appear as lines. The following sections discuss some of the issues surrounding the study of social networks as graphs.

Clustering networks in groups

People tend to form communities — clusters of other people who have similar ideas and sentiments. By studying these clusters, attributing certain behaviors to the group as a whole becomes easier (although attributing a general behavior to an individual is both dangerous and unreliable). The idea behind the study of clusters is that if a connection exists between people, they often have a common set of ideas and goals. By finding clusters, you can determine these ideas by inspecting group membership. For instance, it's common to try to find clusters of people in insurance fraud detection and tax inspection. Unexpected groups of people might raise suspicion that they're part of a group of fraudsters or tax evaders because they lack the usual reasons for people to gather in such circumstances.

Friendship graphs can represent how people connect with each other. The nodes represent individuals and the edges represent their connections, such as family relationships, business contacts, or friendship ties. Typically, friendship graphs are undirected because they represent mutual relationships, and sometimes they're weighted to represent the strength of the bond between two persons.

When looking for clusters in a friendship graph, the connections between nodes in these clusters depend on triads — essentially, special kinds of triangles. Connections between three people can fall into these categories:

- **Closed:** All three people know each other. Think about a family setting in this case, in which everyone knows everyone else.
- **Open:** One person knows two other people, but the two other people don't know each other. Think about a person who knows an individual at work and another individual at home, but the individual at work doesn't know anything about the individual at home.
- **Connected pair:** One person knows one of the other people in a triad but doesn't know the third person. This situation involves two people who know something about each other meeting someone new — someone who potentially wants to be part of the group.
- **Unconnected:** The triad forms a group, but no one in the group knows each other. This last one might seem a bit odd, but think about a convention or seminar. The people at these events form a group, but they may not know anything about each other. However, because they have similar interests, you can use clustering to understand the behavior of the group.

TIP

Many studies focus on undirected graphs that concentrate solely on associations. You can also use directed graphs to show that Person A knows about Person B, but Person B doesn't even know that Person A exists. In this case, you actually have 16 different kinds of triads to consider. For the sake of simplicity, this chapter focuses solely on these four types: closed, open, connected pair, and unconnected.

Triads occur naturally in relationships, and many Internet social networks have leveraged this idea to accelerate the connections among participants. The density of connections is important for any kind of social network because a connected network can spread information and share content more easily. For instance, when LinkedIn, the professional social network (`https://www.linkedin.com/`), decided to increase the connection density of its network, it started by looking for open triads and trying to close them by inviting people to connect. Closing triads is at the foundation of LinkedIn's *Connection Suggestion algorithm.* You can discover more about how it works and improvements that LinkedIn has made by reading `https://engineering.linkedin.com/blog/2021/optimizing-pymk-for-equity-in-network-creation`.

The example in this section relies on the Zachary's Karate Club sample graph described at `https://documentation.sas.com/doc/en/pgmsascdc/v_009/casmlnetwork/casmlnetwork_network_examples06.htm`. It's a small graph that lets you see how networks work without spending a lot of time loading a large dataset. Fortunately, this dataset appears as part of the `networkx` package introduced in Chapter 8. The Zachary's Karate Club network represents the friendship relationships among 34 members of a karate club from 1970 to 1972. Sociologist Wayne W. Zachary used it as a topic of study. He wrote a paper on it entitled "An Information Flow Model for Conflict and Fission in Small Groups." The interesting fact about this graph and its paper is that in those years, a conflict arose in the club between one of the karate instructors (node number 0) and the president of the club (node number 33). By clustering the graph, you can almost perfectly predict the split of the club into two groups shortly after the occurrence.

Because this example also draws a graph showing the groups (so that you can visualize them easier), you also need to use the `matplotlib` package. The following code shows how to graph the nodes and edges of the dataset. (You can find this code in the `A4D2E; 10; Social Networks.ipynb` downloadable source code file; see the Introduction for details.)

```
import networkx as nx
import matplotlib.pyplot as plt
%matplotlib inline

graph = nx.karate_club_graph()

pos=nx.spring_layout(graph)
nx.draw(graph, pos, with_labels=True)
plt.show()
```

To display the graphic onscreen, you also need to provide a layout that determines how to position the nodes onscreen. This example uses the Fruchterman-Reingold force-directed algorithm (the call to `nx.spring_layout`). However, you can choose one of the other layouts described in the Graph Layout section at `https://networkx.github.io/documentation/networkx-1.9/reference/drawing.html`. Figure 10-1 shows the output from the example. (Your output may look different because of how the algorithm generates the graph.)

REMEMBER

The Fruchterman-Reingold force-directed algorithm for generating automatic layouts of graphs creates understandable layouts with separated nodes and edges that tend not to cross by mimicking what happens in physics between electrically charged particles or magnets bearing the same sign. In looking at the graph output, you can see that some nodes have just one connection, some two, and some more than two. The edges form triads, as previously mentioned. However, the most important consideration is that Figure 10-1 clearly shows the clustering that occurs in a social network.

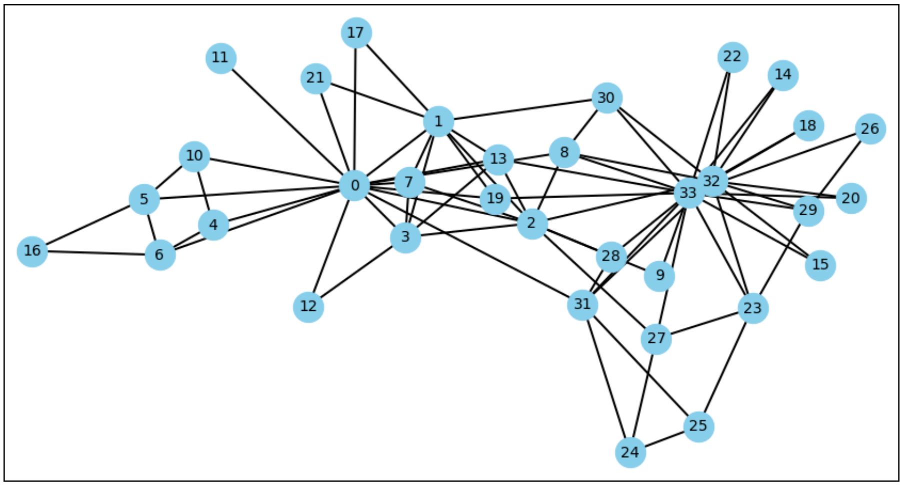


FIGURE 10-1: A graph showing the network clusters of relationships among friends.

Discovering communities

A group of tightly associated people often defines a community. In fact, the term *clique* applies to a group whose membership to the group is exclusive and everyone knows everyone else quite well. Most people have childhood memories of a tight group of friends at school or in the neighborhood who always spent their time together. That's a clique, in which every member of the clique is connected to the other ones.

REMEMBER

Cliques are associated more with undirected graphs than directed ones. In directed graphs focus on connected components, such as when a direct connection path exists between all the node pairs in the component itself. A city is an example of a strongly connected component because you can reach any destination from any starting point by following one-way and two-way streets.

Mathematically, a clique is even more rigorous because it implies a *subgraph* (a part of a network graph that you can separate from other parts as a complete element in its own right) that has maximum connectivity. In looking at various kinds of social networks, picking out the clusters is easy, but what can prove difficult is finding the cliques — the groups with maximum connectivity — within the clusters. By knowing where cliques exist, you can begin to understand the cohesive nature of a community better. In addition, the exclusive nature of cliques tends to create a group that has its own rules outside of those that might exist in the social network as a whole. The following example shows how to extract cliques and communities from the Karate Club graph used in the previous section (note that the import statement on the first two lines should all appear on a single line):

```
from networkx.algorithms.community.kclique import
  k_clique_communities

graph = nx.karate_club_graph()
# Finding and printing all cliques of four
cliques = nx.find_cliques(graph)
print ('All cliques of four: %s'
       % [c for c in cliques if len(c)>=4])

# Joining cliques of four into communities
communities = nx.k_clique_communities(graph, k=4)
communities_list = [list(c) for c in communities]
nodes_list = [node for community in communities_list for
              node in community]
print ('Found these communities: %s' % communities_list)

# Printing the subgraph of communities
subgraph = graph.subgraph(nodes_list)
nx.draw(subgraph, with_labels=True)
plt.show()

All cliques of four: [[0, 1, 2, 3, 13], [0, 1, 2, 3, 7],
                      [33, 32, 8, 30], [33, 32, 23, 29]]
Found these communities: [[0, 1, 2, 3, 7, 13],
                          [32, 33, 29, 23], [32, 33, 8, 30]]
```

The example begins by extracting just the nodes in the Karate Club dataset that have four or more connections, and then prints the cliques with a minimum size of four. Of course, you can set any level of connectivity between the nodes that you deem relevant. Perhaps you consider a clique a community in which each node has 20 connections, but other people might see a clique as a community in which each node has just three connections.

Finally, you can draw the subgraph and display it. Figure 10-2 shows the output of this example, which displays the ensemble of cliques with four or more connections.

Finding cliques in graphs is a complex problem requiring many computations. (It's a difficult problem because the number of cliques can grow exponentially with every added node.) The problem can be solved by using an algorithm based on a brute-force search, which means trying all possible subsets of nodes to determine whether they're cliques. However, you can also try something smarter, such as the algorithm invented by Dutch scientists Coenraad Bron and Joep Kerboschin in 1973, which will list all largest cliques in a given graph.

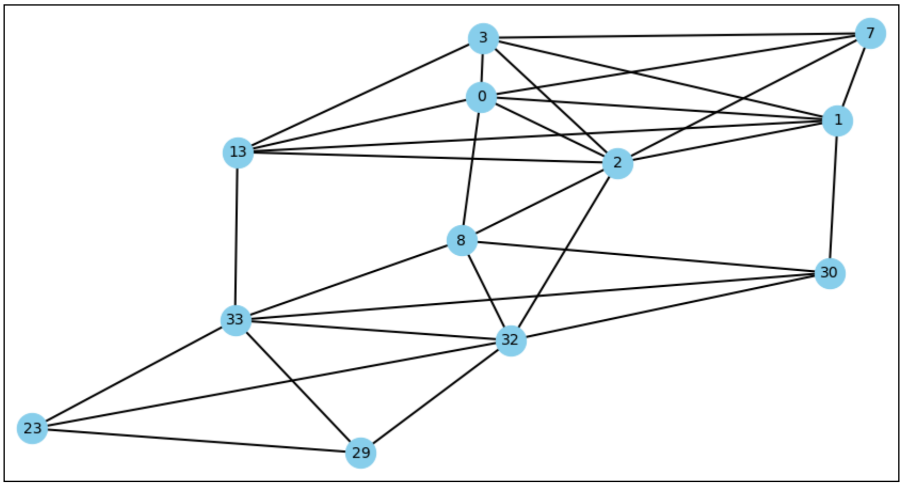


FIGURE 10-2: Communities often contain cliques that can prove useful for SNA.

The algorithm works by recursion and systematic exploration. In the end, it lists all the maximal cliques. A clique is said to be maximal when you can't add more nodes to it. For its operations, the algorithm uses three sets of vertices, conventionally called R, for potential cliques; P, for nodes remaining to explore; and X, for nodes to skip because they have already been explored (the algorithm doesn't repeat itself). At start, R and X are empty and P contains all the nodes of the graph. The algorithm runs by iterating through the nodes in the set P, considering each one as a candidate to a clique. Iteration after iteration, the algorithm considers only the neighbors of the candidate, placing them in R, and moves the others into the set X. At the end of the exploration, the resulting maximal clique is returned from the set R containing all the nodes that are neighbors to each other. In spite of being both recursive and iterative, in practice this algorithm is seen as one of the fastest algorithms in finding cliques because, in the worst-case scenario, its running time in an n-vertex graph is $O(3^{n/3})$.

The list of cliques alone doesn't really help you much, though, if you want to see the communities. To see them, you need to rely on specialized and complex algorithms to merge overlapping cliques and find clusters, such as the clique percolation method described at `https://www.salatino.org/wp/clique-percolation-method-in-python/`. The NetworkX package offers `k_clique_communities`, an implementation of the clique percolation algorithm, which results in the union of all the cliques of a certain size (the k parameter). These cliques of a certain size share k-1 elements (that is, they differ by just one component, a truly strict rule).

Clique percolation provides you with a list of all the communities found. In this example, one clique revolves around the karate instructor and another revolves around the president of the club. In addition, you can extract all the nodes that are part of a community into a single set, which helps you create a subgraph made just of communities.

Navigating a Graph

Navigating or *traversing* a graph means visiting each of the graph nodes. The purpose of navigating a graph can include determining node content or updating it as needed. When navigating a graph, it's entirely possible that the code will visit particular nodes more than once because of the connectivity that graphs provide. Consequently, you also need to consider marking nodes as visited after you see their content. The act of navigating a graph is important in determining how the nodes connect so that you can perform various tasks. Previous chapters discuss basic graph navigation techniques. The following sections help you understand a few of the more advanced graph-navigation techniques.

Counting the degrees of separation

The term *degrees of separation* defines the distance between nodes in a graph. When working with an undirected graph without weighted edges, each edge counts for a value of one degree of separation. However, when working with other sorts of graphs, such as maps, where each edge can represent a distance or time value, the degrees of separation can become quite different. The point is that degrees of separation indicate some sort of distance. The example in this section (and the one that follows) relies on the following graph data. (You can find this code in the `A4D2E; 10; Graph Navigation.ipynb` downloadable source code file; see the Introduction for details.)

```
import networkx as nx
import matplotlib.pyplot as plt
%matplotlib inline

data  = {'A': ['B', 'F', 'H'],
         'B': ['A', 'C'],
         'C': ['B', 'D'],
         'D': ['C', 'E'],
         'E': ['D', 'F', 'G'],
         'F': ['E', 'A'],
         'G': ['E', 'H'],
          'H': ['G', 'A']}

graph = nx.DiGraph(data)
pos=nx.spring_layout(graph)
nx.draw_networkx_labels(graph, pos, font_size=16)
nx.draw_networkx_nodes(graph, pos, node_shape="o",
                    node_color='skyblue', node_size=800)
nx.draw_networkx_edges(graph, pos, width=1, arrows=True,
                       arrowstyle='-|>', arrowsize=20)
plt.show()
```

This is an expansion of the graph used in the "Going beyond trees" section of Chapter 6 (Figure 6-2). Figure 10-3 shows how this graph appears so that you can visualize what the function call is doing. Note that this is a directed graph (`networkx DiGraph`) because using a directed graph has certain advantages when determining degrees of separation (and performing a wealth of other calculations).

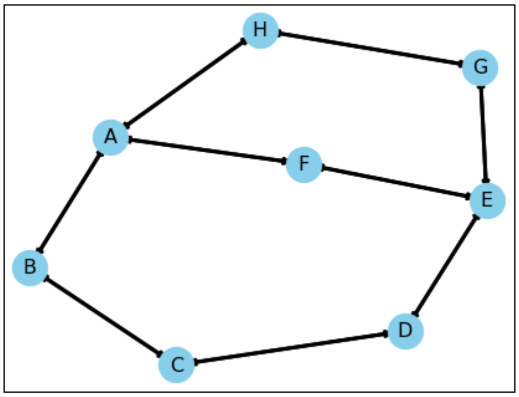


FIGURE 10-3: A sample graph used for navigation purposes.

To discover the degrees of separation between two items, you must have a starting point. For the purpose of this example, you can use node 'A'. The following code shows the required `networkx` package function call and output:

```
nx.shortest_path_length(graph, 'A')

{'A': 0, 'B': 1, 'C': 2, 'D': 3, 'E': 2, 'F': 1, 'G': 2,
 'H': 1}
```

The distance between node A and node A is 0, of course. The greatest degree of separation comes from node A to node D, which is 3. You can use this kind of information to determine which route to take or to perform an analysis of the cost in gas versus the cost in time of various paths. The point is that knowing the shortest distance between two points can be quite important. The `networkx` package used for this example comes with a wide array of distance-measuring algorithms, as described at `https://networkx.org/documentation/stable/reference/algorithms/shortest_paths.html`.

TECHNICAL STUFF

To see how using a directed graph can make a big difference when performing degrees-of-separation calculations, try removing the connection between nodes A and F. Change the data so that it looks like this:

```
data  = {'A': ['B', 'H'],
         'B': ['A', 'C'],
         'C': ['B', 'D'],
         'D': ['C', 'E'],
         'E': ['D', 'F', 'G'],
         'F': ['E', 'A'],
         'G': ['E', 'H'],
         'H': ['G', 'A']}
```

When you perform the call to `nx.shortest_path_length` this time, the output becomes quite different because you can no longer go from A to F directly. Here's the new output from the call:

```
{'A': 0, 'B': 1, 'C': 2, 'D': 3, 'E': 3, 'F': 4, 'G': 2,
 'H': 1}
```

Notice that the loss of the path has changed some of the degrees of separation. The distance to node F is now the longest at 4.

Walking a graph randomly

You might find a need to walk a graph randomly. The act of walking the graph randomly, rather than looking for a specific path, can simulate natural activities, such as an animal foraging for food. It also applies to all sorts of other interesting activities, such as playing games. However, random graph walking can have practical aspects. For example, a car is held up in traffic because of an accident, so the shortest path is no longer available. In some cases, choosing a random alternative might work best because traffic along the second shortest route could be heavy as a result of the traffic jam along the shortest route.

REMEMBER

The networkx package doesn't provide the means for obtaining a random path directly. However, it does provide the means for finding all available paths, after which you can select a path from the list randomly. The following code shows how this process might work using the graph from the previous section:

```
import random
random.seed(0)

paths = nx.all_simple_paths(graph, 'A', 'H')

path_list = []
for path in paths:
    path_list.append(path)
    print("Path Candidate: ", path)
sel_path = random.randint(0, len(path_list) - 1)

print("The selected path is: ", path_list[sel_path])

Path Candidate:  ['A', 'B', 'C', 'D', 'E', 'G', 'H']
Path Candidate:  ['A', 'H']
Path Candidate:  ['A', 'F', 'E', 'G', 'H']
The selected path is:  ['A', 'H']
```

The code sets the seed to a specific value to ensure that you get the same result every time. However, by changing the seed value, you can see different results from the example code. The point is that even the simple graph shown in Figure 10-3 offers three ways to get from node A to node H (two of which are definitely longer than the selected path in this case). Choosing just one of them ensures that you get from one node to the other, albeit by a potentially roundabout way.

IN THIS CHAPTER

» Understanding why finding what you want on the web is hard

» Reviewing problems that PageRank solves

» Implementing the PageRank algorithm with teleporting

» Learning how PageRank usage is evolving

Chapter 11 Getting the Right Web page

The last few chapters review graphs at length. The web is one of the most interesting examples of a graph structure because of the extent and complexity of its interconnected pages. This chapter explains why the ability to search for information was both important and challenging, and how early search engines almost failed in their task until Google and its search algorithm, the PageRank, appeared.

After providing an understanding of the basic algorithms that allow graph traversal and extraction of useful structures (such as the presence of clusters or communities), this chapter completes the discussion of graphs by presenting the PageRank algorithm that has revolutionized people's lives as much as the web and Internet did because it makes the web usable. The PageRank algorithm transforms links on pages into recommendations, akin to the input of expert scholars. Using examples and code, the chapter shows how the growing scale of the web also plays a role in the success of the algorithm. The larger the web, the more likely you are to get good signals for a smart algorithm like PageRank. PageRank isn't only the engine behind Google and many other search engines, but it's a smart way to derive latent information, such as relevance, importance, and reputation, from a graph structure (for instance in fraud detection or natural conservation).

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 11; PageRank.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Finding the World in a Search Engine

Libraries rely on catalogues and librarians to offer an easy way to find particular texts or explore certain subjects. Books aren't all the same: Some are good at presenting certain kinds of information; others are better. Scholar recommendations make a book an authoritative source because these recommendations often appear in other books as quotes and citations. This sort of cross-reference didn't exist on the web initially. The presence of certain words in the title or in the text of the body recommended a particular web page. This approach was practically like judging a book by its title and the number of words it contains.

For many people their personal and professional lives are unimaginable without the Internet and the web today. The Internet network is composed of interconnected pages (among other things). The web is composed of sites that are reachable by domains, each one composed of pages and hyperlinks that connect sites internally and with other sites externally. Service and knowledge resources are available through the web if you know exactly where to look. Accessing the web is unthinkable without search engines — those sites that allow you to find anything on the web using a simple query.

Searching the Internet for data

With an estimated size fluctuating between 35–40 billion pages (`https://www.worldwidewebsize.com/`), the web isn't easy to represent in graph form. Studies describe the web as a bowtie-shaped graph (see `https://immorlica.com/socNet/broder.pdf`). The web mainly consists of an interconnected core and other parts that link to that core. Since its first expansion at the beginning of the 1990s, many noticed a problem in estimating the shape and size of the web. In addition, traverse it to find information wasn't easy; many parts of it were disconnected or difficult to reach.

Search engines were developed to make the web's odd size and shape easier to deal with: to make the web accessible and useful for everyone. By taking any road in the real world, you can go anywhere (you may have to cross the oceans to do it). On the web, though, you can't touch all the sites just by following its structure; some parts aren't easily accessible (they are disconnected, or you're not in a position to reach them). If you want to find something on the web, even when time isn't a problem, you still need an index.

Considering how to find the right data

Finding the right data has been a problem since the early years of the web, but the first search engines didn't appear until the 1990s. Search engines weren't thought of earlier because other solutions, such as simple domain listings or specialized site catalogues, worked fine. Only when these solutions stopped scaling well because of the rapidly growing size of the web did search engines such as Lycos, Magellan, Yahoo!, Excite, Inktomi, and AltaVista appear.

All these search engines worked by having specialized software autonomously visit the web, using domain lists and testing hyperlinks found on the visited pages. These *spiders* explored each new link in a process called *crawling.* Spiders are pieces of software that read the pages as plain text (they can't understand images or other nontextual content).

Early search engines worked by crawling the web, collecting the information from spiders, and processing it in order to create inverted indexes. The indexes allowed the retracing of pages based on the words the pages contained. When you made a query, such inverted indexes reported all the pages containing the terms and helped score the pages, thus creating a ranking that turned into a search result The result was a list of ordered pages, ranging from the anticipated most useful page to the least useful page.

The scoring was quite naive because it often counted how frequently the keywords appeared on pages or whether they appeared in the titles or in the header of the page itself. Sometimes keywords were even scored more if they mixed or clustered together. Such simple indexing and scoring techniques allowed some web users to take advantage by using various tricks:

- **Web spammers:** Used their ability to fill the search results with pages containing poor content and a lot of advertising.
- **Unethical search engine optimization:** Used by people who employ their knowledge of search engines to make the search engine ranking higher for pages they manipulated despite their poor quality. Unfortunately, these issues still persist because search engines, even the most evolved ones, aren't immune to people who want to game the system to obtain a higher search engine ranking. The PageRank algorithm may eliminate many of the older spammers and unethical SEO people, but it's not a panacea.

REMEMBER

It's essential to distinguish unethical SEO from ethical SEO. People who use ethical SEO are professionals who employ their knowledge of search engines to better promote valid and useful pages in a legal and ethical way.

The emergence of such actors and the possibility of manipulating search engines' results created the need for better ranking algorithms in search engines. One such result is the PageRank algorithm.

Explaining the PageRank Algorithm

The PageRank algorithm is named after Google cofounder Larry Page. It made its first public appearance in a 1998 paper entitled "The Anatomy of a LargeScale Hypertextual Web Search Engine," by Sergey Brin and Larry Page, published by the journal *Computer Networks and ISDN Systems* (`http://ilpubs.stanford.edu:8090/361/1/1998-8.pdf`). At that time, both Brin and Page were PhD candidates, and the algorithm, the very foundation of Google's search technology, was initially a research project at Stanford University.

Simply stated, *PageRank* scores the importance of each node in a graph in such a way that the higher the score, the more important the node in a graph. Determining the node importance in a graph like the web means computing whether a page is relevant as part of a query's results, thus better servicing users looking for good web content.

A page is a good response to a query when it matches the query's criteria and has prominence in the system of hyperlinks that ties pages together. The logic behind prominence is that because users build the web, a page has importance in the network for good reason (the quality and authority of the page's content is assessed by its importance in the web's network of hyperlinks).

Understanding the reasoning behind the PageRank algorithm

In 1998, when both Brin and Page were still students at Stanford, the quality of search results was an issue for anyone using the web. Mainstream search engines of the time struggled both with an ever-growing web structure (Part 4 discusses algorithm scaling issues and how to make them work with big data) and with a myriad of spammers.

REMEMBER

The term *spammers* in this case doesn't refer to email spammers (those who send unrequested emails to your Inbox) but rather to web spammers (those who know the economic importance of having pages at the top of search results). This group devised sophisticated and malicious tricks in order to fool search results. Popular hacks by web spammers of the day include:

- **Keyword stuffing:** Implies overusing particular keywords in a page to trick the search engine into thinking the page seriously discusses the keyword topic.
- **Invisible text:** Requires copying the content of a page result on top of a query into a different page using the same color for both characters and background. The copied content is invisible to users but not to the search engine's spiders (which were, and still are, just scanning textual data) and to its algorithms. The trick ranks the page with invisible text as high as the originating page in a search.
- **Cloaking:** Defines a more sophisticated variant of invisible text so that, instead of text, scripts or images provide content to search engine spiders that differs from what users actually see.

Web spammers used such tricks to trick search engines to rank pages highly, even though the page content was poor and, at best, misleading. These tricks have consequences. For instance, a user might look for information relating to university research and instead be exposed to commercial advertising or inappropriate content. Users became disappointed because they often ended up at pages unrelated to their needs, requiring them to restate their queries and to spend time digging for useful information among pages of results, wasting energy in distinguishing good references from bad ones. Scholars and experts, noting the need to cope with spam results and fearing that the development of the web could halt because users had difficulties finding what they really wanted, started working on possible solutions.

As Brin and Page worked on their solving algorithm, other ideas were drafted and publicized, or developed in parallel. One such idea was Hyper Search, by Massimo Marchiori, who first pointed out the importance of web links in determining the prominence of a web page as a factor to consider during a search: `https://www.w3.org/People/Massimo/papers/WWW6/`. Another interesting solution was a web search engine project called HITS (Hypertext-Induced Topic Search), also based on the web links structure and developed by Jon Kleinberg, a young scientist working at IBM Almaden in Silicon Valley. The interesting fact about HITS is that it classifies pages into *hubs* (a page with many links to authoritative pages) and *authorities* (pages considered authoritative by many links from hubs), something that PageRank doesn't do explicitly (but implicitly does in computations) (`http://pi.math.cornell.edu/~mec/Winter2009/RalucaRemus/Lecture4/lecture4.html`).

REMEMBER

When the time is ripe, the same idea or something similar often sprouts in different places. Sometimes sharing of basic ideas occurs between researchers and scientists; sometimes ideas are developed in a completely independent way (see the history of Japanese mathematician Takakazu Seki `https://mathshistory.st-andrews.ac.uk/Biographies/Seki/`, who independently discovered many of the same things as European mathematicians such as Newton, Leibniz, and Bernoulli did around the same period). In 1998, only Brin and Page took steps to create a search engine company based on their algorithm by taking a leave from Stanford University and their doctoral studies to focus on making their algorithm work with more than a billion web pages.

Explaining the nuts and bolts of PageRank

The innovation brought about by PageRank is that an inverted index of terms isn't enough to determine whether a page matches a user's information query. Matching words (or meaning, the semantic query match discussed at the end of the chapter) between a query and the page text is a prerequisite, but it isn't sufficient because hyperlinks are necessary to assess whether the page offers quality content and is authoritative.

When discussing sites, distinguishing between inbound and outbound links is important, and you shouldn't consider internal links that connect within the same site. The links you see on a page are *outbound* when they lead to another page on another site. The links that bring someone to your page from another page on another site are *inbound* links (backlinks). As the page creator, you use outbound links to provide additional information to the page content. You presumably won't use random links on your page (or links pointing to useless or bad content) because that would spoil the page quality. As you point to good content using links, other page creators use links on their pages to point to your page when your page is interesting and of high quality.

It's a chain of trust. Hyperlinks are like endorsements or recommendations for pages. Inbound links show that other page creators trust you, and you share part of that trust by adding outbound links on your pages to point to other pages.

Implementing PageRank

Representing this chain of trust mathematically requires simultaneously determining how much authority your page has, as measured by inbound links, and how much it donates to other pages by outbound links. You can achieve such computations in two ways:

- **Simulation:** Uses the behavior of a web surfer who browses randomly on the web (a *random surfer*). This approach requires that you recreate the web structure and run the simulation.

» **Matrix computation:** Replicates the behavior of a random surfer using a *sparse matrix* (a matrix in which most data is zero) replicating the web structure. This approach requires some matrix operations, as explained in Chapter 5, and a series of computations that reach a result by successive approximation.

Even though it's more abstract, using the matrix computation for PageRank requires fewer programming instructions, and you can easily implement it using Python. (You can try the PageRank algorithm on real-world sites using an automatic PageRank checker, such as `https://checkpagerank.net/index.php`. Unfortunately, the program may produce inaccurate results for newer sites because they haven't been crawled properly yet, it can give you an idea of what PageRank is like in practice.)

Implementing a Python script

PageRank is a function that scores the nodes in a graph with a number (the higher the number, the more important the node). When scoring a web page, the number could represent the probability of a random surfer visit. You express probabilities using a number from 0.0 to a maximum 1.0 and, ideally, when representing the probability of being on a particular site among all available sites, the sum of all the probabilities of the pages on the web should equal 1.0.

REMEMBER

Many versions of PageRank exist, each one changing its recipe a little to fit the kind of graph it has to score. The example in this section presents you with the original version for the web presented in the previously mentioned paper by Brin and Page and in the paper "The PageRank Citation Ranking: Bringing Order to the Web" (`http://ilpubs.stanford.edu:8090/422/1/1999-66.pdf`).

The example creates three different web networks made of six nodes (web pages). The first one is a good working network, and the other two demonstrate problems that a random surfer may encounter because of the web structure or a web spammer's actions. This example also uses the NetworkX commands discussed in Chapter 8 and the NumPy package for matrix computations, as described in Chapter 4.

```
import numpy as np
import networkx as nx
import matplotlib.pyplot as plt

Graph_A = nx.DiGraph()
Graph_B = nx.DiGraph()
Graph_C = nx.DiGraph()
```

```
Nodes = range(1,6)
Edges_OK = [(1,2),(1,3),(2,3),(3,1),(3,2),(3,4),(4,5),
            (4,6),(5,4),(5,6),(6,5),(6,1)]
Edges_dead_end = [(1,2),(1,3),(3,1),(3,2),(3,4),(4,5),
                  (4,6),(5,4),(5,6),(6,5),(6,1)]
Edges_trap = [(1,2),(1,3),(2,3),(3,1),(3,2),(3,4),(4,5),
              (4,6),(5,4),(5,6),(6,5)]
Graph_A.add_nodes_from(Nodes)
Graph_A.add_edges_from(Edges_OK)
Graph_B.add_nodes_from(Nodes)
Graph_B.add_edges_from(Edges_dead_end)
Graph_C.add_nodes_from(Nodes)
Graph_C.add_edges_from(Edges_trap)
```

This code displays the first network, the good one, as shown in Figure 11-1.

```
np.random.seed(2)
pos=nx.shell_layout(Graph_A)
draw_params = {'with_labels':True,
               'arrows': True,
               'node_color':'skyblue',
               'node_size':700, 'width':2,
               'font_size':14}
nx.draw(Graph_A, pos, **draw_params)
plt.show()
```

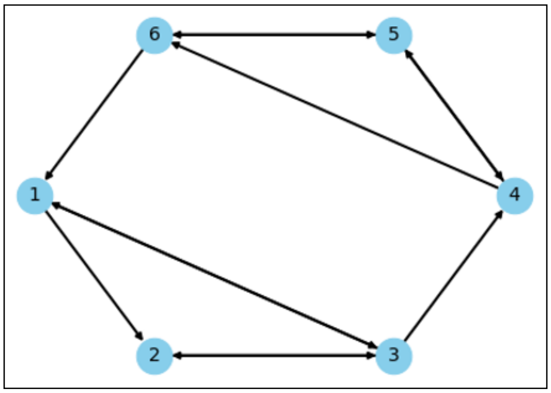


FIGURE 11-1: A strongly connected network.

TIP

All nodes connect with each other. This is an example of a strongly connected graph, which contains no isolated nodes or single nodes and enclaves that act as dead ends. A random surfer can freely run through it and never stop, and any node can reach any other node. The NetworkX representation of a directed graph uses arrows to represent the direction of an edge. For example, a surfer can go from node 4 to node 6 because there is a thick line entering node 6 from node 4. However, the surfer can't go from node 6 to node 4 because the line entering node 4 from node 6 is thin.

The second graph isn't strongly connected. It presents a trap for a random surfer because node 2 has no outbound links, and a user visiting the page could stop there and find no way out. This isn't an unusual event considering the structure of the web, but it could also show a spammer artifact, such that the spammer created a spam factory with many links that direct to a dead end site to trap web surfers. Figure 11-2 shows the output of the following code, which was used to display this graph.

```
np.random.seed(2)
pos=nx.shell_layout(Graph_B)
nx.draw(Graph_B, pos, **draw_params)
plt.show()
```

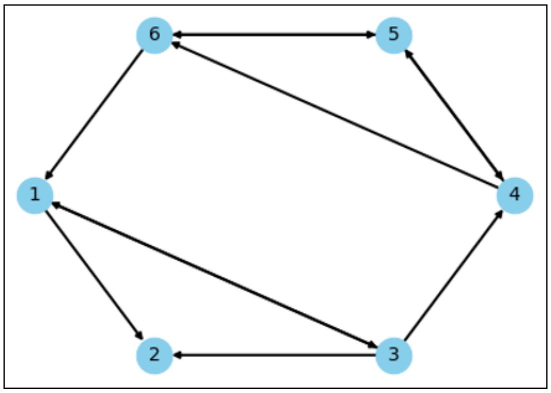


FIGURE 11-2: A network with a dead end in node 2.

Another situation that may be natural or the result of a spammer's action is a spider trap. It's another dead end for a surfer, this time not on a single page but on a closed site that lacks links to an outside network of pages. Figure 11-3 shows the output of the following code, which was used to display this graph.

```
np.random.seed(2)
pos=nx.shell_layout(Graph_C)
nx.draw(Graph_C, pos, **draw_params)
plt.show()
```

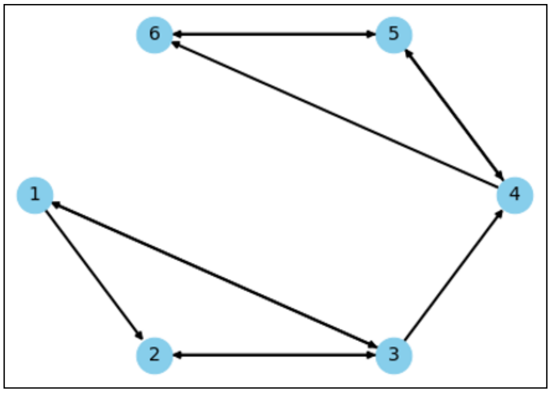


FIGURE 11-3: A network with a spider trap in nodes 4, 5, and 6.

REMEMBER

It's called a *spider trap* because spammers devised it as a way to catch search engine software spiders in a loop and let them believe that the only websites were the ones inside the closed network.

Struggling with a naive implementation

Given a graph made by using Python and NetworkX, you can extract its structure and render it as a *transition matrix*, a matrix that represents nodes in columns and rows:

- **Columns:** Contain the node a web surfer is on
- **Rows:** Contain the probability that the surfer will visit other nodes because of outbound links

In the real web, the transition matrix that feeds the PageRank algorithm is built by spiders' continuous exploration of links.

```
def initialize_PageRank(graph):
    nodes = len(graph)
    M = nx.to_numpy_matrix(graph)
    outbound = np.squeeze(np.asarray(np.sum(M, axis=1)))
    prob_outbound = np.array(
        [1.0/count
         if count>0 else 0.0 for count in outbound])
    G = np.asarray(np.multiply(M.T, prob_outbound))
    p = np.ones(nodes) / float(nodes)
    if np.min(np.sum(G,axis=0)) < 1.0:
        print ('Warning: G is substochastic')
    return G, p
```

The Python code creates the function `initialize_PageRank()`, which extracts both the transition matrix and the initial vector of default PageRank scores.

```
G, p = initialize_PageRank(Graph_A)
print(G)

[[ 0.      0.      0.33333333  0.      0.      0.5 ]
 [ 0.5     0.      0.33333333  0.      0.      0.  ]
 [ 0.5     1.      0.          0.      0.      0.  ]
 [ 0.      0.      0.33333333  0.      0.5     0.  ]
 [ 0.      0.      0.          0.5     0.      0.5 ]
 [ 0.      0.      0.          0.5     0.5     0.  ]]
```

The printed transition matrix `G` represents the transition matrix of the network described in Figure 11-1. Each column represents a node in the sequence 1 through 6. For instance, the third column represents node 3. Each row in the column shows the connections with other nodes (outbound links toward nodes 1, 2, and 4) and values that define the probability of a random surfer using any of the outbound links (that is, 1/3, 1/3, 1/3).

TIP

The diagonal of the matrix is always zero unless a page has an outbound link toward itself (it is a possibility).

The matrix contains more zeros than values. This is also true in reality because estimates show that each site has only ten outbound links on average. Because billions of sites exist, the nonzero values in a transition matrix representing the web are minimal. In this case, it's helpful to use a data structure such as an adjacency list (explained in the "Creating the graph" section of Chapter 9 and mentioned again in the "Distributing files and operations" section of Chapter 13) to represent data without wasting disk or memory space with zero values:

```
from scipy import sparse
sG = sparse.csr_matrix(G)
print (sG)

  (0, 2)   0.333333333333
  (0, 5)   0.5
  (1, 0)   0.5
  (1, 2)   0.333333333333
  (2, 0)   0.5
  (2, 1)   1.0
  (3, 2)   0.333333333333
  (3, 4)   0.5
  (4, 3)   0.5
  (4, 5)   0.5
  (5, 3)   0.5
  (5, 4)   0.5
```

This example has just 12 links out of 30 possible (without counting links to *self*, which is the current site). Another particular aspect of the transition matrix to note is that if you sum the columns, the result should be 1.0. If it is a value less than 1.0, the matrix is *substochastic* (which means that the matrix data isn't representing probabilities properly because probabilities should sum to 1.0) and cannot work perfectly with PageRank estimations.

Accompanying `G` is a vector `p`, the initial estimate of the total PageRank score, equally distributed among the nodes. In this example, because the total PageRank is 1.0 (the probability of a random surfer being in the network, which is 100 percent), it's distributed as 1/6 among the six nodes:

```
print(p)

[ 0.16666667  0.16666667  0.16666667  0.16666667
  0.16666667  0.16666667]
```

To estimate the PageRank, take the initial estimate for a node in the vector `p`, multiply it by the corresponding column in the transition matrix, and determine how much of its PageRank (its authority) transfers to other nodes. Repeat for all nodes and you'll know how PageRank transfers between nodes because of the network structure. You can achieve this computation using a matrix-vector multiplication:

```
print(np.dot(G, p))

[ 0.13888889  0.13888889  0.25        0.13888889
  0.16666667  0.16666667]
```

After the first matrix-vector multiplication, you obtain another estimate of PageRank that you use for redistribution among the nodes. By redistributing multiple times, the PageRank estimate stabilizes (results won't change), and you'll have the score you need. Using a transition matrix containing probabilities and estimation by successive approximation using matrix-vector multiplication obtains the same results as a computer simulation with a random surfer:

```
def PageRank_naive(graph, iters = 50):
    G, p = initialize_PageRank(graph)
    for i in range(iters):
        p = np.dot(G,p)
    return np.round(p,3)

print(PageRank_naive(Graph_A))

[ 0.154  0.154  0.231  0.154  0.154  0.154]
```

The new function `PageRank_naive()` wraps all the previously described operations and emits a vector of probabilities (the PageRank score) for each node in the network. Node 3 emerges as the one with most importance. Unfortunately, the same function doesn't work with the other two networks:

```
print(PageRank_naive(Graph_B))
Warning: G is substochastic
[ 0.  0.  0.  0.  0.  0.]

print(PageRank_naive(Graph_C))
[ 0.     0.     0.     0.222  0.444  0.333]
```

In the first case, the probabilities seem to drain out of the network — the effect of a dead-end website and the resulting substochastic transition matrix. In the second case, the bottom half of the network unfairly gets all the importance, leaving the top part as insignificant.

Introducing boredom and teleporting

Both dead ends (*rank sinks*) and spider traps (*cycles*) are common situations on the web because of users' choices and spammers' actions. The problem, however, is easily solved by making the random surfer randomly jump to another network node (*teleporting*, as in the sci-fi devices that take you instantaneously from one place to another). The theory is that a surfer will get bored at one point or another and move away from deadlocking situations. Mathematically, you define an alpha value representing the probability of continuing the random journey on the graph by the surfer. The alpha value redistributes the probability of being on a node independently of the transition matrix.

TIP

The value originally suggested by Brin and Page for alpha (also called the damping factor) is 0.85 (or only a 0.15 chance of teleporting), but you can change it according to your needs. For the web, it works the best between 0.8 and 0.9 (read about why at `https://www.cise.ufl.edu/~adobra/DaMn/talks/damn05-santini.pdf`). The smaller the alpha value, the shorter the trip of the surfer on the network, on average, before restarting somewhere else.

```
def PageRank_teleporting(graph, iters=50, alpha=0.85,
                         rounding=3):
```

```
    G, p = initialize_PageRank(graph)
    u = np.ones(len(p)) / float(len(p))
    for i in range(iters):
        p = alpha * np.dot(G,p) + (1.0 - alpha) * u
    return np.round(p / np.sum(p), rounding)

print('Graph A:', PageRank_teleporting(Graph_A,
                                    rounding=8))
print('Graph B:', PageRank_teleporting(Graph_B,
                                    rounding=8))
print('Graph C:', PageRank_teleporting(Graph_C,
                                    rounding=8))

Graph A: [ 0.15477863  0.15346061  0.22122243  0.15477863
           0.15787985  0.15787985]
Warning: G is substochastic
Graph B: [ 0.16502904  0.14922238  0.11627717  0.16502904
           0.20222118  0.20222118]
Graph C: [ 0.0598128   0.08523323  0.12286869  0.18996342
           0.30623677  0.23588508]
```

After applying the modifications to a new function, `PageRank_teleporting()`, you can get similar estimates for the first graph as well as much more realistic (and useful) estimates for both the second and third graphs, without falling into the traps of dead ends or rank sinks. Interestingly, the function is equivalent to the one provided by NetworkX: `https://networkx.org/documentation/stable/reference/algorithms/generated/networkx.algorithms.link_analysis.pagerank_alg.pagerank.html`.

```
nx.pagerank(Graph_A, alpha=0.85)

{1: 0.15477892494151968,
 2: 0.1534602056628941,
 3: 0.2212224378270561,
 4: 0.15477892494151968,
 5: 0.1578797533135051,
 6: 0.15787975331350507}
```

Looking inside the life of a search engine

Though it reports only on the web hyperlink structure, PageRank reveals how authoritative a page can become. However, Google's ranking algorithm isn't composed only of PageRank. The algorithm provides solid foundations for any query, and it initially bootstrapped Google's fame as a reliable search engine. Today, PageRank is just one of the many ranking factors that intervene when processing a query.

Specialized sources in SEO knowledge quote more than 200 factors as contributing to the results that Google provides. To see what other sorts of ranking factors Google considers, consult the lists at `https://moz.com/learn/seo/on-page-factors` and `https://moz.com/learn/seo/off-site-seo` (made by MOZ, a U.S. company).

You must also consider that the Google algorithm has received many updates, and at this point, it's more of an ensemble of different algorithms, each one named with a fantasy name (Caffeine, Panda, Penguin, Hummingbird, Pigeon, Mobile Update). You can find a complete, curated list by year at `https://www.searchenginejournal.com/google-algorithm-history/` thanks to SEJ, the Search-Engine Journal. Many of these updates have caused shake-ups of previous search rankings and were motivated by the need to fix spamming techniques or make surfing the web more useful for users; for instance, the Mobile Update induced many sites to render their interfaces mobile-phone friendly.

Considering other uses of PageRank

Although PageRank provides better search results, its applicability isn't limited to Google or search engines. You can use PageRank anywhere you can reduce your problem to a graph. Just modify and tune the algorithm to your needs. Cornell University has enumerated some other potential uses of PageRank in different sectors (`https://blogs.cornell.edu/info2040/2014/11/03/more-than-just-a-web-search-algorithm-googles-pagerank-in-non-internet-contexts/`), and surprising reports have emerged of the algorithm being successfully used in computational biology (`https://www.wired.com/2009/09/googlefoodwebs/`). By creating a teleportation tied to specific nodes that you want to explore, you see the algorithm shining at diverse applications such as the following:

- **Fraud detection:** Revealing how certain persons and facts are related in unexpected ways
- **Product recommendation:** Suggesting products that a person with a certain affinity might like

Going Beyond the PageRank Paradigm

In recent years, Google has done more than introduce more ranking factors that modify the original PageRank algorithm. It has introduced some radical changes that leverage page content better (to avoid being fooled by the presence of certain keywords) and has adopted AI algorithms that rank the relevance of a page in a search result autonomously. These changes have led some search experts to declare that PageRank doesn't determine the position of a page in a search any longer (see `https://www.entrepreneur.com/article/269574`). They still debate the question, but it's most likely safe to assume that PageRank is still powering the Google engine as a ranking factor, albeit not sufficiently to enlist a page into the best results after a query.

Introducing semantic queries

If you currently try to pose questions, not just chains of keywords, to Google, you'll notice that it tends to answer smartly and gets the sense of the question. As of 2012, Google became better able to understand synonyms and concepts. However, after August 2013, the Hummingbird update (`https://searchengineland.com/google-hummingbird-172816`) truly changed the game because the search engine became capable of understanding conversational searches (queries in which you ask something as you would say it to another person) as well as the semantics behind queries and a page's contents.

Since this update, the Google algorithm has worked by disambiguating both users' intentions and the meanings expressed by pages, not just by the keywords. The update made the search engine work more in a semantic way, which means understanding what words imply on both sides: the query and resulting web pages. In this sense, it can't be tricked anymore by playing with keywords. Even without much support from PageRank, the search engine can look at how a page is written and get a sense of whether the page contains content good enough for inclusion in the results of a query.

Using AI for ranking search results

PageRank is still at the core of search result ranking, but the results have less weight because of the introduction of machine learning technology into ranking, the so-called RankBrain. According to some sources (see `https://www.searchenginejournal.com/google-algorithm-history/rankbrain/`), the machine learning algorithm now acts as a preconditioner, a filtering device that assesses the received query and computes proper weights for the signals it spots in the query.

Even though RankBrain is still cloaked in secrecy, its importance has grown, and the algorithm seems to be capable of guessing, with much higher accuracy than performed by a human being, whether the contents of a page can appear in search results. It overrides all other ranking factors in cases that are difficult to judge. This is another example of an additional algorithm that limits the role played by the original PageRank algorithm.

4 Wrangling Big Data

IN THIS PART . . .

Interacting with and managing big data

Processing big data in more efficient ways

Making data smaller

Hiding data using encryption

IN THIS CHAPTER

» Becoming familiar with Moore's Law and its implications

» Understanding big data and its 4 Vs

» Discovering how to deal with infinite streaming data

» Leveraging sampling, hashing, and sketches for stream data

Chapter 12 Managing Big Data

Big data is more than a buzzword used by vendors to propose innovative ways to store data and analyze it. Big data is also not a fad. Instead, it's a reality and a driving force of our times. You may have heard it mentioned in many specialized scientific and business publications and even wondered what *big data* really means (no, it isn't about placing information on billboards in large letters). From a technical point of view, big data refers to large and complex amounts of computer data, so large (as the name implies) and intricate that the data you can't deal with it by making more storage available on your computers or by making new computers more powerful and faster in their computations. The first part of this chapter discusses the implications of big data and what it means with regard to algorithms.

You need to know more about data than where it comes from or its implications for hardware, software, and analysis. The second part of the chapter looks at the idea of *streaming data,* which involves putting it into a form for it to be reviewed in an orderly fashion. This means applying algorithmic tools such as sampling and hashing, which you can read about in the second section of this chapter. You also consider the effects of *sampling,* which is the process of reserving the correct data for various uses. (Hashing is covered in detail in the "Relying on Hashing" section of Chapter 7.)

The third section of the chapter looks at *sketching,* which is a method of creating a simple and approximate data summary. This process begins with hashing, but then moves on to creating the data summary using various algorithms.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `\A4D2E\A4D2E; 12; Managing Big Data .ipynb` file of the downloadable source. See the Introduction for details on how to find these source files.

Transforming Power into Data

In 1965, Gordon Moore, cofounder of Intel and Fairchild Semiconductor (two giant companies that produce electronic components for electronics and computers), stated in an *Electronics* magazine paper entitled "Cramming More Components Onto Integrated Circuits" that the number of components found in integrated circuits would double every year for the next decade (`https://www.britannica.com/technology/Moores-law`). (He later revised his prediction to every two years.) At that time, transistors dominated electronics. Being able to stuff more transistors into a circuit using a single electronic component that gathered the functionalities of many of them (an integrated circuit), meant being able to make electronic devices more capable and useful. This process is *integration* and implies a strong process of electronics miniaturization (making the same circuit much smaller, which makes sense because the same volume should contain double the circuitry as the previous year).

As miniaturization proceeds, electronic devices, the final product of the process, become smaller or simply more powerful. For instance, today's computers aren't larger than computers of a decade ago, yet they are decisively more powerful. The same goes for mobile phones. Even though they're the same size as their predecessors, they have become able to perform more tasks. Other devices, such as sensors, are simply smaller, which means that you can put them everywhere and even find new unforeseen uses.

Understanding Moore's implications

What Moore stated in the article mentioned at the beginning of this section proved true for many years, and the semiconductor industry calls it Moore's Law (see `http://www.mooreslaw.org/` for details). Doubling did occur for the first ten years, as predicted. In 1975, Moore corrected his statement, forecasting a doubling every two years. Figure 12-1 shows the effects of this doubling. This rate of doubling is still valid (`https://www.wired.com/beyond-the-beyond/2020/03/preparing-end-moores-law/`), but some naysayers aren't happy about it, so they say it's going to end. (Others disagree.) Starting in 2012, a mismatch occurs between the expectation of cramming more transistors into a component to make it faster and what semiconductor companies can achieve with regard to miniaturization. In truth, physical barriers exist to integrating more circuitry into an integrated circuit using the present silica components. (However, innovation will continue; you can read the article at `https://www.nature.com/news/the-chips-are-down-for-moore-s-law-1.19338` for more details.) In addition, Moore's Law isn't actually a law — it's an observation, or even a tentative, implicit goal for the industry to strive to achieve (a self-fulfilling prophecy, in a certain sense).

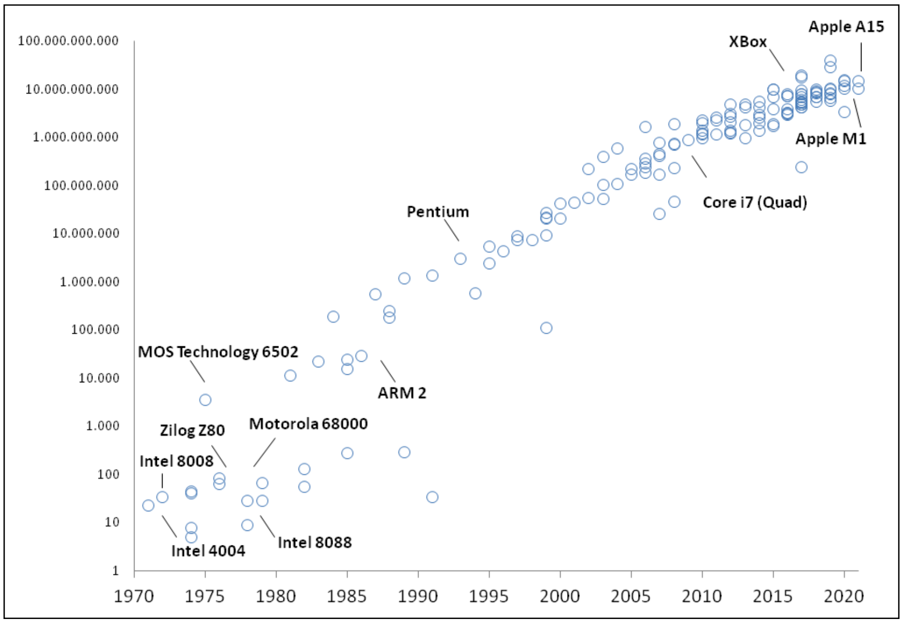


FIGURE 12-1: Stuffing more and more transistors into a CPU.

Eventually, Moore's Law may not apply anymore because industry will switch to new technology, such as making components by using optical lasers instead of transistors (see the article at `https://sciencenordic.com/computers-denmark-forskerzonen/optical-computers-light-up-the-horizon/1454763` for details about optical computing) or turning to quantum computing (see the article at `https://www.nasa.gov/feature/ames/quantum-supremacy`). What matters is that since 1965, about every two years the computer industry experienced great advancements in digital electronics that had consequences.

REMEMBER

Some people advocate that Moore's Law already no longer holds. The chip industry has kept up the promise so far, but now it's lowering expectations. Intel has already increased the time between its generations of CPUs, saying that in five years, chip miniaturization will hit a wall. (Read about the waves in chip development at `https://scitechdaily.com/twilight-for-silicon-end-of-moores-law-in-view-as-silicon-chip-density-nears-physical-limit/`.)

POLITICS AND THE LEGAL STUFF

Depending on whom you talk with, the whole issue of whether a law will stand the test of time can look different because that person will have a different perspective. This book isn't here to convince you of one point of view or another; it simply reports the prevalent view. For example, Moore's Law is arguably every bit as proven as the laws of thermodynamics. If you look into conventional physics more, you can find many discrepancies with its laws and many of its assumptions. It's not a matter of devaluing science in any way — just pinpointing the fact that everything in science, including its laws, is a work in progress.

As to whether Moore's Law will cease to exist, generally speaking, laws don't stop applying; scientists refurbish them so that they are more in line with the facts. Really? Did we say that? Well, what we really meant was that Moore's Law may undergo the same transformation. Linear or overly simplistic laws rarely apply in a general sense because there are no straight lines anywhere in nature, including its temporal models. Therefore, the most likely scenario is that Moore's Law will change into a more sigmoidal function in an attempt to adhere to reality.

Moore's Law has a direct effect on data. It begins with smarter devices. The smarter the devices, the more the diffusion. (Electronics are everywhere in our day and age.) The greater the diffusion, the lower the price becomes, creating an endless loop that drove and is driving the use of powerful computing machines and small sensors everywhere. With large amounts of computer memory available and larger storage disks for data, the consequences are an expansion of the availability of data, such as websites, transaction records, a host of various measurements, digital images, and other sorts of data flooding in from everywhere.

Finding data everywhere

Scientists began fighting against impressive amounts of data for years before anyone coined the term *big data.* At this point, the Internet didn't produce the vast sums of data that it does today. It's useful to remember that big data is not just simply a fad created by software and hardware vendors but has a basis in many of the following fields:

- **Astronomy:** Consider the data received from spacecraft on a mission (such as Voyager or Galileo) and all the data received from radio telescopes, which are specialized antennas used to receive radio waves from astronomical bodies. A common example is the Search for Extraterrestrial Intelligence (SETI) project (`https://www.seti.org/`), which looks for extraterrestrial signals by observing radio frequencies arriving from space. The data is based on technosignatures, millions of them, that generate huge amounts of data (`https://www.sciencealert.com/scientists-detected-26-million-possible-technosignatures-they-all-came-from-us`) even if they mostly come from human sources. Proxima Centauri did recently call (`https://theconversation.com/seti-new-signal-excites-alien-hunters-heres-how-we-could-find-out-if-its-real-152498`), but it's the exception rather than the rule (making everyone feel like moms who don't hear from their kids).

Another example of the astonishing amount of data generated from different telescopes is the assembly of the first image of a black hole located at the center of the galaxy M87 (for more details, read: `https://www.jpl.nasa.gov/edu/news/2019/4/19/how-scientists-captured-the-first-image-of-a-black-hole/`).

- **Meteorology:** Think about trying to predict weather for the near term given the large number of required measures, such as temperature, atmospheric pressure, humidity, winds, and precipitation at different times, locations, and altitudes. Weather forecasting is really one of the first problems in big data, and quite a relevant one. According to Weather Analytics, a company that provides climate data, more than 33 percent of Worldwide Gross Domestic Product (GDP) is determined by how weather conditions affect agriculture, fishing, tourism, and transportation, just to name a few. Dating back to the 1950s, the first supercomputers of the time were used to crunch as much data as possible because, in meteorology, the more data, the more accurate the forecast (see `https://bigdataanalyticsnews.com/big-data-enhance-weather-forecasting/` for details).
- **Physics:** Consider the large amounts of data produced by experiments using particle accelerators in an attempt to determine the structure of matter, space, and time. For example, the Large Hadron Collider (`https://home.cern/science/accelerators/large-hadron-collider`), the largest particle accelerator ever created, produces 15PB (petabytes, or 1 million gigabytes) of data every year as a result of particle collisions (`https://home.cern/science/computing`).
- **Genomics:** Sequencing a single DNA strand, which means determining the precise order of the many combinations of the four bases — adenine, guanine, cytosine, and thymine — that constitute the structure of the molecule, requires quite a lot of data. For instance, a single chromosome, a structure containing the DNA in the cell, may require from 50MB to 300MB. A human being has 46 chromosomes, and the DNA data for just one person consumes an entire DVD. Just imagine the massive storage required to

document the DNA data of a large number of people or to sequence other life forms on earth (see `https://www.zymergen.com/blog/the-art-of-biological-data-science-bringing-biologys-great-unknowns-into-focus/`).

- **Oceanography:** There are many sensors placed in the oceans measure temperature, currents, and other useful information. In addition, by using hydrophones, it's possible to record sounds for acoustic monitoring for scientific purposes (discovering facts about fish, whales, and plankton) and for military defense purposes (finding sneaky submarines from other countries). Oddly enough, Covid-19 has made collecting even more data less difficult (read `https://www.eurekalert.org/news-releases/749064` for details).
- **Satellites:** Recording images from the entire globe and sending them back to earth in order to monitor the Earth's surface and its atmosphere isn't a new business (TIROS 1, the first satellite to send back images and data, dates back to 1960). The question of just how many satellites are up there is a complex one, but you can get an idea of the number active satellites and their purpose at `https://www.geospatialworld.net/blogs/how-many-satellites-are-orbiting-the-earth-in-2021/`. The amount of data arriving on earth is astonishing, and it serves both military (surveillance) and civilian purposes, such as tracking economic development, monitoring agriculture, and monitoring changes and risks. A single European Space Agency's satellite, Sentinel 1A, generates 5PB of data during two years of operation, as you can read at `https://spaceflightnow.com/2016/04/28/europes-sentinel-satellites-generating-huge-big-data-archive/`.

Accompanying these older data trends, new amounts of data are now generated or carried about by the Internet, creating new issues and requiring solutions in terms of both data storage and algorithms for processing:

- The statistics of Internet usage are ever growing, and you can't determine whether the numbers you read one day are still valid the next (`https://www.internetadvisor.com/key-internet-statistics`). In recent years, more people have gained access to Internet, not just by means of computers but also by mobile devices such as smart phones. The COVID-19 pandemic has even heightened this trend because it forced many to stay at home and shop or work from there.
- The Internet of Things (IoT) has become a reality. You may have heard the term many times in the last 20 years, but now the growth of the stuff connected to the Internet has exploded. The idea is to put sensors and transmitters on everything and use the data to both better control what happens in the world and to make objects smarter (plus, it's also a handy way for the government to monitor people, if you're a conspiracy theorist). Transmitting

devices are getting tinier, cheaper, and less power-demanding; some are already so small that they can be put everywhere. IoT devices also come in forms that you might not expect (`https://www.asme.org/topics-resources/content/9-cool-iot-devices-for-our-daily-lives`). Experts estimate that in 2019, IoT devices already produced around 17.3ZB (a zettabyte corresponds to one million petabytes) of data. That figure is expected to grow by more than four times and become 73.1ZB by 2025 (`https://dataprot.net/statistics/iot-statistics/`).

Getting algorithms into business

The human race is now at an incredible intersection of technologies: unprecedented volumes of data that are generated by increasingly smaller and more powerful hardware and are being analyzed by algorithms that this same process helped develop. It's not simply a matter of volume, which by itself is a difficult challenge. As formalized by the research company Gartner in 2001 and then reprised and expanded by other companies, such as IBM, big data can be summarized by four *V*s representing its key characteristics (`https://edudataonline.com/4-vs-of-big-data/`):

- **Volume:** The amount of data
- **Velocity:** The speed of data generation
- **Variety:** The number and types of data sources
- **Veracity:** The quality and authoritative voice of the data (quantifying errors, bad data, and noise mixed with signals), a measure of the uncertainty of the data

Read on for more details of these key characteristics.

Volume

Each big data characteristic offers a challenge and an opportunity. For instance, volume is a challenge for storage systems, forcing an organization to revise its prevalent methods and solutions and pushing present technologies and algorithms to look ahead. However, volume is also an opportunity because you can expect a certain amount of useful information in all that data. This useful information provides new capabilities and helps achieve results that weren't possible before. As an example, consider how more data can help in understanding shifting consumer preferences in global markets or in serving a company's customers in the best way.

Velocity

In addition to the challenges of volume, velocity requires that you catch data in a timely manner or it will slip out of sight. For the organizations that are fast enough to grasp it, velocity opens up the ability to react to threats in real time and presents additional opportunities for gains of various sorts (such as a financial gain). It doesn't matter whether the data is from security threats or financial markets, it can inform you about anything that happens under the sun.

Variety

Variety requires that you to cope with data in many formats. Some of the formats are expected because you planned and devised them; others are unexpected and complicated because other entities produced them. Variety implies that you can't count on finding what you're looking for in specific places, or written in ways you can immediately understand. Techniques used to search for and process information become much more flexible in the time of big data, requiring skills more similar to those of a researcher or an investigator than of a librarian or warehouser.

Veracity

The veracity characteristic helps the democratization of data itself. In the past, organizations hoarded data because it was precious and difficult to obtain. At this point, various sources create data in such growing amounts that hoarding it is meaningless (90 percent of the world's data has been created in the last two years), so limiting access is pointless. Data is turning into such a commodity that many open data programs go on all around the world. (The United States has a long tradition of open access; the first open data programs date back to the 1970s when the National Oceanic and Atmospheric Administration, NOAA, started releasing weather data freely to the public.) However, because data has become a commodity, the uncertainty of that data has become an issue. You no longer know whether the data is completely true because you may not even know its source.

REMEMBER

Data has become so ubiquitous that its value is no longer in the actual information (such as data stored in a firm's database). The value of data exists in how you use it. Here, algorithms come into play and change the game. A company like Google feeds itself from freely available data, such as the content of websites or the text found in publicly available texts and books. Yet, the value Google extracts from the data mostly derives from its algorithms. For example, data value resides in the PageRank algorithm (discussed in Chapter 11), which is the very foundation of Google's business. The value of algorithms is true for other companies as well. Amazon's recommendation engine contributes a significant part of the company's revenues. Many financial firms use algorithmic trading and robo-advice, leveraging freely available stock data and economic information for investments.

Streaming Flows of Data

When data flows in huge amounts, storing it all may be difficult or even impossible. In fact, storing it all might not even be useful. Here are some figures from the most recent statistics, from 2019–2020, of just some of what you can expect to happen within a single minute on the Internet:

- 188 million emails sent
- 350,000 new tweets sent on Twitter
- 3.8 million queries requested on Google
- 1,000,000 people logged in to their account on Facebook

Given such volumes, accumulating the data all day for incremental analysis might not seem efficient. You simply store it away somewhere and analyze it some other day (which is the widespread archival strategy that's typical of databases and data warehouses). However, useful data queries tend to ask about the most recent data in the stream, and data becomes less useful when it ages (in some sectors, such as financial, a day can be a lot of time). Moreover, you can expect even more data to arrive tomorrow (the amount of data increases daily), and that makes it difficult, if not impossible, to pull data from repositories as you push new data in. Pulling old data from repositories as fresh data pours in is akin to the punishment of Sisyphus. Sisyphus, as a Greek myth narrates, received a terrible punishment from the god Zeus: being forced to eternally roll an immense boulder up to the top of a hill, only to watch it roll back down each time (see `https://www.mythweb.com/encyc/gallery/sisyphus_c.html` for additional details).

Sometimes data can arrive so fast and in such large quantities that writing it to disk is impossible: New information arrives faster than the time required to write it to the hard disk. This is a problem typical of particle experiments with particle accelerators such as the Large Hadron Collider, requiring scientists to decide what data to keep (`https://home.cern/science/computing/storage`). Of course, you may queue data for some time, but not for too long, because the queue will quickly grow and become impossible to maintain. For instance, if kept in memory, queue data will soon lead to an out-of-memory error.

Because new data flows may render the previous processing of old data obsolete, and procrastination is not a solution, people have devised multiple strategies to deal instantaneously with massive and changeable data amounts. People use three ways to deal with large amounts of data:

- **Stored:** Some data is stored as it is because it may help answer unclear questions later. This method relies on techniques to store it immediately and process it later very fast, no matter how massive it is.

- **Summarized:** Some data is summarized because keeping it all as it is makes no sense; only the important information is kept.
- **Consumed:** The remaining data is consumed because its usage is predetermined. Algorithms can instantly read, digest, and turn the data into signals or actions. After that, the system forgets the data forever.

The book deals with the first point in Chapter 13, which is about distributing data among multiple computers and understanding the algorithms used to deal with it (a divide-and-conquer strategy). The following sections address the second and third points, applying them to data that streams in systems.

TIP

When talking of massive data arriving into a computer system, you will often hear a water metaphor: streaming data, data streams, data fire hose. You discover how working with data streams is like consuming tap water: For the latter, opening the tap lets you collect water for storage in cups or drinking bottles, or you can use it for cooking, scrubbing food, cleaning plates, or washing hands. In any case, after any of these uses, most or all of the water is gone, yet it has been very useful and indeed vital.

Analyzing streams with the right recipe

Streaming data needs streaming algorithms, and the key point to know about streaming algorithms is that, apart from a few measures that it can compute exactly, a streaming algorithm necessarily provides approximate results. The algorithm output is almost correct; it doesn't guess the precise answer, but one close to it.

In addition to the water metaphor of the previous section, another useful metaphor for understanding streams relates to combining ingredients in a recipe. (We're truly not trying to make you soggy or hungry.) When dealing with streams, you clearly have to concentrate only on the measures of interest and leave out many details. You could be interested in a statistical measurement, such as mean, minimum, or maximum. Moreover, you could want to count elements in the stream or distinguish old information from new. There are many algorithms to use, depending on the problem, yet the recipes always use the same ingredients. The trick of cooking the perfect stream is to use one or all of these algorithmic tools as ingredients:

- **Sampling:** Reduce your stream to a more manageable data size; represent the entire stream or the most recent observations using a shifting data window.

- **Hashing:** Reduce infinite stream variety to a limited set of simple integer numbers (as seen in the "Relying on Hashing" section of Chapter 7).
- **Sketching:** Create a short summary of the measure you need, removing the less useful details. This approach lets you leverage a simple working storage, which can be your computer's main memory or its hard disk.

Another characteristic to keep in mind about algorithms operating on streams is their simplicity and low computational complexity. Data streams can be quite fast. Algorithms that require too many calculations can miss essential data, which means that the data is gone forever. When you view the situation in this light, you can appreciate how hash functions prove useful because they're prompt in transforming inputs into something easier to handle and search. Hash functions are prompt because for both operations, complexity is O(1) (see the "Working with functions" section of Chapter 2 for a discussion of complexity). You can also appreciate the sketching and sampling techniques, which bring about the idea of *lossy compression* (see more on compression in Chapter 14). Lossy compression enables you to represent something complex by using a simpler form. You lose some detail but save a great deal of computer time and storage.

Sampling means drawing a limited set of examples from your stream and treating them as if they represented the entire stream. Sampling is a well-known tool in statistics through which you can make inferences about a larger context (technically called the *universe* or the *population*) by using a small part of it.

Reserving the right data

Statistics was born in a time when obtaining a complete census was almost impossible. A *census* is a systematic investigation of a population, which includes counting it and acquiring useful data from it. The government asks all the people in a country about where they live, their family, their daily life, and their work. The census has its origins in ancient times. In the Bible, a census occurs in the book of Numbers; the Israelite population is counted after the exodus from Egypt. For tax purposes, the ancient Romans periodically held a census to count the population of their large empire. Historical documents provide accounts of similar census activities in ancient Egypt, Greece, India, and China.

Statistics, in particular the branch of statistics called *inferential statistics,* can achieve the same outcome as a census, with an acceptable margin of error, by interrogating a smaller number of individuals (called a *sample*). Thus, by querying a few people, pollsters can determine the general opinion of a larger population on a variety of issues, such as who will win an election. In the United States, for instance, the statistician Nate Silver made news by predicting the winner of the 2020 presidential election in all 50 states, using data from samples (`https://projects.fivethirtyeight.com/2020-election-forecast/`).

Clearly, holding a census implies huge costs (the larger the population, the greater the costs) and requires a lot of organization (which is why censuses are infrequent), whereas a statistical sample is faster and cheaper. Reduced costs and lower organizational requirements also make statistics ideal for big data streaming: Users of big data streaming don't need every scrap of information, and they can summarize the data's complexity.

However, there's a problem with using statistical samples. At the core of statistics is sampling, and sampling requires randomly picking a few examples from the pool of the entire population. The key element of the recipe is that every element from the population has exactly the same probability of being part of the sample. If a population consists of a million people and your sample size is one, each person's probability of being part of the sample is one out of a million. In mathematical terms, if you represent the population using the variable N and the sample size is n, the probability of being part of a sample is n/N, as shown in Figure 12-2. The represented sample is a *simple random sample.* (Other sample types have greater complexity; this is the simplest sample type, and all the others build upon it.)

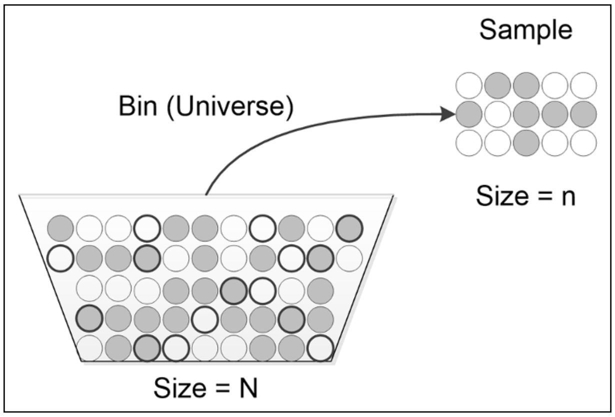


FIGURE 12-2: How sampling from a bucket works.

Using a simple random sample is just like playing the lottery, but you need to have all the numbers inside a container in order to extract a few to represent the whole. You can't easily put data streams into a repository from which you can extract a sample; instead, you have to extract your sample on the fly. What you really need is another sample type named *reservoir sampling.* Just as a reservoir retains water for later use, yet its water isn't still because some enters and some leaves, so this algorithm works by randomly choosing elements to keep as samples until other elements arrive to replace them. You can find this algorithm used in monitoring Internet communication networks as well as in running query systems on databases and search engines, such as Google's. It is most useful in taming large flows of data into more manageable sets bound to produce approximate, yet reliable, information.

The reservoir sampling algorithm is more sophisticated than another algorithmic strategy, called *windowing,* in which you create a queue and let new elements enter the queue (see Figure 12-3). Older elements leave the queue based on a trigger. This method applies when you want reports from the stream at exact time intervals. For instance, you may want to know how many pages users request from an Internet server each minute. Using windowing, you start queuing page requests at a particular minute of time, accumulate page count elements for a specific interval, count the elements in the queue, report the number, discard the content of the queue, and start queuing again.

Another motivation for using windowing is to have a fixed amount of the most recent data. In that case, every time you insert an element into the queue, the oldest element leaves. A queue is a first in/first out (FIFO) structure, which is mentioned in Chapter 6.

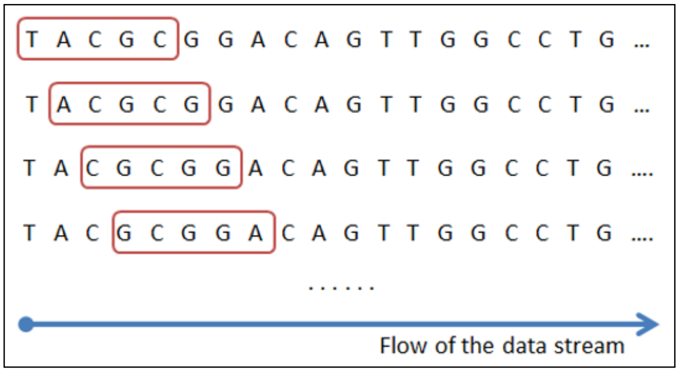

T A C G C G G A C A G T T G G C C T G ...
T A C G C G G A C A G T T G G C C T G ...
T A C G C G G A C A G T T G G C C T G ....
T A C G C G G A C A G T T G G C C T G ....
Flow of the data stream

FIGURE 12-3: An example of windowing a stream of DNA data.

Windowing looks at samples using a sliding window — it shows the elements under the window, which represent a certain time slice or a certain segment of the stream. Reservoir sampling represents the entire stream scope instead by offering a manageable amount of data, which is a statistical sample of the stream.

Here is how reservoir sample works: Given a stream of data containing many elements, you initialize the reservoir sample with elements taken from the stream until the sample is complete. For instance, if the sample contains 1,000 elements, a number that usually fits in the computer's internal memory, you start by picking the first 1,000 stream elements. The number of elements you want in the sample is k, and k implies a sample that fits into the computer's memory. At the point when you reserve the first k stream elements, the algorithm starts making its selections:

1. From the beginning of the stream, the algorithm counts every new element that arrives. It tracks the counting using the variable named n. When the algorithm gets into action, the value of n is equivalent to k.
2. Now, new elements arrive, and they increment the value of n. A new element arriving from the stream has a probability of being inserted into the reservoir sample of k/n and a probability of not being inserted equal to (1 – k/n).
3. The probability is verified for each new element that arrives. It's like a lottery: If the probability is verified, the new element is inserted. On the other hand, if it isn't inserted, the new element is discarded. If it's inserted, the algorithm discards an old element in the sample according to some rule (the easiest being to pick an old element at random) and replaces it with the new element.

The following code shows a simple example in Python so that you can see this algorithm in action. The example relies on a sequence of alphabet letters (pretend that they are a data stream) and creates a sample of five elements. (You can find this code in the `A4D2E; 12; Managing Big Data.ipynb` downloadable source code file; see the Introduction for details.)

```
import string
datastream = list(string.ascii_uppercase)
datastream += list(string.ascii_lowercase)
print(datastream)

['A', 'B', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'J', 'K', 'L',
 'M', 'N', 'O', 'P', 'Q', 'R', 'S', 'T', 'U', 'V', 'W', 'X',
 'Y', 'Z', 'a', 'b', 'c', 'd', 'e', 'f', 'g', 'h', 'i', 'j',
 'k', 'l', 'm', 'n', 'o', 'p', 'q', 'r', 's', 't', 'u', 'v',
 'w', 'x', 'y', 'z']
```

Apart from strings, the example uses functions from the random package to create a seed (for stable and replicable solutions) and, drawing a random integer number, it checks whether it needs to change an element in the reservoir. Apart from the seed value, you can experiment with modifying the sample size or even feeding the algorithm a different stream (it should be in a Python list for the example to work correctly).

```
from random import seed, randint
seed(9) # change this value for different results
sample_size = 5
sample = []

for index, element in enumerate(datastream):
        # Until the reservoir is filled, we add elements
        if index < sample_size:
                sample.append(element)
        else:
                # Having filled the reservoir, we test a
                # random replacement based on the elements
                # seen in the data stream
                drawn = randint(0, index)
                # If the drawn number is less or equal the
                # sample size, we replace a previous
                # element with the one arriving from the
                # stream
                if drawn < sample_size:
                        sample[drawn] = element

print(sample)

['y', 'e', 'v', 'F', 'i']
```

This procedure assures you that, at any time, your reservoir sample is a good sample representing the overall data stream. In this implementation, the variable `index` plays the role of n and the variable `sample_size` acts as k. Note two particular aspects of this algorithm:

- As the variable `index` grows because the stream floods with data, the probability of being part of the sample decreases. Consequently, at the beginning of the stream, many elements enter and leave the sample, but the rate of change decreases as the stream continues to flow.
- If you check the probability of adding an individual `element` from `datastream` to `sample` and you average them all, the average will approximate the probability of a particular `element` found in `datastream` (the population) being picked into any sample (not necessarily this specific `sample`), which is `k/n`.

Sketching an Answer from Stream Data

Sampling is an excellent strategy for dealing with streams but it doesn't answer all the questions you may have from your data stream. For instance, a sample can't tell you when you've already seen a stream element because the sample doesn't contain all the stream information. The same holds true for problems such as counting the distinct number of elements in a stream or computing element frequency.

To achieve such results, you need hash functions (as seen in Chapter 7) and sketches, which are simple and approximate data summaries. The following sections start with hashes, and you discover how to be correct in finding when an arriving stream element has appeared before, even if your stream is infinite and you can't keep an exact memory of everything that flowed before.

Filtering stream elements by heart

At the heart of many streaming algorithms are Bloom filters. Created almost 50 years ago by Burton H. Bloom, at a time when computer science was still quite young, the original intent of this algorithm's creator was to trade space (memory) and/or time (complexity) against what he called *allowable errors.* His original paper is entitled *Space/Time Trade-offs in Hash Coding with Allowable Errors* (see: `https://dl.acm.org/doi/10.1145/362686.362692` for details).

You may wonder about the space and time that Bloom considers motivators for his algorithm. Imagine that you need to determine whether an element has already appeared in a stream using some previously created or processed data structure. Such can be useful for a variety of applications, especially in cyber security, safe Internet browsing, and even in electronic wallets (for instance, using digital currencies such as Bitcoin). You can find a detailed list at `https://iq.opengenus.org/applications-of-bloom-filter/`.

Finding something in a stream implies that recording and searching are fast, so a hash table seems an ideal choice. *Hash tables,* as discussed in Chapter 7, simply require adding the elements that you want to record and storing them. Recovering an element from a hash table is fast because the hash table uses easily manipulated values to represent the element, rather than the element itself (which could be quite complex). Yet, storing both elements and an index to those elements has limitations. If a hash table faces more elements than it can handle, such as the elements in a continuous and potentially infinite stream, you'll end up incurring memory problems at some point.

REMEMBER

An essential consideration for Bloom filters is that false positives can occur, but false negatives can't. For example, a data stream might contain real-time monitoring data for a power plant. When using a Bloom filter, the analysis of the data stream would show that expected readings are probably part of the set of allowed readings, with some errors allowed. However, when an error occurs in the system, the same analysis shows that the readings aren't part of the set of allowed readings. The false positives are unlikely to cause problems, but the absence of false negatives means that everyone remains safe. Because of the potential for false positives, filters such as the Bloom filter are probabilistic data structures — they don't provide a certain answer but rather a probable one.

REMEMBER

Hashes, the individual entries in a hash table, are fast because they act like the index of a book. You use a *hash function* to produce the hash; the input is an element containing complex data, and the output is a simple number that acts as an index to that element. A hash function is deterministic because it produces the same number every time you feed it a specific data input. You use the hash to locate the complex information you need. Bloom filters are helpful because they're a frugal way to record traces of many elements without having to store them away as a hash table does. They work in a simple way and use the following as main ingredients:

- **A bit vector:** A list of *m* bit elements, where each bit in the element can have a value of 0 or 1. The greater m is, the better, though there are ways of optimally defining its size.
- **A series of hash functions:** Each hash function represents a different value. The hash functions can quickly crunch data as an index into a list and produce uniformly distributed results within the list of m bit elements, which are results equally ranging from the minimum to the maximum output values of the hash.

Adding elements to Bloom filters

Generally, you create Bloom filters of a fixed size (recently developed versions allow you to resize the filter). You operate them by adding new elements to the filter and looking them up when already present. It's not possible to remove an element from the filter after adding it (the filter has an indelible memory). When adding an element to a bit vector, the bit vector has some bits set to 1, as shown in Figure 12-4. In this case, the Bloom filter adds X to the bit vector.

You can add as many elements as is necessary to the bit vector. For example, Figure 12-5 shows what happens when adding another element, Y, to the bit vector. Note that bit 7 is the same for both X and Y. Consequently, bit 7 represents a collision between X and Y. These collisions are the source of the potential false positives; because of them, the algorithm could say that an element is already added to the bit vector when it isn't. Using a larger bit vector makes collisions less likely and improves the performance of the Bloom filter, but does so at the cost of both space and time.

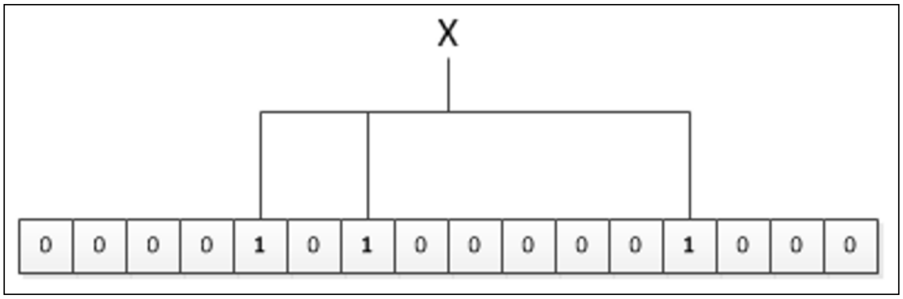


FIGURE 12-4: Adding a single element to a bit vector.

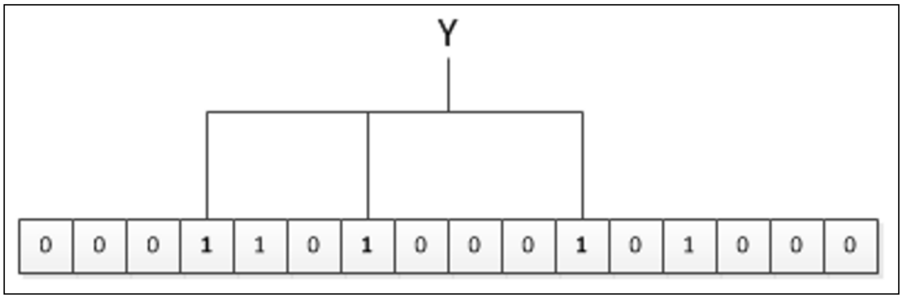


FIGURE 12-5: Adding a second element can cause collisions.

Searching a Bloom filter for an element

Searching a Bloom filter lets you determine whether a particular element appears in the bit vector. During the search process, the algorithm looks for the presence of a 0 in the bit vector. For example, the previous section added elements X and Y to the bit vector. In searching for element Z, the algorithm finds a 0 in the second bit, as shown in Figure 12-6. The presence of a 0 means that Z isn't part of the bit vector.

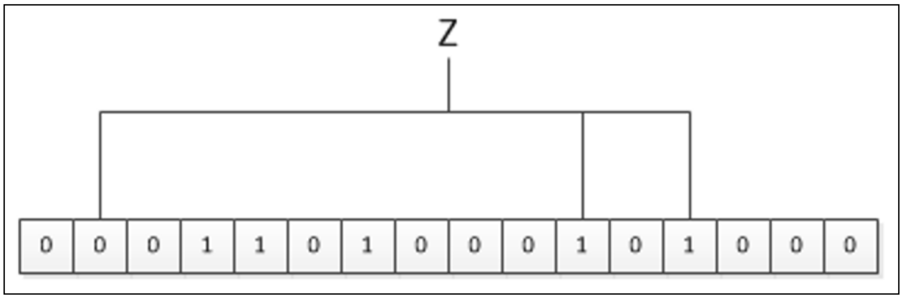


FIGURE 12-6: Locating an element and determining that it exists means searching for 0s in the bit vector.

Demonstrating the Bloom filter

This example uses Python to demonstrate a Bloom filter and shows the result with a graphical visualization. Say that you're using a crawler, which is specialized software that journeys the web to check whether something has changed in the monitored websites (which may imply copying part of the website's data, an activity known as *scraping*). The example uses a short bit vector and three hash functions, which isn't the best setting for handling a large number of elements (the bit vector will get filled quickly), but it's enough for a working example.

```
hash_functions = 3
bit_vector_length = 10
bit_vector = [0] * bit_vector_length

from hashlib import md5, sha1

def hash_f(element, i, length):
    """ This is a magic function """
    h1 = int(md5(element.encode('ascii')).hexdigest(),16)
    h2 = int(sha1(element.encode('ascii')).hexdigest(),16)
    return (h1 + i*h2) % length

def insert_filter(website):
    result = list()
    for hash_number in range(hash_functions):
        position = hash_f(website, hash_number,
                          bit_vector_length)
        result.append(position)
        bit_vector[position] = 1
    print ('Inserted in positions: %s' % result)

def check_filter(website):
    result = list()
    for hash_number in range(hash_functions):
        position = hash_f(website, hash_number,
                          bit_vector_length)
        result.append((position,bit_vector[position]))
    print ('Bytes in positions: %s' % result)
```

The code begins by creating a bit vector and some functions that can do the following:

- Generate multiple hash functions (see the "Creating your own hash function" section in Chapter 7 for details) based on the md5 and sha1 hashing algorithms

» Insert an object into the bit vector

» Check whether the bytes relative to an object in the bit vector are turned on

All these elements together constitute a Bloom filter (though the bit vector is the key part of it). This example has the crawler first visiting the website `wikipedia.org` to take some information from a few pages:

```
insert_filter('wikipedia.org')
print(bit_vector)
```

Here are the results:

```
Inserted in positions: [0, 8, 6]
[1, 0, 0, 0, 0, 0, 1, 0, 1, 0]
```

That activity turns on the bits in positions 0, 6, and 8 of the bit vector. The example now crawls the `youtube.com` website (which has some new videos of kittens) and so the crawler inserts the information of the visit into the Bloom filter:

```
insert_filter('youtube.com')
print(bit_vector)
```

Here are the updated results:

```
Inserted in positions: [3, 0, 7]
[1, 0, 0, 1, 0, 0, 1, 1, 1, 0]
```

Here the Bloom filter is activated on positions 0, 3, and 7. Given the short length of the bit vector, there is already a collision on position 0, but positions 3 and 7 are completely new. At this point, because the algorithm can't remember what it visited before (but visited sites can be verified using the Bloom filter), the example verifies that it hasn't visited `yahoo.com` in order to avoid redoing things, as shown in Figure 12-7:

```
check_filter('yahoo.com')

Bytes in positions: [(7, 1), (5, 0), (3, 1)]
```

As graphically represented, in this case you can be sure that the example never visited `yahoo.com` because the Bloom filter reports at least one position, position 5, whose bit was never set on.

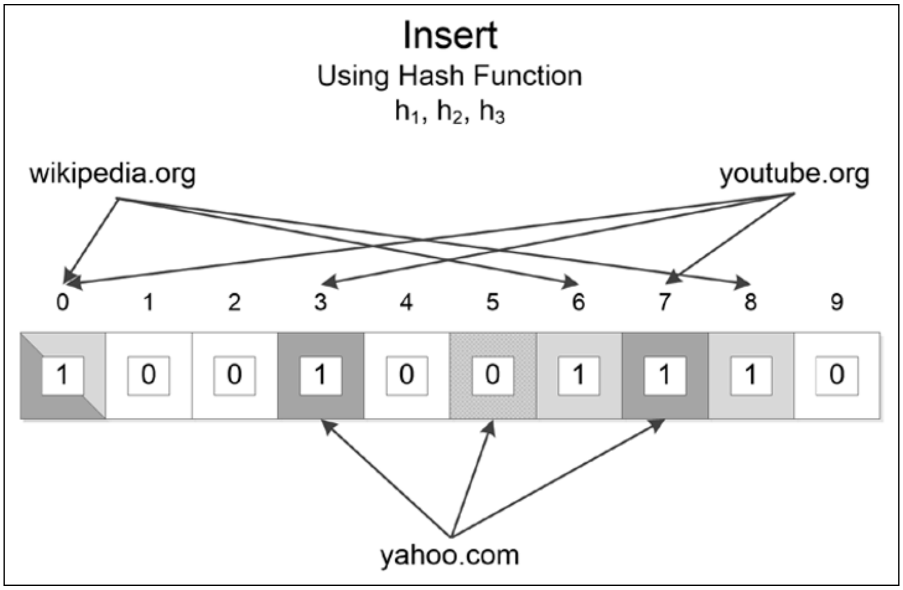


FIGURE 12-7: Testing membership of a website using a Bloom filter.

TIP

A crawler is often concerned with getting new content from websites and not copying data that it has already recorded and transmitted. Instead of hashing the domain or the address of a single page, you can directly populate a Bloom filter using part of the website content, and you can use it to check the same website for changes later.

There is a simple and straightforward way of decreasing the probability of having a false positive. You just increase the size of the bit vector that is the core of a Bloom filter. More addresses equate fewer chances for a collision by the hash functions' results. Ideally, the size m of the bit vector can be calculated by estimating n, the number of distinct objects that you expect to add by keeping m much larger than n. The ideal number k of hash functions to use to minimize collisions can then be estimated by using the following formula (ln is the natural logarithm):

```
k = (m/n)*ln(2)
```

After you have m, n, and k defined, this second formula helps you estimate the probability of a collision (a false positive rate) using a Bloom filter:

```
false positive rate = (1-exp(-kn/m))^k
```

If you can't determine n because of the variety of the data in the stream, you have to change m, the bit vector size (which equates to memory space), or k, the number of hash functions (which equates to time), to adjust the false positive rate. The trade-off reflects the relationships that Bloom considers in the original paper between space, time, and probability of an error.

Finding the number of distinct elements

Even though a Bloom filter can track objects arriving from a stream, it can't tell how many objects are there. A bit vector filled by ones can (depending on the number of hashes and the probability of collision) hide the true number of objects being hashed at the same address.

Knowing the distinct number of objects is useful in various situations, such as when you want to know how many distinct users have seen a certain website page or the number of distinct search engine queries. Storing all the elements and finding the duplicates among them can't work with millions of elements, especially coming from a stream. When you want to know the number of distinct objects in a stream, you still have to rely on a hash function, but the approach involves taking a numeric sketch.

Sketching means taking an approximation, that is an inexact yet not completely wrong value as an answer. Approximation is acceptable because the real value is not too far from it. In one kind of sketching algorithm, *HyperLogLog,* which is based on probability and approximation, you observe the characteristics of numbers generated from the stream. HyperLogLog derives from the studies of computer scientists Nigel Martin and Philippe Flajolet. Flajolet improved their initial algorithm, *Flajolet–Martin* (or the LogLog algorithm), into the more robust HyperLogLog version, which works like this:

1. A hash converts every element received from the stream into a number.
2. The algorithm converts the number into binary, the base 2 numeric standard that computers use.
3. The algorithm counts the number of initial zeros in the binary number and tracks of the maximum number it sees, which is n.
4. The algorithm estimates the number of distinct elements passed in the stream using n. The number of distinct elements is 2^n.

For instance, the first element in the string is the word *dog.* The algorithm hashes it into an integer value and converts it to binary, with a result of 01101010. Only one zero appears at the beginning of the number, so the algorithm records it as the maximum number of leading zeros seen. The algorithm then sees the words *parrot* and *wolf,* whose binary equivalents are 11101011 and 01101110, leaving n unchanged. However, when the word *cat* passes, the output is 00101110, so n becomes 2. To estimate the number of distinct elements, the algorithm computes 2^n, that is, 2^2=4. Figure 12-8 shows this process.

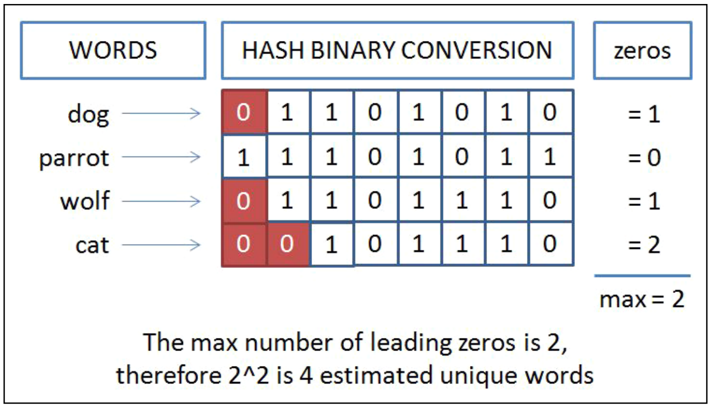


FIGURE 12-8: Counting only leading zeros.

The trick of the algorithm is that if your hash is producing random results, equally distributed (as in a Bloom filter), by looking at the binary representation, you can calculate the probability that a sequence of zeros appeared. Because the probability of a single binary number to be 0 is one in two, for calculating the probability of sequences of zeros, you just multiply that 1/2 probability as many times as the length of the sequence of zeros:

- 50 percent (1/2) probability for numbers starting with 0
- 25 percent (1/2 * 1/2) probability for numbers starting with 00
- 12.5 percent (1/2 * 1/2 * 1/2) probability for numbers starting with 000
- (1/2)^k probability for numbers starting with k zeros (you use powers for faster calculations of many multiplications of the same number)

TIP

The fewer the numbers that HyperLogLog sees, the greater the imprecision. Accuracy increases when you use the HyperLogLog calculation many times using different hash functions and average together the answers from each calculation. As an alternative, you can resort to *stochastic averaging*, which means to use the same hash but divide the stream into groups (such as by separating the elements into groups as they arrive based on their arrival order) and for each group, you keep track of the maximum number of trailing zeros. In the end, you compute the distinct element estimate for each group and compute the arithmetic average of all the estimates.

Learning to count objects in a stream

This last algorithm in the chapter also leverages hash functions and approximate sketches. It does so after filtering duplicated objects and counting distinct elements that have appeared in the data stream. Learning to count objects in a stream can help you find the most frequent items or rank usual and unusual events. You use this technique to solve problems like finding the most frequent queries in a search engine, the bestselling items from an online retailer, the highly popular pages in a website, or the most volatile stocks (by counting the times a stock is sold and bought).

You apply the solution to this problem, *Count-Min Sketch*, to a data stream. It requires just one data pass and stores as little information as possible. This algorithm is applied in many real-world situations (such as analyzing network traffic or managing distributed data flows). The recipe requires using a bunch of hash functions, each one associated with a count vector, in a way that resembles a Bloom filter, as shown in Figure 12-9:

1. Initialize all the count vectors to zeroes in all positions.
2. Apply the hash function for each count vector when receiving an object from a stream. Use the resulting numeric address to increment the value at that position.
3. Apply the hash function to an object and retrieve the value at the associated position when asked to estimate the frequency of an object. Of all the values received from the count vectors, you take the smallest as the number of times the object occurred in the stream.

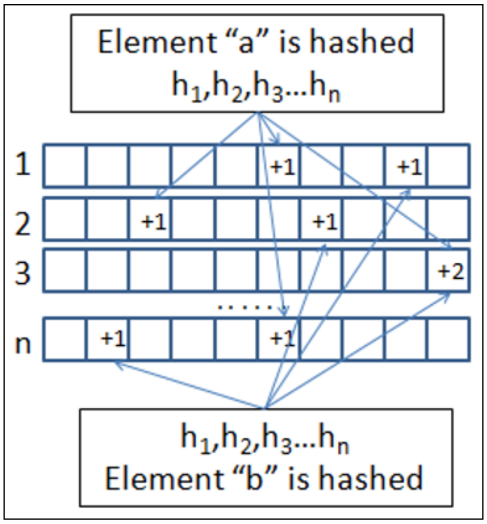


FIGURE 12-9: How values are updated in a Count-Min Sketch.

REMEMBER

Because collisions are always possible when using a hash function, especially if the associated count vector has few slots, having multiple count vectors at hand makes it more likely that at least one of them keeps the correct value. The value of choice should be the smallest because it isn't mixed with as many false positive counts due to collisions.

IN THIS CHAPTER

- » **Understanding why simply bigger, larger, and faster isn't always the right solution**
- » **Looking inside the storage and computational approaches of Internet companies**
- » **Figuring out how using clusters of commodity hardware reduces costs**
- » **Reducing complex algorithms into separable parallel operations by MapReduce**

Chapter 13 Parallelizing Operations

Managing immense amounts of data using streaming or sampling strategies has clear advantages (as discussed in Chapter 12) when you have to deal with massive data processing. Using streaming and sampling algorithms helps you obtain a result even when your computational power is limited (for instance, when using your own computer). However, some costs are associated with these approaches:

- » **Streaming:** Handles infinite amounts of data. Yet your algorithms perform at low speed because they process individual pieces of data and the stream speed rules the pace.
- » **Sampling:** Applies any algorithms on any machine. Yet the obtained result is imprecise because you have only a probability, not a certainty, of getting the right answer. Most often, you just get something plausible.

The first part of this chapter discusses some problems that require handling great amounts of data in both a precise and a timely fashion, and how to avoid costs of streaming and sampling. Examples abound in the digital world, such as making a keyword query among billions of websites or processing multiple pieces of information (searching for an image in a video repository or a match in multiple DNA sequences). Doing such calculations sequentially would take a lifetime.

The mainstream solution for solving the problem of speed with precision is using *distributed computing,* as explained in the "Distributing files and operations" section, which means interconnecting many computers in a network and using their computational capabilities together, combined with algorithms running on them in an independent, parallel manner. This is where the second part of the chapter comes into play. After presenting MapReduce in the "Employing the MapReduce solution" section, the chapter shows examples of how to set up MapReduce processing in detail.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `\A4D2E\A4D2E; 13; Map_Reduce.ipynb` file of the downloadable source. See the Introduction for details on how to find the source files.

Managing Immense Amounts of Data

The use of the Internet to perform a wide range of tasks, along with the increase in popularity of its most successful applications such as search engines or social networking, has required professionals in many fields to rethink how to apply algorithms and software solutions to cope with a deluge of data. Searching for topics and connecting people drive this revolution.

Just imagine the progression, in terms of available websites and pages, that has occurred in the last 15 years. Even if you use a smart algorithm, such as PageRank (discussed and explored in Chapter 11), coping with ever larger and changeable data is still hard. The same goes for social networking services offered by companies such as Facebook, Twitter, Pinterest, LinkedIn, and so on. As the number of users increases and their reciprocal relationships unfold, the underlying graph connecting them turns massive in scale. With such a large scale, handling nodes and links to find groups and connections becomes incredibly difficult. (Part 3 of the book discusses graphs in detail.)

In addition to communication-based data, consider online retailers that provide virtual warehouses of thousands and thousands of products and services (books, films, games, and so on). Even though you understand why you bought something, the retailer sees the items in your basket as small pieces of a purchase decision-making puzzle to solve to understand buying preferences. Solving the puzzle enables a retailer to suggest and sell alternative or supplementary products.

Understanding the parallel paradigm

CPU makers found a simple solution when challenged to stuff more computing power into microprocessors (as forecasted and partially prescribed by Moore's law, discussed in Chapter 12). Yet, bigger, larger, and faster isn't always the right solution. When they found that power absorption and heat generation limited the addition of more CPUs to a single chip, engineers compromised by creating *multicore processing units*, which are CPUs made by stacking two or more CPUs together. The use of multicore technology provided access to parallel computing to a larger audience.

Parallel computing has existed for a long time, but it mainly appeared in high-performance computers, such as the Cray super-computers created by Seymour Cray at Control Data Corporation (CDC) starting in the 1960s. Simply stated, the associative and commutative properties in math express the core idea of parallelism. In a math addition, for instance, you can group part of the sums together, or you can add the parts in a different order than the one shown by the formulas:

```
Associative property
2 + (3 + 4) = (2 + 3) + 4

Commutative property
2 + 3 + 4 = 4 + 3 + 2
```

The same concepts apply to computing algorithms, regardless of whether you have a series of operations or a mathematical function. Most often, you can reduce the algorithm to a simpler form when you apply associative and commutative properties, as shown in Figure 13-1. Then you can split the parts and have different units perform atomic operations separately, summing the result at the end.

In this example, two CPUs split a simple function with three inputs (x, y, and z) by leveraging both associative and commutative properties. The equation solution requires sharing common data (CPU1 needs x and y values; CPU2 needs y and z values). The processing proceeds in parallel until the two CPUs emit their results, which are summed to obtain the answer.

Parallelism allows processing of large numbers of calculations simultaneously. The more processes, the higher the speed of computation execution, although the time spent is not linearly proportional to the number of parallel executors. (It isn't completely true that two CPUs imply double speed, three CPUs imply three times the speed, and so on.) In fact, you can't expect the associative or commutative properties to work on every part of your algorithm or computer instructions. The algorithm simply can't make some parts parallel as stated by Amdahl's law, which helps determine the parallelism speed advantage of your computation (for details, see `https://www.geeksforgeeks.org/computer-organization-amdahls-law-and-its-proof/`). In addition, other aspects can dampen the positive effect of parallelism:

- **Overhead:** You can't sum the results in parallel.
- **Housekeeping:** The underlying conversion from a human-readable language to machine language requires time. Keeping the processors working together increases the conversion costs, making it impossible to see a doubling effect from two processors even if you can perform every part of the task in parallel.
- **Asynchronous Outputs:** Because parallel executors don't perform tasks at the same exact speed, the overall speed is bound to the slowest one. (As with a fleet, the speed of the fleet is determined by the slowest boat.)

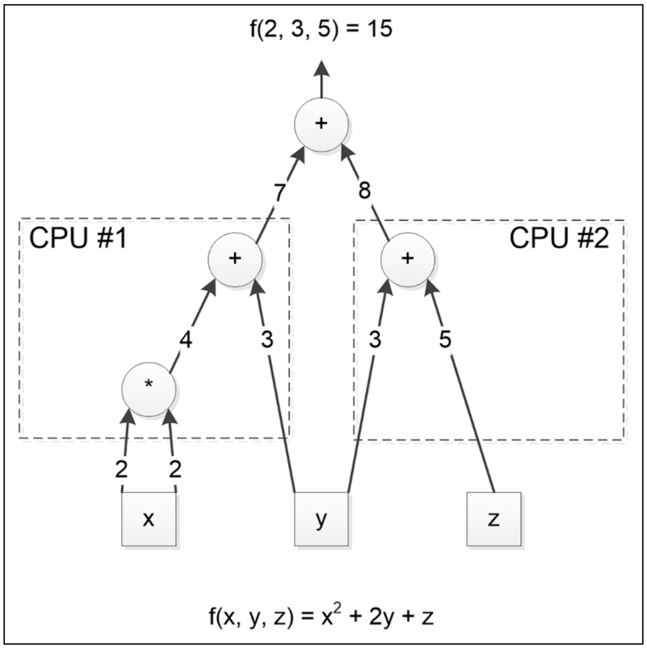


FIGURE 13-1: Associative and commutative properties allow parallelism.

Even if not always as beneficial as expected, parallelism can potentially address the problem of handling a massive number of operations faster than using a single processor (if a massive number of executors can process them in parallel). Yet, parallelism can't address the massive amounts of data behind the computations without another solution: distributed computing on distributed systems.

REMEMBER

When you buy a new computer, the seller likely tells you about cores and threads. *Cores* are the CPUs that are stacked inside the single CPU chip and that work in a parallel fashion using multiprocessing. Because each core is independent, the tasks occur simultaneously. *Threads* refer instead to the capability of a single core to split its activity between multiple processes, in an almost parallel way. However, in this case, each thread takes its turn with the processor, so the tasks don't occur simultaneously. This is called *multithreading.*

Distributing files and operations

Large graphs; huge amounts of text files, images, and videos; and immense adjacency relation matrices call forth the parallel approach. Fortunately, you no longer need a supercomputer to deal with them, but can instead rely on parallelism by a bunch of much less powerful computers. The fact that these large data sources keep growing means that you need a different approach than using a single computer specially designed to handle them. The data grows so fast that when you finish designing and producing a supercomputer for crunching the data, it may well be no longer suitable because the data has already grown too large.

Everything started in 2004 when the MapReduce concept became public in "MapReduce: Simplified Data Processing On Large Clusters," written by Jeffery Dean and Sanjay Ghemawat (at `https://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.324.78&rep=rep1&type=pdf`). The paper describes how Google collected and analyzed data for websites to optimally power up its search system. The authors' description of the MapReduce approach, and how it worked on the Google File System (GFS), sprouted much interest by the open source community, and the Apache open source foundation started quite a few projects. One such project was Nutch (`http://nutch.apache.org/`), an open source search engine; another was Apache Lucene (`https://lucene.apache.org/`), which was used for powering text searches in databases. Things got more interesting in 2006 when Doug Cutting, an employee of Yahoo!, designed Hadoop and named it after his son's toy elephant. Released as an open source project in 2007, it took the spotlight and became a top-level project at the Apache Software Foundation. The same core ideas behind Hadoop also inspired many other parallel analogous projects or large-scale data processing, with Spark (`https://spark.apache.org/`), a research project at the U.C. Berkeley AMPLab and then passed to Apache Software Foundation, being the best known one.

Most of these projects for large data processing work in a similar fashion. Engineers put many existing technological ideas together and create a Distributed File System (DFS) of some sort. When using a DFS, data isn't stored in a single powerful computer with a giant hard disk; instead, the DFS spreads it among multiple smaller computers, similar to a personal computer. The engineers arrange the computers into a *cluster,* a physical system of racks and cable connections. Racks are the true backbone of the network, in which multiple computers are stored next to each other. In a single rack of the network, you may find a variable number of computers, from eight to 64, each one connected to the other. Each rack connects to other racks by means of a cable network, created by interconnecting the racks not directly between themselves, but to various layers of *switches*, which are computer-networking devices able to efficiently handle and manage the data exchange between racks, as shown in Figure 13-2.

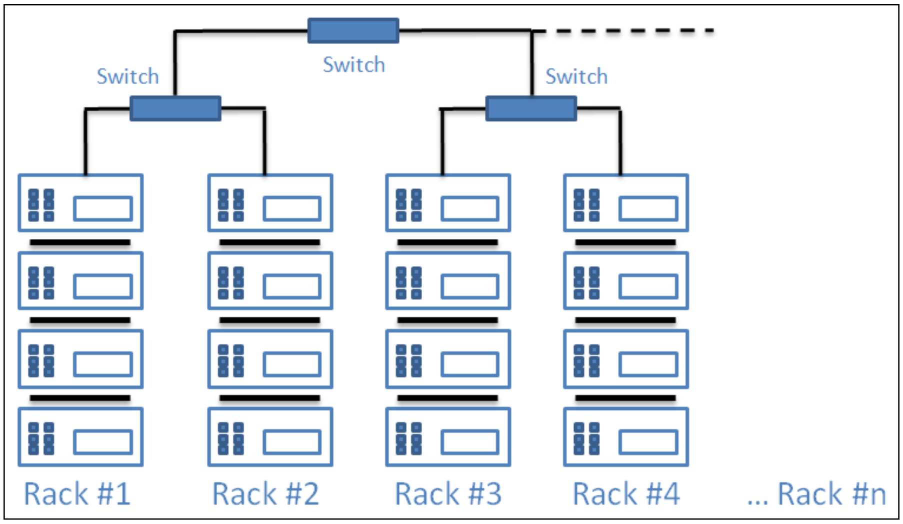


FIGURE 13-2: A schema representing a computing cluster.

You can find all this hardware at any computer store, yet it's exactly what makes the DFS infrastructure viable. Theoretically, you could find a million or more computers interconnected in a network. (You can read about the Google version of this setup, based on the most recent available estimates, at `https://www.datacenterknowledge.com/archives/2017/03/16/google-data-center-faq`.) The interesting point is that these services increase computational power when needed by adding more computers, not by creating new networks.

In this system, as data arrives, the DFS splits it into chunks (each one up to 64MB in size). The DFS copies the chunks into multiple duplicates and then distributes each copy to a computer on the network. The action of splitting data into chunks, duplicating it, and distributing it is quite fast, no matter how the data is structured (tidy and ordered information or messy ensemble). The only requirement pertains to the recording of the chunks' address in the DFS, which is achieved by an index for each file (itself replicated and distributed), called the master node. The DFS execution speed is due to how the DFS handles the data. Contrary to previous storage techniques (such as data warehouses), a DFS doesn't require any particular sorting, ordering, or cleaning operation on the data itself; on the contrary, it does the following:

- Handles data of any size because the data is split into manageable chunks
- Stores new data by piling it next to the old data; a DFS never updates any previously received data
- Replicates data redundantly so that you don't need to back it up; duplication is in itself a backup

REMEMBER

Computers fail in a number of ways: hard disk, CPU, power system, or some other component. Statistically, you can expect a computer serving in a network to work for about 1,000 days (about three years). (The precise mean time between failures, or MTBF, is a little complicated to calculate because there are so many variables, but the article at `https://www.trentonsystems.com/blog/how-to-calculate-a-rackmount-computer-failure-rate` provides you with some idea of what is involved.) Consequently, a service with a million computers can expect 1,000 of its computers to fail every day. That is why the DFS spreads three or more copies of your data inside multiple computers in the network. Replication reduces the likelihood of losing data because of a failure. The probability of having a failure that involves only computers where the same chunk of data is stored is about one out of a billion (assuming that the DFS replicates the data three times), making this a tiny, acceptable risk.

Employing the MapReduce solution

Even though distributed systems store data quickly, retrieving data is much slower, especially when performing analysis and applying algorithms. The same sort of problem occurs when you break a jigsaw puzzle into pieces and scatter the pieces around (easy). You must then pick the pieces up and recreate the original image (hard and time consuming). When working with data in a DFS:

1. Get the master node and read it to determine the location of the file parts.
2. Dispatch a fetch order to the computers in the network to obtain the previously stored data chunks.
3. Gather the data chunks stored on multiple computers onto a single computer (if doing so is possible; some files may be too large to store on a single machine).

Obviously, this process can become complex, so web service engineers have decided that it's better not to recompose files before processing them. A smarter solution is to leave them in chunks on the source computers and let the hosting computer process them. Only a `reduce` version, which is already almost completely processed, would have to move across the network, limiting the data transmission. MapReduce is the solution that provides the means to process algorithms in parallel in a data-distributed system. As an algorithm itself, MapReduce consists of just two parts, `map` and `reduce`.

USING A PACKAGE SOLUTION FOR MAPREDUCE

Even though the book demonstrates how to create a MapReduce solution from scratch, you don't need to reinvent the wheel every time you want to perform this task. Packages such as MrJob (actually stands for "Map Reduce Job": `https://mrjob.readthedocs.io/en/latest/index.html`) enable you to test and perform MapReduce tasks quickly and easily on your local computer. In addition, by using a package such as MrJob, you can make it easy to transmit and execute the task using cloud-based resources, such as Amazon Web Services using Elastic MapReduce (EMR) (`https://aws.amazon.com/emr/`) or with Hadoop (`http://hadoop.apache.org/`). The point is that you do need to know how the algorithm works, which is the point of this book, but having to write all the required code may be unnecessary in the right situation.

Explaining map

The first phase of the MapReduce algorithm is the `map` part, a function found in many *functional programming languages* (a style of programming that treats computing as a mathematical function). `map()` is straightforward: You begin with a one-dimensional array (which, in Python, could be a list) and a function. By applying the function on each array element, you obtain an identically shaped array whose values are transformed. The following example contains a list of ten numbers that the function transforms into their power equivalent:

```
def mapper(fun, *iter):
    for i in zip(*iter):
        yield fun(*i)

L = [0, 1, 2, 3, 4, 5, 6, 7, 8, 9]
m = list(mapper(lambda x: x**2, L))
print(m)def mapper(fun, *iter):
    for i in zip(*iter):
```

The output shows that each of the outputs is the square of the input.

```
[0, 1, 4, 9, 16, 25, 36, 49, 64, 81]
```

The `mapper()` function applies the Python `lambda` function A *lambda* function is a function defined on the fly (see *Functional Programming For Dummies*, by John Paul Mueller [Wiley] for help in understanding lambda functions). In the preceding example, the `lambda` function transforms each element in the initial list into a resulting element. Figure 13-3 shows the result of this mapping process.

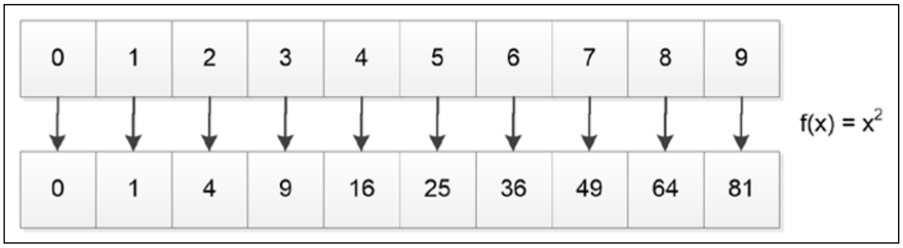


FIGURE 13-3: Mapping a list of numbers by a square function.

Note that each list element transformation is independent of the others. You can apply the function to the list elements in any order. (However, you must store the result in the right position in the final array.) The capability to process the list elements in any order creates a scenario that is naturally parallelized without any particular effort.

REMEMBER

Not all problems are naturally parallel, and some will never be. However, sometimes you can rethink or redefine your problem in order to achieve a set of computations that the computer can deal with in a parallel way.

Explaining reduce

The second phase of the MapReduce algorithm is the `reduce` part (there is also an intermediate step, shuffle and sort, explained in the next section, but not important for now unless you feel like dancing). When given a list, `reduce` applies a function in a sequence that cumulates the results. Thus, when using a summation function, `reduce` applies the summation to all the input list elements. `reduce` takes the first two array elements and combines them. Then it combines this partial result with the next array element, and so on until it completes the array.

TIP

You can also supply a starting number. When you supply a starting number, `reduce` starts by combining the starting number with the first list element to obtain the first partial result. The following example uses the result from the mapping phase and reduces it using a summation function (as displayed in Figure 13-4):

```
def reducer(fun, seq):
    if len(seq)==1:
        return seq[0]
    else:
        return fun(reducer(fun, seq[:-1]), seq[-1])

L = [0, 1, 2, 3, 4, 5, 6, 7, 8, 9]
m = list(mapper(lambda x: x**2, L))
r = reducer(lambda x, y: x+y, m)
print(r)defreducer(fun,seq):
    if len(seq)==1:
        return seq[0]
    else:
        return fun(reducer(fun, seq[:-1]), seq[-1])
```

The output is the sum of the previous squared numbers as shown here:

```
285
```

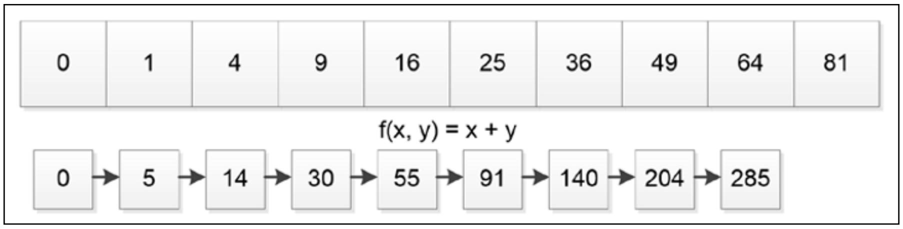


FIGURE 13-4: Reducing a list of numbers to its sum.

REMEMBER

The reducer() function operates on the input array as if it were a data stream (as discussed in Chapter 12). It usually works with one element at a time and tracks the intermediate results.

Distributing operations

Between the map() and reduce() phases is an intermediate phase, shuffling and sorting. As soon as a map task completes, the host redirects the resulting tuples of key and value pairs to the right computer on the network to apply the reduce() phase. This is typically done by grouping matching key pairs into a single list and using a hash function on the key in a manner similar to Bloom filters (see Chapter 12). The output is an address in the computing cluster for transferring the lists.

On the other end of the transmission, the computer performing the reduce() phase starts receiving lists of tuples of one or multiple keys. Multiple keys occur when a hash collision occurs, which happens when different keys result in the same hashed value, so they end up going to the same computer. The computer performing the reduce phase sorts them into lists containing the same key before feeding each list into the reduce phase, as shown in Figure 13-5.

As shown in the figure, MapReduce takes multiple inputs at each computer in the computing cluster where they are stored, maps the data, and transforms it into tuples of key and value pairs. Arranged into lists, the host transmits these tuples to other computers over the network, where the receiving computers operate sort and reduce operations that lead to a result.

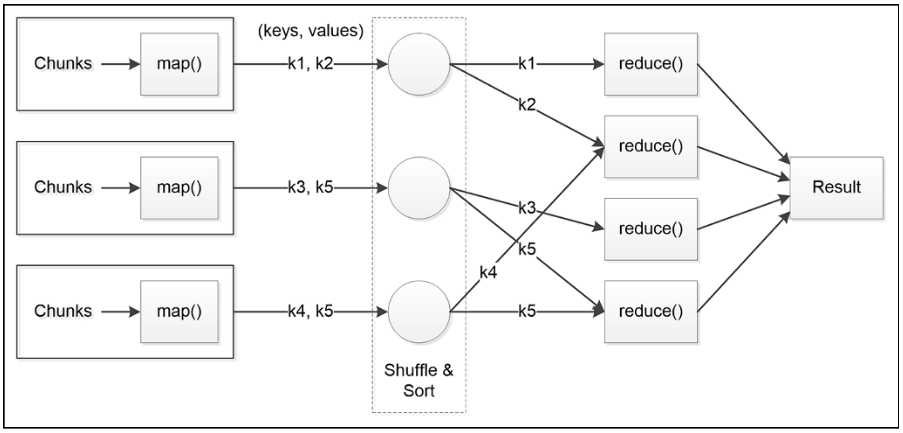


FIGURE 13-5: An overview of the complete MapReduce computation.

Working Out Algorithms for MapReduce

Contrary to other examples in this book, you can think of MapReduce as more of a style of computing or a Big Data framework than an algorithm. As a framework, it enables you to combine different distributed algorithms (parallel algorithms that spread computations across different computers) and allow them to work efficiently and successfully with large amounts of data. You can find MapReduce algorithms in many applications, and you can read about them at the Apache wiki regarding Hadoop, with details about the company that uses it, how it is used, and on what kind of computing cluster: `https://cwiki.apache.org/confluence/display/HADOOP2/PoweredBy`. Even though the possibilities are many, you most often find MapReduce used to perform these tasks:

- Text algorithms for splitting the text into elements (tokens), creating indexes, and searching for relevant words and phrases
- Graph creation and graph algorithms
- Data mining and learning new algorithms from data (machine learning)

One of the most common uses of the MapReduce algorithm is to process text. The example in this section demonstrates how to solve a simple task, counting certain words in a text passage using a map-and-reduce approach, and leveraging multithreading or multiprocessing (depending on the operating system installed on your computer).

TECHNICAL STUFF

The Python programming language is not the ideal computer language for parallel operations. Technically, because of synchronization and shared memory access problems, the Python interpreter isn't thread safe, which means that it can experience errors when executing applications using multiple processes or threads on multiple cores. Consequently, Python limits multithreading to a single thread (code is distributed but no performance increase occurs), and multicore parallelism by multiple processes is indeed tricky to achieve, especially on computers running on Windows. You can learn more about the difference in threads and processes by reading the Microsoft article at https://docs.microsoft.com/windows/win32/procthread/about-processes-and-threads.

Setting up a MapReduce simulation

This example processes text that is in the public domain, obtained from the nonprofit Project Gutenberg organization (https://www.gutenberg.org/) site. The first text processed is the novel *War and Peace*, by Leo Tolstoy (who is also known by other names in other languages, such as Lev Tolstoj). The following code loads the data into memory:

```
from  urllib import request

url = 'https://github.com/lmassaron/datasets/releases/'
url += 'download/1.0/2600.txt'
response = request.urlopen(url)
text = response.read().decode('utf-8')[627:]
  from urllib import request

url='https://github.com/lmassaron/datasets/releases/
  download/1.0/2600.txt'
response=request.urlopen(url)
text=response.read().decode('utf-8')[627:]

print (text[:37])
```

Here is the output you see:

```
WAR AND PEACE

By Leo Tolstoy/Tolstoi
```

Be patient! Loading the book takes time (just try reading it in as short a time as the computer does). When complete, the code displays the first few lines with the title. The code stores the data in the text variable. Part of the process splits the text into words and stores them in a list, as shown in the following code:

```
words = text.split()
print ('Number of words: %i' % len(words))
```

The output shows that there are a lot words in the text (Tolstoy's fingers must have been mighty tired):

```
Number of words: 566218
```

The `words` variable now contains individual words from the book. It's time to import the necessary Python packages and the functions for the example using the following code:

```
import os
if os.name == "nt":
    #Safer multithreading on Windows
    from multiprocessing.dummy import Pool
else:
    #Multiprocessing on Linux,Mac
    from multiprocessing import Pool
from multiprocessing import cpu_count
from functools import partial
import string
```

Depending on your operating system, the example relies on multiprocessing or multithreading. Windows uses multithreading, which splits the task into multiple threads processed at the same time by the same core. On Linux and Mac systems, the code executes in parallel instead, and each operation is taken care of by a different computer core.

The code that comes next counts words from a list that corresponds to a set of keywords. After removing any punctuation, the code compares words, and if it finds any match with a keyword, the function returns a tuple consisting of a key, the matched keyword, and a unit value, which is a count. This output represents the core of the MapReduce map:

```
def remove_punctuation(text):
    return ''.join([l for l in text if l in
                    string.ascii_letters])

def count_words(list_of_words, keywords):
    results = list()
    for word in list_of_words:
        for keyword in keywords:
            if keyword == remove_punctuation(
                              word.upper()):
                results.append((keyword,1))
    return results
```

The functions that follow partition the data. This approach is similar to the way in which a distributed system partitions the data. The code distributes the computation and gathers the results:

```
def Partition(data, size):
    return [data[x:x+size] for x in range(0, len(data),
                                     size)]

def Distribute(function, data, cores):
    pool = Pool(cores)
    results = pool.map(function, data)
    pool.close()
    return results
```

Finally, the following functions shuffle and order the data to reduce the results. This step represents the last two phases of a MapReduce job:

```
def Shuffle_Sort(L):
    # Shuffle
    Mapping = dict()
    for sublist in L:
        for key_pair in sublist:
            key, value = key_pair
            if key in Mapping:
                Mapping[key].append(key_pair)
            else:
                Mapping[key] = [key_pair]
    return [Mapping[key] for key in Mapping]

def Reduce(Mapping):
  return (Mapping[0][0], sum([value for (key, value
                                  ) in Mapping]))
```

Inquiring by mapping

The following code simulates a distributed environment using multiple processor cores. It begins by requesting the number of available cores from the operating system. The number of cores you see will vary by the number of cores available in your computer. Most modern computers provide four or eight cores.

```
n = cpu_count()
print ('You have %i cores available for MapReduce' % n)
```

In this case, the output shows four cores (your output may show a different number of cores):

```
You have 4 cores available for MapReduce
```

REMEMBER

If you're running the code on Windows, for technical reasons you work with a single core, so you won't take advantage of the total number of available cores. The simulation still appears to work, but you won't see any increase in speed.

In order to start, the code first defines the map operation. It then distributes the map function to threads, each of which processes a partition of the initial data (the list containing the words from *War and Peace*). The map operation finds the words *peace, war* (is there more war or peace in *War and Peace*?), *Napoleon,* and *Russia:*

```
Map = partial(count_words,
              keywords=['WAR', 'PEACE', 'RUSSIA',
                        'NAPOLEON'])
map_result = Distribute(Map,
                        Partition(
        words,len(words)//n+1), n)
print ('map_result is a list made of %i elements' %
       len(map_result))
print ('Preview of one element: %s]'% map_result[0][:5])
```

After a while, the code prints the results (the number of elements shown may vary):

```
Map is a list made of 4 elements
Preview of one element: [('WAR', 1), ('PEACE', 1), ('WAR', 1),
  ('WAR', 1), ('RUSSIA', 1)]]
```

In this case, the resulting list contains four elements because the host system has four cores (you may see greater or fewer elements, depending on the number of cores on your machine). Each element in the list is another list containing the results of the mapping on that part of the word data. By previewing one of these lists, you can see that it's a sequence of coupled keys (depending on the keyword found) and unit values. The keys aren't in order; they appear in the order in which the code generated them. Consequently, before passing the lists to the `reduce` phase for summing the total results, the code arranges the keys in order and sends them to the appropriate core for reducing:

```
Shuffled = Shuffle_Sort(map_result)
print ('Shuffled is a list made of %i elements' %
       len(Shuffled))
print ('Preview of first element: %s]'% Shuffled[0][:5])
print ('Preview of second element: %s]'% Shuffled[1][:5])
```

As shown in the example, the `Shuffle_Sort` function creates a list of four lists, each one containing tuples featuring one of the four keywords (your list might vary from that shown):

```
Shuffled is a list made of 4 elements
Preview of first element: [('RUSSIA', 1), ('RUSSIA', 1),
 ('RUSSIA', 1), ('RUSSIA', 1), ('RUSSIA', 1)]]
Preview of second element: [('NAPOLEON', 1), ('NAPOLEON',
 1), ('NAPOLEON', 1), ('NAPOLEON', 1), ('NAPOLEON', 1)]]
```

In a cluster setting, this processing equates to having each mapping node pass through the emitted results, and, by using some kind of addressing (for instance, using a hash function, as seen in the bit vector of a Bloom filter Chapter 12), they send (shuffle phase) the tuple data to the appropriate reducing node. The receiving node places each key in the appropriate list (order phase):

```
result = Distribute(Reduce, Shuffled, n)
print ('Emitted results are: %s' % result)
```

The reduce phase sums the distributed and ordered tuples and reports the total summation for each key, as seen in the result printed by the code that replicates a MapReduce (your output may vary from that shown):

```
Emitted results are: [('RUSSIA', 162), ('NAPOLEON', 475),
   ('WAR', 295), ('PEACE', 111)]
```

Reading the results, you can see that Tolstoy mentions war more than peace in *War and Peace,* but he mentions Napoleon even more often.

You can easily repeat the experiment on other texts or, even hack the map function in order to apply a different function to the text. For instance, you could choose to analyze some of the most famous novels by Sir Arthur Conan Doyle and try to discover how many times Sherlock Holmes used the phrase "Elementary, Watson":

```
from  urllib import request

url = 'https://github.com/lmassaron/datasets/releases/'
url += 'download/1.0/1661-0.txt'
```

```
response = request.urlopen(url)
text = response.read().decode('utf-8')[932:]
words = text.split()

print (text[:60])
print ('\nTotal words are %i' % len(words))

Map = partial(count_words,
              keywords=['WATSON', 'ELEMENTARY'])
result = Distribute(Reduce,
                    Shuffle_Sort(Distribute(Map,
                    Partition(words,len(words)//n), n)),
                    1)
print ('Emitted results are: %s' % result)
```

The result may be surprising!

```
The Adventures of Sherlock Holmes

by Arthur Conan Doyle



Total words are 107411
Emitted results are: [('WATSON', 81), ('ELEMENTARY', 1)]
```

You never actually find that phrase in the novels; it's a catchphrase that authors inserted later into the film screenplays: `https://www.phrases.org.uk/meanings/elementary-my-dear-watson.html`.

IN THIS CHAPTER

» Creating efficient and smart encodings

» Leveraging statistics and building Huffman trees

» Compressing and decompressing using the Lempel-Ziv-Welch (LZW) algorithm

» Performing encryption tasks

Chapter 14 Compressing and Concealing Data

The last decade has seen the world flooded by data. In fact, data is the new oil, and specialists of all sorts hope to extract new knowledge and richness from it. As a result, you find data piled everywhere, and it's often archived as soon as it arrives. The first part of this chapter focuses on using various compression techniques to store data efficiently. It's split into two major subsections: encoding techniques and data compression. The discussion in the first part begins with encoding techniques.

The first part also discusses data compression in a second subsection. Data compression algorithms offer the solution of compacting data to store more of it on a single device at the cost of computer processing time. Trading disk space for computer time reduces costs. Compression is also handy in situations in which data infrastructure growth doesn't match data growth, which is especially true of both wireless and mobile bandwidth in developing countries. In addition, compression helps deliver complex web pages faster, stream videos efficiently, store data on a mobile device, or reduce mobile phone data-transmission costs. The data compression discussion relies on two popular compression techniques: Huffman encoding and the Lempel-Ziv-Welch (LZW) algorithm.

The second part of this chapter discusses the use of encoding for another purpose, encryption. Making data unreadable by those who shouldn't see it has a long history. Even the ancient Egyptians used cryptography, as explained at `http://www.cs.trincoll.edu/~crypto/historical/intro.html`. Of course, modern ciphers are far more complicated than those ancient methods.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 14; Compression.ipynb` and `A4D2E; 14; Cryptography.ipynb` files of the downloadable source. See the Introduction for details on how to find this source file.

Making Data Smaller

Computer data is made of bits — sequences of zeros and ones. This chapter explains the use of zeros and ones to create data in more depth than previous chapters because compression leverages these zeros and ones in multiple ways. To understand compression, you must know how a computer creates and stores binary numbers. The following sections discuss the use of binary numbers in computers.

Understanding encoding

Zeros and ones are the only numbers in the binary system. They represent the two possible states in an electric circuit: absence and presence of electricity. Computers started as simple circuits made of tubes or transistors; using the binary system instead of the human decimal system made things easier. Humans use ten fingers to count numbers from 0 to 9. When they have to count more, they add a unit number to the left. You may never have thought about it, but you can express counting by using powers of ten. Therefore, a number such as 199 can be expressed as $10^2 * 1 + 10^1 * 9 + 10^0 * 9 = 199$; that is, you can separate hundreds from tens and units by multiplying each figure by the power of ten relative to its position: 10^0 for units; 10^1 for tens; 10^2 for hundreds; and so on.

REMEMBER

Knowing this information helps you understand binary numbers better because they actually work in exactly the same way. However, binary numbers use powers of two rather than powers of ten. For instance, the number 11000111 is simply

```
2^7*1+2^6*1+2^5*0+2^4*0+2^3*0+2^2*1+2^1*1+2^0*1 =
128*1+64*1+32*0+16*0+8*0+4*1+2*1+1*1 =
128+64+4+2+1 = 199
```

You can represent any number as a binary value in a computer. A value occupies the memory space required by its total length. For example, binary 199 is 8 figures, each figure is a bit, and 8 bits are called a byte. The computer hardware knows data only as bits because the circuitry can store only bits. However, from a higher point of view, computer software can interpret bits as letters, ideograms, pictures, films, and sounds, which is where encoding comes into play.

Encoding uses a sequence of bits to represent something other than the number expressed by the sequence itself. For instance, you can represent a letter using a particular sequence of bits. Computer software commonly represents the letter *A* using the number 65, or binary 01000001 when working with the American Standard Code for Information Interchange (ASCII) encoding standard. You can see sequences used by ASCII system at `https://www.asciitable.com/`. ASCII uses just 7 bits for its encoding (8 bits, or a byte, in the extended version), which means that you can represent 128 different characters (the extended version has 256 characters). Python can represent the string "Hello World" using bytes:

```
print (''.join(['{0:08b}'.format(ord(l))
                for l in "Hello World"]))
```

This example provides the following output:

```
0100100001100101011011000110110001101111001000000 1010111
01101111011100100110110001100100
```

When using extended ASCII, a computer knows that a sequence of exactly 8 bits represent a character. It can separate each sequence into 8-bit bytes and, using a conversion table called a *symbolic table*, it can turn these bytes into characters.

REMEMBER

ASCII encoding can represent the standard Western alphabet, but it doesn't support the variety of accented European characters or the richness of non-European alphabets, such as the ideograms used by the Chinese and Japanese languages. Chances are that you're using a robust encoding system such as UTF-8 or another form of Unicode encoding (see `https://home.unicode.org/` for more information). Unicode encoding is the default encoding in Python 3.

Using a complex encoding system requires that you use longer sequences than those required by ASCII. Depending on the encoding you choose, defining a character may require up to 4 bytes (32 bits). When representing textual information, a computer creates long bit sequences. It decodes each letter easily because encoding uses fixed-length sequences in a single file. Encoding strategies, such as Unicode Transformation Format 8 (UTF-8), can use variable numbers of bytes (1 to 4 in this case). You can read more about how UTF-8 works at `https://www.fileformat.info/info/unicode/utf8.htm`.

Considering the effects of compression

The use of fixed-sized character sequences leaves a lot of room for improvement. You may not use all the letters in an alphabet, or you use some letters more than others. This is where compression comes into play. By using variable-length character sequences, you can greatly reduce the size of a file. However, the file also requires additional processing to turn it back into an uncompressed format that applications understand. Compression removes space in an organized and methodical manner; decompression adds the space back into the character strings. It's like those *just add water* drinks you buy at the store: First they were a drink, then a powder, and then a drink again. When it's possible to compress and decompress data in a manner that doesn't result in any data loss, you're using *lossless* compression.

The same idea behind compression goes for images and sounds that involve framing sequences of bits of a certain size in order to represent video details or to reproduce a second of a sound using the computer's speakers. Videos are simply sequences of bits, and each bit sequence is interpreted by software as a *pixel,* which is composed of small points that constitute an image. Likewise, audio is composed of sequences of bits that represent an individual sample. Audio files store a certain number of samples per second to recreate a sound. The discussions at `https://www.wowza.com/blog/video-codecs-encoding` and `https://developer.mozilla.org/docs/Web/Media/Formats/Audio_codecs` provide more information about both video and audio storage. Computers store data in many predefined formats of long sequences of bits (commonly called *bit streams*). Compression algorithms can exploit the way each format works to obtain the same result using a shorter, custom format.

You can compress data that represents images and sounds further by eliminating details that you can't process. Humans have both visual and aural limits, so they aren't likely to notice the loss of detail imposed by compressing the data in specific ways. You may have heard of MP3 compression that allows you to store entire collections of CDs on your computer or on a portable reader. The MP3 file format simplifies the original cumbersome WAV format used by computers. WAV files contain all the sound waves received by the computer, but MP3 saves space by removing and compacting waves that you can't hear. (For more information about MP3, see the article at `https://arstechnica.com/features/2007/10/the-audiofile-understanding-mp3-compression/`).

TIP

Removing details from data creates *lossy* compression. JPEG, DjVu, MPEG, MP3, and WMA are all lossy compression algorithms specialized in a particular kind of media data (images, video, sound), and there are many others. Lossy compression is fine for data meant for human input; however, by removing the details, you can't revert to the original data structure. Thus, you can get good digital photo compression and represent it in a useful way on a computer's screen. Yet when you print the compressed photo on paper, you may notice that the quality, though acceptable, is not as good as the original picture. The display provides output at 96 dots per inch (dpi), but a printer typically provides output at 300 to 1200 dpi (or higher). The effects of lossy compression become obvious because a printer is able to display them in a manner that humans can see.

REMEMBER

Choosing between lossless and lossy compression is important. Discarding details is a good strategy for media, but it doesn't work so well with text, because losing words or letters may change the meaning of the text. (Discarding details doesn't work for programming languages or computer instructions for the same reason.) Even though lossy compression is an effective compression solution when details aren't as important, it doesn't work in situations in which precise meaning must be retained.

Choosing a particular kind of compression

Lossless algorithms simply compress data to reduce its size and decompress it to its original state. Lossless algorithms have more general applications than lossy compression because you can use them for any data problem. (Even when using lossy compression, you remove some detail and further compress what remains using lossless compression.) Just as you can find many lossy algorithms that are specialized for use with different media, so can you find many lossless algorithms, each one adept at exploiting some data characteristics. (To get an idea of how large the lossless algorithm family is, read more details at `http://ethw.org/History_of_Lossless_Data_Compression_Algorithms`.)

AN EXAMPLE OF LOSSY COMPRESSION BENEFITS

An example of the difference that lossy compression can make is in photography. A raw formatted picture file contains all the information originally provided by the camera's sensor, so it doesn't include any sort of compression. When working with a certain camera, you might find that this file consumes 29.8MB of hard drive space. A raw file often uses the `.raw` file extension to show that no processing has occurred. Opening the file and saving it as a lossy `.jpeg` might result in a file size of only 3.7MB, but with a corresponding loss of detail. To save some of the detail but obtain some savings in file size as well, you might choose to use the `.jpeg` file format with less compression. In this case, the file size might be 12.4MB, which represents a good compromise in file size savings to loss of image data.

REMEMBER

It's essential to remember that the goal of both lossy and lossless compression is to reduce the redundancy contained in data. The more redundancies the data contains, the more effective the compression.

Chances are that you have many lossless data compression programs installed on your computer that output files such as ZIP, LHA, 7-Zip, and RAR, and you aren't sure which one is better. A "best" option may not exist, because you can use bit sequences in many different ways to represent information on a computer; also, different compression strategies work better with different bit sequences. This is the no-free-lunch problem discussed in Chapter 1. The option you choose depends on the data content you need to compress.

To see how compression varies by the sample you provide, you should try various text samples using the same algorithm. The following Python example uses the ZIP algorithm to compress the text of *The Adventures of Sherlock Holmes*, by Arthur Conan Doyle, and then to reduce the size of a randomly generated sequence of letters. (You can find the complete code for this example in the Compression Performances section of the `A4D2E; 14; Compression.ipynb` file of the downloadable source code for this book; see the Introduction for details.)

```
from  urllib import request
import zlib
from random import randint

url = 'https://github.com/lmassaron/datasets/releases/'
url += 'download/1.0/1661-0.txt'
response = request.urlopen(url)
sh = response.read().decode('utf-8')[932:]
sh_length = len(sh)
rnd = ''.join([chr(randint(0, 126)) for k in
               range(sh_length)])

def zipped(text):
    return len(zlib.compress(text.encode("utf-8'")))

print ("Original size for both texts: %s characters" %
       sh_length)
print ("The Adventures of Sherlock Holmes to %s" %
       zipped(sh))
print ("Random file to %s " % zipped(rnd))
```

The output of the example is enlightening. Even though the example application can reduce the size of the short story to less than half of its original size, the size reduction for the random text is much less (both texts have the same original length).

```
Original size for both texts: 592905 characters
The Adventures of Sherlock Holmes to 227478
Random file to 519679
```

The output implies that the ZIP algorithm leverages the characteristics of the written text but doesn't do as well on random text that lacks a predictable structure.

TIP

When performing data compression, you can measure performance by calculating the compression ratio: Just divide the new compressed size of the file by the original size of the file. The compression ratio can tell you about algorithm efficiency in saving space, but high-performance algorithms also require time to perform the task. In case time is your concern, most algorithms let you trade some compression ratio for speedier compression and decompression. In the preceding example for the *Sherlock Holmes* text, the compression ratio is 226824 / 594941; that is, about 0.381. The `compress()` method found in the example has a second optional parameter, `level`, which controls the level of compression. Changing this parameter controls the ratio between the time to perform the task and the amount of compression achieved.

Choosing your encoding wisely

The example in the preceding section shows what happens when you apply the ZIP algorithm to random text. The results help you understand why compression works. Boiling down all the available compression algorithms, you discover four main reasons:

- **Shrinking character encoding:** Compression forces characters to use fewer bits by coding them according to some feature, such as commonality of use. For example, if you use only some of the characters in a character set, you can reduce the number of bits to reflect that level of usage. It's the same difference that occurs between ASCII, which uses 7 bits, and extended ASCII, which uses 8 bits. This solution is particularly effective with problems like DNA encoding, in which you can devise a better encoding than the standard one.
- **Shrinking long sequences of identical bits:** Compression uses a special code to identify multiple copies of the same bits and replaces those copies with just one copy, along with the number of times to repeat it. This option is very effective with images (it works fine with fax black and white images) or with any data that you can rearrange in order to group similar characters together (DNA data is one of this kind).

- **Leveraging statistics:** Compression encodes frequently used characters using a shorter numeric sequence than less frequently used characters, which use a longer numeric sequence. For example, the letter *E* appears commonly in English, so if the letter *E* uses only 3 bits, rather than a full 8 bits, you save considerable space. This is the strategy used by Huffman encoding, in which you recreate the symbolic table and save space, on average, because common characters have shorter encodings.
- **Encoding frequent long sequences of characters efficiently:** This is similar to shrinking long sequences of identical bits, but it works with character sequences rather than single characters. This is the strategy used by LZW, which learns data patterns on the fly and creates a short encoding for long sequences of characters.

To understand how rethinking encoding can help in compression, start with the first reason. Scientists working on the Genome Project around 2008 (`https://www.genome.gov/human-genome-project`) managed to drastically reduce the size of their data using a simple encoding trick. Using this trick made the task of mapping the entire human DNA simpler, helping scientists understand more about the life, disease, and death scripted into our body cells.

Scientists describe DNA using sequences of the letters A, C, T, and G (representing the four nucleotides present in all living beings). The human genome contains six billion nucleotides (you find them associated in couples, called bases) that add up to more than 50GB using ASCII encoding. In fact, you can represent A, C, T, and G in ASCII encoding as follows:

```
print (' '.join(['{0:08b}'.format(ord(l))
                 for l in "ACTG"]))

01000001 01000011 01010100 01000111
```

The sum of the preceding line is 32 bits, but because DNA maps just four characters, you can use 2 bits each, saving 75 percent of the previously used bits:

```
00 01 10 11
```

REMEMBER

Such a gain demonstrates the reason to choose the right encoding. The encoding works fine in this case because the DNA alphabet is made of four letters, and using a full ASCII table based on 8 bits is overkill. If a problem requires that you use the complete ASCII alphabet, you can't compress the data by redefining the encoding used. Instead, you have to approach the problem using Huffman compression.

If you can't shrink the character encoding (or you have already done it), you can still shrink long sequences, reducing them to a simpler encoding. Observe how binary data can repeat long sequences of ones and zeros:

```
00000000 00000000 01111111 11111111 10000011 11111111
```

In this case, the sequence starts from zero. You can therefore count the number of zeros, and then count the number of ones that follow, and then repeat with the next count of zeros, and so on. Because the sequence has only zeros and ones, you can count them and obtain sequence of counts to compress the data. In this case, the data compresses into values of 17 15 5 10. Translating these counts into bytes shortens the initial data in an easily reversible way:

```
00010001 00001111 00000101 00001010
```

Instead of using 6 bytes to represent the data, you now need only 4 bytes. To use this approach, you limit the maximum count to 255 consecutive values, which means:

- You can encode each sequence in a byte.
- The first value is a zero when the sequence starts from 1 instead of 0.
- When a block of values is longer than 255 elements, you insert a 0 value (so the decoder switches to the other value for 0 counts and then starts counting the first value again).

This algorithm, *run-length encoding* (RLE), is very effective if your data has many long repetitions. This algorithm enjoyed great success in the 1980s because it could reduce fax transmission times. Fax machines worked on just black-and-white images, and by land-line telephone, so shrinking the long sequences of zeros and ones that made up images and text proved to be convenient. Though businesses seldom use fax machines now, scientists still use RLE for DNA compression in combination with the Burrows-Wheeler Transform (an advanced algorithm that you can read about at `https://marknelson.us/posts/1996/09/01/bwt.html`), which rearranges (in a reversible way) the genome sequence in long runs of the same nucleotide. You also find RLE used for compression of other data formats, such as JPEG and MPEG (see `https://motorscript.com/mpeg-jpeg-compression/` for additional details).

TIP

Data characteristics rule the success of a compression algorithm. By knowing how algorithms work and exploring your data characteristics, you can choose the best-performing algorithm or combine more algorithms in an effective way. Using multiple algorithms together creates an *ensemble of algorithms.*

Encoding using Huffman compression

Redefining an encoding, such as when mapping nucleotides in DNA, is a smart move that works only when you use a part of the alphabet that the encoding represents. When you use all the symbols in the encoding, you can't use this solution. David A. Huffman discovered another way to encode letters, numbers, and symbols efficiently even when using all of them. He achieved this accomplishment when he was a student at MIT in 1952 as part of a term paper required by his professor, Prof. Robert M. Fano. His professor and another famous scientist, Claude Shannon (the father of information theory), had struggled with the same problem.

In his paper, "A Method for the Construction of Minimum-Redundancy Codes," Huffman describes in just three pages his mind-blowing encoding method. It changed the way we stored data until the end of 1990s. You can read the details about this incredible algorithm in a September 1991 *Scientific American* article at `http://www.huffmancoding.com/my-uncle/scientific-american`. Huffman codes have three key ideas:

- **Encode frequent symbols with shorter sequences of bits.** For instance, if your text uses the letter *a* often, but rarely uses the letter *z,* you can encode *a* using a couple of bits and reserve an entire byte (or more) for *z*. Using shorter sequences for common letters means that overall your text requires fewer bytes than when you rely on ASCII encoding.
- **Encode shorter sequences using a unique series of bits.** When using variable length bit sequences, you have to ensure that you can't misinterpret a shorter sequence in place of a longer one because they are similar. For instance, if the letter *a* in binary is 110 and *z* is 110110, you could misinterpret the letter *z* as a series of two-letter *a* characters. Huffman encoding avoids this problem by using prefix-free codes: The algorithm never reuses shorter sequences as initial parts of longer sequences. For example, if *a* is 110, then *z* will be 101110 and not 110110.
- **Manage prefix-free coding using a specific strategy.** Huffman encoding manages prefix-free codes by using binary trees in a smart way. Binary trees are a data structure discussed in Chapters 6 and 7. The Huffman algorithm uses binary trees (called Huffman trees) in an advanced fashion. You can read more about the internals of the algorithm in the tutorial at `https://www.tutorialspoint.com/huffman-trees-in-data-structure`.

TECHNICAL STUFF

The algorithm used to perform Huffman encoding uses an iterative process that relies on *heaps*, which are specialized tree-based data structures (mentioned in Chapter 6). A heap is a complex data structure. Because of the manner in which you use a heap to arrange data, it's useful for achieving a *greedy* strategy. In the next chapter, which is devoted to greedy algorithms, you test Huffman encoding yourself, using the working examples in the downloadable code accompanying the book (the Huffman Compression example in the `A4D2E; 15; Greedy Algorithms.ipynb` file; see the Introduction for details on where to file this file).

For the moment, as an example of a Huffman encoding output, Figure 14-1 shows the Huffman encoding binary tree used to encode a long sequence of *ABCDE* letters distributed in a way that *A* is more frequent than *B*, *B* more than *C*, *C* more than *D*, and *D* more than *E*.

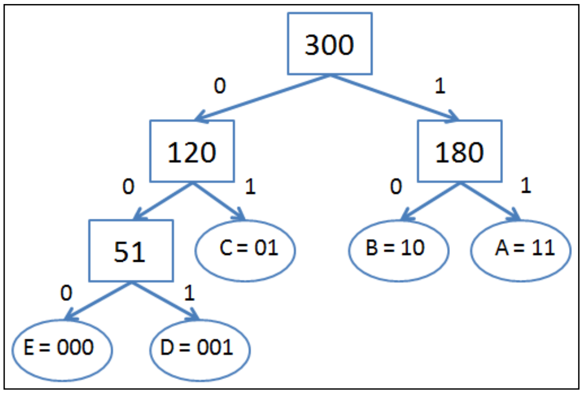


FIGURE 14-1: A Huffman tree and its symbolic table of conversion.

The square nodes represent *branch nodes*, where the algorithm places the number of the remaining letters it distributes to the *child nodes* (those that are below the branch nodes in the hierarchy). The round nodes represent *leaf nodes*, where you find the successfully encoded letters. The tree starts at the *root* with 300 letters left to distribute (the length of the text). It distributes the letters by branching the 0 and 1 bits, respectively, on the left and on the right branches until it reaches all the leaves necessary for encoding. By reading from the top of the sequence of branches to a specific letter, you determine the binary sequence representing that letter. Less frequent letters (*D* and *E*) get the longest binary sequences.

TIP

Following the Huffman tree from bottom to top lets you compress a symbol into a binary sequence. By following the tree from top to bottom, you can decompress a binary sequence into a symbol (as represented by the first leaf node you encounter).

REMEMBER

For decompression, you need to store both the compressed binary sequence and the Huffman tree that made the compression possible. When your text or data is too short, the Huffman tree could require more space than the compressed data, thus making compression ineffective. Huffman code works best on larger data files.

Remembering sequences with LZW

Huffman encoding takes advantage of the most frequent characters, numbers, or symbols in data and shortens their encoding. The LZW algorithm performs a similar task but extends the encoding process to the most frequent sequences of characters. The LZW algorithm dates to 1984 and was created by Abraham Lempel, Jacob Ziv, and Terry Welch based on an earlier LZ78 algorithm (developed in 1978 by Lempel and Ziv alone). Both Unix compression and the GIF image format rely on this algorithm. LZW leverages repetitions, so it's also ideal for document and book text compression because humans often use the same words when writing. In addition, LZW can operate on streaming data, but Huffman can't; Huffman needs the full dataset to build its mapping table.

As the algorithm skims through the data-bit stream, it learns sequences of characters from it and assigns each sequence to a short code. Thus, when later reencountering the same series of characters, LZW can compress them using a simpler encoding. Interestingly, this algorithm starts from a symbolic table made of single characters (usually the ASCII table) and then enlarges that table using the character sequences it learns from the data it compresses.

Moreover, LZW doesn't need to store the learned sequences in a table for decompression; it can rebuild them easily by reading the compressed data. LZW can reconstruct the steps it took when compressing the original data and the sequences it encoded. This capability comes at a price: LZW isn't efficient at first. It works best with large pieces of data or text (a characteristic common to other compression algorithms).

LZW isn't a complex algorithm, but you need to see a number of examples to understand it fully. You can find quite a few good tutorials at `https://marknelson.us/posts/2011/11/08/lzw-revisited.html` and `http://www.matthewflickinger.com/lab/whatsinagif/lzw_image_data.asp`. The second tutorial explains how to use LZW to compress images. The following example shows a Python implementation. (You can find the complete code for this example in the LZW section of the `A4D2E; 14; Compression.ipynb` file of the downloadable source code for this book; see the Introduction for details).

```
def lzw_compress(text):
    dictionary = {chr(k): k for k in range(256)}
    encoded = list()
    s = text[0]
    for c in text[1:]:
        if s+c in dictionary:
            s = s+c
        else:
            print ('> %s' %s)
            encoded.append(dictionary[s])
            print ('found: %s compressed as %s' %
                   (s,dictionary[s]))
            dictionary[s+c] = max(dictionary.values()) + 1
            print ('New sequence %s indexed as %s' %
                   (s+c, dictionary[s+c]))
            s = c
    encoded.append(dictionary[s])
    print ('found: %s compressed as %s'
           %(s,dictionary[s]))
    return encoded
```

In this example, the algorithm scans the text by checking the text a character at a time. It begins by encoding characters using the initial symbolic table, which is actually the ASCII table in this case. The best way to see how this code works is to see a series of output messages and then analyze what has taken place, as shown here:

```
text = "ABABCABCABC"
compressed = lzw_compress(text)
print('\nCompressed: %s \n' % compressed)
```

As the output shows, the data really is compressed:

```
> A
found: A compressed as 65
New sequence AB indexed as 256
> B
found: B compressed as 66
New sequence BA indexed as 257
> AB
found: AB compressed as 256
New sequence ABC indexed as 258
> C
found: C compressed as 67
New sequence CA indexed as 259
> ABC
found: ABC compressed as 258
New sequence ABCA indexed as 260
found: ABC compressed as 258
```

Here is a quick synopsis of what these output messages mean:

1. The first letter, *A,* appears in the initial symbolic table, so the algorithm encodes it as 65.
2. The second letter, *B,* is different from *A* but also appears in the initial symbolic table, so the algorithm encodes it as 66.
3. The third letter is another *A,* so the algorithm reads the next letter, which is a *B,* and encodes the two-letter combination, *AB,* as 256.
4. The fourth letter, a *C,* is different from any of the previous letters and also appears in the initial symbolic table, so the algorithm encodes it as 67.
5. The next letter has already appeared before; it's an *A.* The next letter is a *B,* which makes the *AB* letter combination; this also appears in the symbolic table. However, the next letter is a *C,* which makes a new sequence and which the algorithm now encodes as 258.
6. The final three letters are another set of *ABC,* so the code for them is 258 again. Consequently, the encoded output for *ABABCABCABC* is

   ```
   Compressed: [65, 66, 256, 67, 258, 258]
   ```

All the learning and encoding operations translate into final compression data consisting of just six numeric codes (costing 8 bits each) against the initial 11 test letters. The encoding results in a good compression ratio of about half the initial data: 6/11 = 0.55.

Retrieving the original text from the compressed data requires a different, inverse procedure, which accounts for the only situation when LZW decoding may fail to reconstruct the symbolic table when a sequence starts and ends with the same character. This particular case is taken care of by Python using an if-then-else command block, so you can safely use the algorithm to encode and decode anything:

```
def lzw_decompress(encoded):
    reverse_dictionary = {k:chr(k) for k in range(256)}
    current = encoded[0]
    output = reverse_dictionary[current]
    print ('Decompressed %s ' % output)
    print ('>%s' % output)
    for element in encoded[1:]:
        previous = current
        current = element
        if current in reverse_dictionary:
            s = reverse_dictionary[current]
```

```
            print ('Decompressed %s ' % s)
            output += s
            print ('>%s' % output)
            new_index = max(reverse_dictionary.keys()) + 1
            reverse_dictionary[new_index
            ] = reverse_dictionary[previous] + s[0]
            print ('New dictionary entry %s at index %s' %
                    (reverse_dictionary[previous] + s[0],
                     new_index))
        else:
            print ('Not found:',current,'Output:',
                   reverse_dictionary[previous
                    ] + reverse_dictionary[previous][0])
            s = reverse_dictionary[previous
                    ] + reverse_dictionary[previous][0]
            print ('New dictionary entry %s at index %s' %
                   (s, max(reverse_dictionary.keys())+1))
            reverse_dictionary[
                max(reverse_dictionary.keys())+1] = s
            print ('Decompressed %s' % s)
            output += s
            print ('>%s' % output)
    return output
```

Running the function on the previously compressed sequence recovers the original information by scanning through the symbolic table, as shown here:

```
print ('\ndecompressed string : %s' %
       lzw_decompress(compressed))
print ('original string was : %s' % text)

Decompressed A
> A
Decompressed B
> AB
New dictionary entry AB at index 256
Decompressed AB
> ABAB
New dictionary entry BA at index 257
Decompressed C
> ABABC
New dictionary entry ABC at index 258
Decompressed ABC
> ABABCABC
```

```
New dictionary entry CA at index 259
Decompressed ABC
> ABABCABCABC
New dictionary entry ABCA at index 260

decompressed string : ABABCABCABC
original string was : ABABCABCABC
```

Hiding Your Secrets with Cryptography

In an age in which everyone seems to be prying into everyone else's business, *cryptography*, the art of making text unreadable in a manner that those in the know can reverse later, has taken on added meaning. Cryptography is all about keeping secret text out of the hands of people who don't need to know about it. As mentioned earlier in this chapter, cryptography is an old art (because one has to be creative to define a unique cryptographic technique) and science (because the cryptography has to be reversible), originating with the Egyptians. The basics of cryptography haven't changed in thousands of years. The process

1. Uses *plain text* (the original data)
2. *Encrypts* it (to become unreadable)
3. Sends the data to a recipient as *cipher text* (which is unreadable)
4. *Decrypts* it (to make it readable again)

Modern cryptography relies on all sorts of advanced mathematical methods to perform the encryption and decryption steps. It would require several books (or even more) to discuss the topic at any depth, and by then your brain would be pure jelly (it happens to everyone). The following sections provide you with a brief overview of cryptography — just enough for you to act smart at your next office party, but not enough to turn your brain to jelly.

WARNING

The examples in the sections that follow are toy examples that are meant to teach principles, not create unbreakable cryptographic output. Consequently, you should use the examples to understand how cryptography works, not encrypt your next secret missive to your best friend and hope that no one else can read it. After all, anyone who reads this book will be able to read your message and let the entire world know!

Substituting characters

Character substitution is one of the simplest and fastest methods to encrypt data. It's also one of the most breakable because this form of encryption doesn't hide the natural patterns of data very well (as evidenced by those puzzle books that allow you to solve this form of encryption with nothing more than pattern recognition). One of the first character substitution methods was devised by Julius Caesar, and you can read about it at `https://www.dcode.fr/caesar-cipher`. Still, with a little ingenuity, you can create a character-substitution cipher using Python that provides variable encryption:

```
import random

random.seed(input("Provide an encryption value: "))

letters = ["a", "b", "c", "d", "e", "f", "g", "h", "i",
           "j", "k", "l", "m", "n", "o", "p", "q", "r",
           "s", "t", "u", "v", "w", "x", "y", "z", "!",
           "A", "B", "C", "D", "E", "F", "G", "H", "I",
           "J", "K", "L", "M", "N", "O", "P", "Q", "R",
           "S", "T", "U", "V", "W", "X", "Y", "Z", " "]
randomLetters = letters.copy()
random.shuffle(randomLetters)
print(letters)
print(randomLetters)
```

The example starts with a list of letters, the space, and the exclamation mark. It copies these letters to `randomLetters` and then shuffles them based on the `random.seed()` value you provide. The seed value is a *key*, essentially a secret value known only to you. Because it isn't hard coded in the application, you must know the key to decrypt the input string later. When you run this code with a seed value of 5, you see the following output:

```
Provide an encryption value: 5
['a', 'b', 'c', 'd', 'e', 'f', 'g', 'h', 'i', 'j', 'k', 'l',
            'm', 'n', 'o', 'p', 'q', 'r', 's', 't', 'u', 'v',
            'w', 'x', 'y', 'z', '!', 'A', 'B', 'C', 'D', 'E',
            'F', 'G', 'H', 'I', 'J', 'K', 'L', 'M', 'N', 'O',
            'P', 'Q', 'R', 'S', 'T', 'U', 'V', 'W', 'X', 'Y',
            'Z', ' ']
['x', 'q', 'i', 'y', 'l', 'B', 'u', 'a', 'z', 'L', 'v', 'A',
            'P', 'O', 'X', 'e', 'c', 'D', 't', 'f', 'Z', 'p',
            'k', 'V', 'm', 'S', 's', '!', ' ', 'H', 'R', 'Q',
            'U', 'E', 'h', 'j', 'Y', 'n', 'b', 'I', 'M', 'J',
            'g', 'N', 'K', 'C', 'o', 'F', 'd', 'T', 'G', 'W',
            'r', 'w']
```

This example doesn't use any sort of complex algorithm to encrypt or decrypt the input string, but the steps are similar to any other algorithm. To decrypt a string, you must reverse whatever you did to encrypt it, as shown here:

```
def encrypt(text):
    result=""
    for i in range(len(text)):
        char = text[i]
        result += randomLetters[letters.index(char)]
    return result

def decrypt(text):
    result=""
    for i in range(len(text)):
        char = text[i]
        result += letters[randomLetters.index(char)]
    return result
```

The algorithm uses simple substitution to perform the task. Consequently, when you run this code:

```
encrypted = encrypt("Hello There!")
print(encrypted)
```

you see an output that's precisely the same length as the input string, but also quite hard to read:

```
hlAAXwoalDls
```

The decryption process needs to be sure that you're the originator of the encrypted string, so it again asks for the seed value, as shown here:

```
random.seed(input("Provide a decryption value: "))
randomLetters = letters.copy()
random.shuffle(randomLetters)

decrypted = decrypt(encrypted)
print(decrypted)
```

Inputting the wrong seed value, the wrong key, will result in a string that's not decrypted properly. This process is much the same as the one that more complicated encryption techniques use. The difference is in the algorithm. For example, the Advanced Encryption Standard (AES) provides an incredibly complex algorithm, as described at https://www.geeksforgeeks.org/advanced-encryption-standard-aes/. You can find other examples of Python encryption techniques at https://www.tutorialspoint.com/cryptography_with_python/cryptography_with_python_quick_guide.htm.

Working with AES encryption

Now that you've seen a basic example, it's time to look at basic code you could use in the real world. However, before you can use this example, you need to install the PyCrypto package (https://pypi.org/project/pycrypto/) using the following command at the Anaconda prompt (don't use the normal prompt and you may have to open the Anaconda prompt with administrative privileges):

```
conda install pycrypto
```

The example in this section uses a process very similar to the one in the previous section, but the algorithm is more complex and the results much harder to break. The encryption and decryption code looks like this:

```
import base64, re
from Crypto.Cipher import AES
from Crypto import Random

def encrypt(key, blk_sz, raw):
    raw = raw + '\0' * (blk_sz - len(raw) % blk_sz)
    raw = raw.encode('utf-8')
    secretKey = Random.new().read(AES.block_size)
    cipher = AES.new(key.encode('utf-8'), AES.MODE_CBC,
                     secretKey)
    return base64.b64encode(
        secretKey + cipher.encrypt(raw) ).decode(
            'utf-8')

def decrypt(key, enc):
    enc = base64.b64decode(enc)
    secretKey = enc[:16]
    cipher = AES.new(key.encode('utf-8'), AES.MODE_CBC,
                     secretKey)
    return re.sub(b'\x00*$', b'',
                  cipher.decrypt(enc[16:])).decode(
                    'utf-8')
```

FIXING THE TIME.CLOCK() ERROR

After you install PyCrypto, you may need to perform an additional step. The `time.clock()` call is deprecated in Python 3.3 and removed in Python 3.8 and above. If you receive an error of `AttributeError: module 'time' has no attribute 'clock'` when running this example, the fix is relatively easy. You can read about it at `https://stackoverflow.com/questions/58569361/attributeerror-module-time-has-no-attribute-clock-in-python-3-8`. Essentially, you open the `C:\Users\<Your Name>\anaconda3\Lib\site-packages\Crypto\Random\_UserFriendlyRNG.py` file on your system, and then search for `t = time.clock()`. Change each of these entries to `t = time.time()` and save the file. This problem should be fixed when a new version of the PyCrypto library is released.

The encryption process begins by *padding* (adding nulls at the end) the text to decrypt so that it divides equally into the block size. For example, if the original message has 25 characters (and the block size is 32 characters), this padding process adds 7 nulls to make the message 32 characters long. The text is also encoded as UTF-8, so the nulls don't appear as control character 0 but rather as `\x00`. The reason you need to pad the message is that the example is using a block cipher.

The next step of the process generates a secret key for encrypting the message, as described at `https://www.dlitz.net/software/pycrypto/doc/#crypto-publickey-public-key-algorithms`. This secret key is in contrast to the public key you provide when calling the `encrypt()` function. Because the secret key is unknown, it's nearly impossible to guess it to make the message content known without having the public key (the one that is known). The secret key is now used to encode the message using `AES.new()` (described at `https://pycryptodome.readthedocs.io/en/latest/src/cipher/aes.html`) and output it as `cipher`. Finally, the `encrypt()` function outputs a combination of the secret key (used for decrypting the message later) and the cipher decoded in UTF-8 form and encoded in base64 form.

TECHNICAL STUFF

Base64 encoding ensures that strings remain in human-readable form and aren't hindered by platform differences in handling special character types like control characters. You can read more about base64 encoding at `https://levelup.gitconnected.com/what-is-base64-encoding-4b5ed1eb58a4`. The sites at `https://www.base64encode.org/` and `https://www.base64decode.org/` demonstrate how base64 encoding works.

Decryption follows a somewhat opposite process from encryption. The code begins by decoding the base64 encrypted message, It then extracts the `secretKey` from the first 16 characters of the combined message and uses the `key` and `secretKey` to create the cipher object, which you then use to decrypt the message. The call to `re.sub()` (see `https://docs.python.org/3/library/re.html`) removes the previously added padding, and you end up with the original message. The following code shows how to use these two functions:

```
encryp_msg = encrypt("1234567890ABCDEF", 16,
                     "This is a secret message.")
print(encryp_msg)

msg = decrypt("1234567890ABCDEF", encryp_msg)
print(msg)
```

The code first calls `encrypt()` with the public key, block size, and message to encrypt. Note that the public key is 16 characters long. You can't use a smaller key unless you pad it to 16 characters in this case because the block size is 16 characters. When you run this code, you see jumbled output similar to this:

```
r6KPOR0pbHqE7oZzCrpF4wVgV6/YrakgD7pSwHBVTPYUrOwmZpbknqZADtvxOxBN
```

The call to `decrypt()` provides the public key again, along with the encrypted message. When you run this code, you see your original message again.

5 Challenging Difficult Problems

IN THIS PART . . .

Using greedy, dynamic, and randomized algorithms

Reaching a compromise using local search

Employing linear programming techniques

Exploring the different flavors of heuristics

IN THIS CHAPTER

» Understanding how to design new algorithms and use solving paradigms

» Explaining how an algorithm can act greedy and get great results

» Drafting a greedy algorithm of your own

» Revisiting Huffman coding and illustrating some other classical examples

Chapter 15 Working with Greedy Algorithms

After taking your first steps into the world of algorithms by presenting what algorithms are and discussing ordering, searching, graphs, and big data, it's time to enter a more general part of the book. In this latter part of the book, you deal with some difficult examples and see general algorithmic approaches that you can use under different circumstances when solving real-world problems.

By taking new routes and approaches, this chapter goes well beyond the divide-and-conquer recursion approach that dominates in most sorting problems. Some of the discussed solutions aren't completely new; you've seen them in previous chapters. However, this chapter discusses those previous algorithms in greater depth, under the new *paradigms* that the chapter discusses. These paradigms include a look at the application rules and conditions, the general approach and steps to the solution of a problem, and analysis of problem complexity, limitations, and caveats.

Making some solutions general and describing them as widely applicable paradigms is a way to offer hints to solve new practical problems and is part of the analysis and design of algorithms. The remainder of this book discusses other general approaches.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 15; Greedy Algorithms.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Deciding When It Is Better to Be Greedy

Greedy algorithms come in handy for solving a wide array of problems, especially when drafting a global solution is difficult. Sometimes, it's worth giving up complicated plans and simply starting to look for low-hanging fruit that resembles the solution you need. In algorithms, you can describe a shortsighted approach like this as *greedy* (unlike those times where you want a second dessert, which could also be considered greedy). Looking for easy-to-grasp solutions constitutes the core distinguishing characteristic of greedy algorithms. A greedy algorithm reaches a problem solution using sequential steps during which, at each step, it makes a decision based on the best solution at that time, without considering future consequences or implications.

REMEMBER

Two elements are essential for distinguishing a greedy algorithm:

- » At each turn, you always make the best decision you can at that particular instant.
- » You hope that making a series of best decisions results in the best final solution.

Greedy algorithms are simple, intuitive, small, and fast because they usually run in *linear time* (the running time is proportional to the number of inputs provided). Unfortunately, they don't offer the best solution for all problems, but when they do, they provide the best results quickly. Even when they don't offer the top answers, they can give a nonoptimal solution that may suffice or that you can use as a starting point for further refinement by another algorithmic strategy. It's sort of like those times when you need to make a quick decision that's good enough.

Interestingly, greedy algorithms resemble how humans solve many simple problems without using much brainpower or with limited information. For instance, when working as cashiers and making change, a human naturally uses a greedy approach. You can state the *make-change* problem as paying a given amount (the change) using the least number of bills and coins among the available denominations. The following Python example demonstrates the make-change solution using a greedy approach:

```
def change(to_be_changed, denomination):
    resulting_change = list()
    for bill in denomination:
        while to_be_changed >= bill:
            resulting_change.append(bill)
            to_be_changed = to_be_changed - bill
    return resulting_change, len(resulting_change)

currency = [100, 50, 20, 10, 5, 1]
amount = 367
print ('Change: %s (using %i bills)'
       % (change(amount, currency)))

Change: [100, 100, 100, 50, 10, 5, 1, 1] (using 8 bills)
```

The algorithm, encapsulated in the `change()` function, scans the denominations available, from the largest to the smallest. It uses the largest available currency to make change until the amount due is less than the denomination. It then moves to the next denomination and performs the same task until it finally reaches the lowest denomination. In this way, `change()` always provides the largest bill possible for the amount to deliver. (This is the greedy principle in action.)

Greedy algorithms are appreciated for scheduling problems, optimal caching (making your computer operating system and web browser work better), and compression using Huffman coding. They also work fine for some graph problems. For instance, Kruskal's and Prim's algorithms for finding a minimum-cost spanning tree, and Dijkstra's shortest-path algorithm, are all greedy ones (see Chapter 9 for details). A greedy approach can also offer a nonoptimal yet acceptable first approximation solution to difficult problems such as the traveling salesman problem (TSP). In addition greedy algorithms can also solve special cases of problems that are otherwise solvable by more complicated algorithms, such as the knapsack problem when quantities aren't discrete (Chapter 16 discusses both problems).

Understanding why greedy is good

It shouldn't surprise you that a greedy strategy works so well in the make-change problem. In fact, some problems don't require farsighted strategies: The solution is built using intermediate results (a sequence of decisions), and at every step the right decision is always the best one according to an initially chosen criteria.

Acting greedy is also a very human (and effective) approach to solving economic problems. In the 1987 film *Wall Street*, Gordon Gecko, the protagonist, declares that "Greed, for lack of a better word, is good" and celebrates greediness as a positive act in economics. Greediness (not in the moral sense, but in the sense of using a greedy algorithm) is at the core of the neoclassical economy. Economists such as Adam Smith, in the 18th century, theorized that the individual's pursuit of self-interest greatly benefits society as a whole and renders it prosperous in economy: `https://plus.maths.org/content/adam-smith-and-invisible-hand`.

Detailing how a greedy algorithm works (and under what conditions it can work correctly) is straightforward, as explained in the following four steps:

1. You can divide the problem into partial problems. The sum (or other combination) of these partial problems provides the right solution. In this sense, a greedy algorithm isn't much different from a divide-and-conquer algorithm (like Quicksort or Mergesort, both of which appear in Chapter 7).
2. The successful execution of the algorithm depends on the successful execution of every partial step. This is the *optimal substructure characteristic* because an optimal solution is made only of optimal subsolutions. You can confirm that your problem has an optimal substructure analytically or by retracing systematically from an optimal solution.
3. To achieve success at each step, the algorithm considers the input data only at that step. That is, situation status (previous decisions) determines the decision the algorithm makes, but the algorithm doesn't consider consequences. This complete lack of a global strategy is the *greedy choice property* because being greedy at every phase is enough to offer ultimate success. As an analogy, it's akin to playing the game of chess by not looking ahead more than one move, and yet winning the game.
4. The greedy choice property provides hope for success, so a greedy algorithm lacks a complex decision rule because it needs, at worst, to consider all the available input elements at each phase. There is no need to compute possible decision implications; consequently, the computational complexity is at worst linear `O(n)`. Greedy algorithms take the simple route to solving highly complex problems that other algorithms take forever to compute because they look too deeply.

Keeping greedy algorithms under control

When faced with a new difficult problem, it's not hard to come up with a greedy solution using the four steps described in the previous section. All you have to do is divide your problem into phases and determine which greedy rule to apply at each step. That is, you do the following:

- Choose how to make your decision (determine which approach is the simplest, most intuitive, smallest, and fastest).
- Start solving the problem by applying your decision rule.
- Record the result of your decision (if needed) and determine the status of your problem.
- Repeatedly apply the same approach at every step until reaching the problem conclusion.

No matter how you apply the previous steps, you must determine whether you're accomplishing your goal by relying on a series of myopic decisions. The greedy approach works for some problems, but it doesn't work for every problem. For instance, the make-change problem works perfectly with U.S. currency but produces less-than-optimal results with other currencies. To see this problem, consider a fictional currency (credits) with denominations of 1, 15, and 25 credits, the previous algorithm fails to deliver the optimal change for a due sum of 30 credits:

```
print ('Change: %s (using %i bills)'
       % (change(30, [25, 15, 1])))

Change: [25, 1, 1, 1, 1, 1] (using 6 bills)
```

Clearly, the optimal solution is to return two 15 credit bills, but the algorithm, being shortsighted, started with the highest denomination available (25 credits) and then used five 1 credit bills to make up the residual 5 credits.

TECHNICAL STUFF

Some complex mathematical frameworks called *matroids* (see `https://jeremykun.com/2014/08/26/when-greedy-algorithms-are-perfect-the-matroid/` for details) can help verify whether you can use a greedy solution to optimally solve a particular problem. If phrasing a problem using a matroid framework is possible, a greedy solution will provide an optimal result. Yet there are problems that have optimal greedy solutions that don't abide by the matroid framework. (You can read about matroid structures being sufficient, but not necessary, for an optimal greedy solution in the article found at `http://cstheory.stackexchange.com/questions/21367/does-every-greedy-algorithm-have-matroid-structure`.) There is also an interesting video, "Matroids for Greedy Algorithms," at `https://www.youtube.com/watch?v=VWRm1IZAsVE`.

The greedy algorithms user should know that greedy algorithms do perform well but don't always provide the best possible results. When they do, it's because the problem consists of known examples or because the problem is compatible with matroid mathematical framework. Even when a greedy algorithm works best in one setting, changing the setting may *break the toy* and generate just good or acceptable solutions. In fact, the cases of just good or acceptable results are many, because greedy algorithms don't often outperform other solutions, as shown by

- The make-change problem solutions earlier show how a change in setting can cause a greedy algorithm to stop working.
- The scheduling problem (described in the "Finding Out How Greedy Can Be Useful" section, later in this chapter) illustrates how a greedy solution works perfectly with one worker, but not with more than one.
- The Dijkstra shortest-path algorithm works only with edges having positive weights. (Negative weights will cause the algorithm to loop around some nodes indefinitely.)

Demonstrating that a greedy algorithm works the best is a hard task, requiring a solid knowledge of mathematics. Otherwise, you can devise a proof in a more empirical way by testing the greedy solution against one of the following:

- One of the techniques used to prove the correctness of greedy algorithms is *greedy exchange*. The greedy exchange proof morphs a solution produced by any other algorithm into the solution produced by your greedy algorithm in a way that doesn't worsen the solution's quality. Using this technique shows that any other solution is no better than the greedy solution, which proves that the greedy solution does return the optimal solution.
- Another algorithm when, as you see the greedy solution unfolding, you notice that the greedy solution *stays ahead* of the optimal algorithm; that is, the greedy solution always provides a better solution at every step than is provided by another algorithm.

TIP

Even considering that it's more the exception than a rule that a successful greedy approach will determine the top solution, greedy solutions often outperform other tentative solutions. You may not always get the top solution, but the solution will provide results that are good enough to act as a starting point (as a minimum), which is why you should start by trying greedy solutions first on new problems.

Considering NP complete problems

Usually you think of a greedy algorithm because other choices don't compute the solution you need in a feasible time. The greedy approach suits problems for which you have many choices and have to combine them. As the number of possible combinations increases, complexity explodes, and even the most powerful computer available fails to provide an answer in a reasonable time. For example, when attempting to solve a puzzle, you could try to solve it by determining all the possible ways you can fit the available pieces together. A more reasonable way is to start solving the problem by choosing a single location and then finding the best-fitting piece for it. Solving the puzzle this way means using time to find the best fitting piece, but you don't have to consider that location again, reducing the total number of pieces for each iteration.

Puzzle problems, in which the number of possible decisions can become huge, are more frequent than you expect. Some problems of this type have already been solved, but many others aren't, and it isn't possible to transform them (yet) into versions with known solutions. Until someone is smart enough to find a generic solution for these problems, a greedy approach may be the easiest way to approach them, provided that you accept that you won't always get the best solution, but a roughly acceptable one instead (in many cases).

These difficult problems vary in characteristics and problem domain. One example of a difficult problem is that of protein unfolding (which can help cure cancer and recently made great advancements thanks to Google DeepMind and its deep learning–powered AI named AlphaFold 2: `https://www.nature.com/articles/d41586-020-03348-4`). Another example of a difficult problem is that of breaking strong password encryption, such as the popular RSA cryptosystem (`https://www.okta.com/identity-101/rsa-encryption/`). In the 1960s, researchers found a common pattern for all strong password encryption: They are all equally difficult to solve. This pattern is called the NP-completeness theory (NP stands for nondeterministic polynomial). In a sense, difficult problems distinguish themselves from others because it's not yet possible to find a solution in a reasonable time — that is, in polynomial time.

Polynomial time means that, in the worst case, an algorithm runs in powers of the number of inputs (known as P problems). Linear time is polynomial time because it runs $O(n^1)$. Also quadratic $O(n^2)$ and cubic $O(n^3)$ complexities are polynomial time, and though they grow quite fast, they don't compare to exponential time, that is, $O(c^n)$. *Exponential time* complexity makes it impossible to find a reasonable solution for any of these problems using brute force. In fact, if *n* is large enough, you may easily have to try a number of solutions larger than the number of atoms present in the known universe. This issue enters the territory of NP problems, and at present, you can hope to solve any of these problems in polynomial time only if you have a nondeterministic Turing machine available. Such a machine is a kind of a magic machine (therefore it is just theoretical) that could potentially work thanks to infinite parallel processors. Each parallel stream of computations, though it doesn't communicate with the other ones, can take care of a part of the solution, hence in theory at the end it can solve difficult problems in polynomial time, thus escaping the trap of exponential time.

Because nondeterministic Turing machines are theoretical, no way to quickly solve any NP problem is at hand, but they get solved anyway because people are smart enough to devise a solution. Also, when we find a solution to an NP problem, it's easy to check whether the solution is valid because, by definition, it can take only polynomial time to verify the solution. For instance, linear programming has long been reputed a NP problem, but in 1979 it was shown to be a P problem by the ellipsoid algorithm of the Russian mathematician Leonid Khachiyan. Therefore, don't despair; sooner or later, many NP problems become P ones thanks to the efforts of many researchers and scientists.

Among NP problems, there is a subset called NP-complete problems (see Figure 15-1). These problems are very special problems because we know that solving them could be the key to solving in polynomial time many other NP problems simultaneously. The hope of algorithm experts is that someone will find a way to solve any one of these problems in the future, thus opening the door to solving all the NP problems at one time. Solving NP-complete problems is one of the "Millennium Prize Problems" proposed by the Clay Mathematics Institute, which offers an award of one million USD to anyone who can devise a solution (`http://www.claymath.org/millennium-problems/p-vs-np-problem`).

However, NP-complete problems do not really complete the number of hard problems that you can solve and unlock all the NP problems simultaneously, as you can see in Figure 15-1. Actually, NP-complete are part of a much larger set of problems called NP-Hard problems. The fact that NP-complete problems are also part of NP makes them reasonably verifiable (as mentioned previously, they can checked in polynomial time), but NP-hard are not in NP. This fact implies that checking their solutions also requires exponential time, which makes solving and checking them a real nightmare for current algorithmic capabilities. If scientists can break through a hard problem and find the Holy Grail of algorithms, probably it will happen solving an NP-complete, not an NP-hard problem.

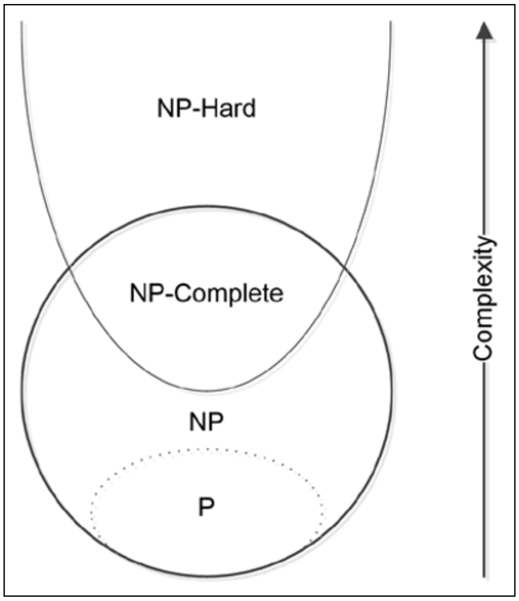


FIGURE 15-1: The sets of P, NP, NP-complete and NP-hard problems.

Finding Out How Greedy Can Be Useful

Previous sections of the chapter offer a general understanding of greedy algorithms. This part of the chapter shows some of these algorithms in detail to give you a deeper look and help you determine how to reuse their strategies for solving other problems. The following sections describe how a *computer cache* (an algorithm always found under the hood of any computer) works. In addition, you discover how to schedule tasks correctly to achieve deadlines and priorities. The production of material goods relies strongly on greedy algorithms to schedule resources and activities. Usually, activity algorithms appear at the core of Material Requirements Planning (MRP) software, and they help run a factory efficiently (`http://searchmanufacturingerp.techtarget.com/definition/Material-requirements-planning-MRP`). Finally, the following sections review the Huffman coding algorithm to provide more insight on how it works to create new efficient encoding systems.

Arranging cached computer data

Computers often process the same data multiple times, making some people think that they're obsessive, when they're really being thorough. Obtaining data from disk or the Internet requires sufficient bandwidth and costs computational time. Consequently, it's useful to store often-used data in local storage, where it's easier to access (and maybe already preprocessed). A *cache,* which is usually a series of memory slots or space on disk reserved for that need, fulfills the purpose.

For instance, when reviewing your web browser's history, you likely notice that only a part of traffic is made of new websites, whereas you spend a large amount of time and page requests on sites you know well. Storing in cache some parts of commonly seen websites (such as the header, background, some pictures, and some pages that seldom change) can really improve your web experience because it reduces the need to download data again. All you need is the new data from the Internet because most of what you want to see is already somewhere in your computer. (The cache of a web browser is a disk directory.)

The problem isn't new. In the 1960s, László Bélády, a Hungarian computer scientist working at IBM Research, hypothesized that the best way to store information in a computer for prompt reuse is to know what data is needed in the future and for how long. You can't implement such forecasting in practice because computer usage can be unpredictable and not predetermined.

Yet, as a principle, the idea of anticipating the future can inspire an *optimal replacement strategy,* a greedy choice based on the idea of keeping the pages that you expect to use soon based on previous requests to the cache. Bélády's optimal page replacement policy (also known as the *clairvoyant replacement algorithm*) works on a greedy principle: to discard data from the cache whose next use will likely occur farthest in the future in order to minimize the chance of discarding something you need soon. To implement this idea, the algorithm follows these steps:

1. **Fill the computer cache by recording data from every request made.** Only when the cache is full do you start discarding past stuff to make room for new data.
2. **Define a method for determining recent usage.** This algorithm can use file date stamps or a system of memory flags (which flags recently used pages and clears all the flags after a certain time) to make the determination.
3. **When you have to fit new data, you discard data that hasn't been used recently from the cache.** The algorithm picks one piece of data randomly among the ones not used.

For instance, if your cache has only four memory slots, and it is filled by four alphabet letters that arrive in the following order:

```
A          B          C          D
```

when a new letter is processed, such as the letter *E,* the computer makes space for it by removing one of the letters that are less likely to be requested at this point. In this example, good candidates are *A, B,* or *C* (*D* is the most recent addition). The algorithm will pick one slot randomly and evict its data from the cache in order to let *E* in.

Competing for resources

No, this section isn't about a new game show whose winning contestants walk off with amazing prizes. Instead, it's about solving a common problem that arises when you want to achieve an objective, such as to create a service or produce a material object. The problem is scheduling several competing activities that require exclusive access to resources. Resources can include time on a production machine. Examples of such situations abound in the real world, ranging from scheduling your attendance at university courses to arranging the supplies of an army, or from assembling a complex product such as a car to organizing a computational job sequence in a data center. Invariably, common goals in such situations are to

- Achieve getting the most jobs done in a certain amount of time
- Manage jobs as quickly as possible, on average
- Respect some strict priorities (hard deadlines)
- Respect some priority indications (soft deadlines)

Job scheduling falls into two categories:

- Jobs that are hard to solve properly and require advanced algorithms to solve
- Jobs that are easier to deal with and can be solved by simple greedy algorithms

Most of the scheduling you perform actually falls among those solvable by greedy algorithms. For instance, managing jobs as quickly as possible is a common requirement for industrial production or the service industry when each job serves the needs of a client and you want to do your best for all your clients. Here's how you can determine a context for such an algorithm:

- You have a single machine (or worker) that can work out orders.
- Orders arrive in batches, so you have many to choose from at a time.
- Orders differ in length, each requiring a different execution time.

For instance, you receive four jobs from four business customers requiring 8, 4, 12, and 3 hours, respectively, to execute. Even though the total execution time remains the same, changing the job-execution order changes the time when you complete the jobs and dictates how long each business customer has to wait before having its job done. The following sections consider different methods for meeting business customer needs given specific goals.

Addressing customer satisfaction

Business is about keeping customers happy. If you execute the jobs in the order presented, the work takes 8 + 4 + 12 + 3 = 27 hours to execute completely. Yet, the first customer will receive its job after 8 hours, the last one after 27 hours. In fact, the first job completes in 8 hours, the second in 8 + 4 = 12 hours, the third in 8 + 4 + 12 = 24 hours, the last in 8 + 4 + 12 + 3 = 27 hours.

If you aim at to keep all your customers happy and satisfied, you should strive to minimize the average waiting time for each of them. This measure is given by the average of the delivery times: (8 + 12 + 24 + 27) / 4 = 17.75 hours on average to wait for a job. To reduce the average wait time, you could start simulating all the possible combinations of order execution and recalculate the estimate. This is feasible for a few jobs on a single machine, but if you have hundreds of them on multiple machines, that becomes a very heavy computational problem. A greedy algorithm can save the day without much planning: just execute the shortest first. The resulting average will be the smallest possible: (3 + (3 + 4) + (3 + 4 + 8) + (3 + 4 + 8 + 12)) / 4 = 13 hours on average.

REMEMBER

To obtain the average wait time, you take the average of the cumulated sums of runtimes. If you instead take the average of raw times, you obtain the average length of a task, which doesn't represent the customer's waiting time.

The greedy principle is simple: Because you sum cumulative times, if you start by running the longest tasks, you extend the longest run to all successive execution times (because it is a cumulative sum). If instead you start with the shortest jobs, you draw the smallest times first, positively affecting the average (and your customers' average level of satisfaction — but the customer with the longest job may still not be happy).

Meeting deadlines

Sometimes, more than just wanting to make your customers wait for less time, you also have to respect their time requirements, meaning that you have deadlines. When you have deadlines, the greedy mechanism changes. Now you don't start from the shortest task but with the task that you must deliver the earliest, according to the principle *the earlier, the better*. This is the problem of hard deadlines, and it's a problem you can actually fail to solve. (Some deadlines are simply impossible to meet.)

TIP

If you try a greedy strategy and can't solve the problem, you can acknowledge that no solution to the required deadline exists. When hard deadlines can't work, you can try to solve the problem using soft deadlines instead, meaning that you have to respect a priority (executing certain tasks first).

In this example, you have both the lengths of the tasks, as discussed in the previous section, and you have a value (a *weight*) that defines the task importance (larger weights have higher priority). It's the same problem, but this time you must minimize the weighted average completion time. To achieve this goal, you create a priority score by dividing the time lengths by the weights, and you start with the tasks that have the lowest score. If a task has the lowest score, it's because it is high priority or very short.

For instance, reprising the previous example, you now have tuples of both weights and lengths: (40, 8), (30, 4), (20, 12), (10, 3), where 40 in the first tuple is a weight and 8 is a length. Divide each length by the weight and you get priority scores of 0.20, 0.13, 0.60, and 0.30. Start from the lowest-priority score and, adding the lowest priority score that's left, you obtain a best schedule that assures that you both minimize times and respect priorities: (30, 4), (40, 8), (10, 3), (20, 12).

Revisiting Huffman coding

As seen in the previous chapter, Huffman coding can represent data content in a more compact form by exploiting the fact that some data (such as certain characters of the alphabet) appear more frequently in a data stream. By using encodings of different length (shorter for the most frequent characters, longer for the least frequent ones), the data consumes less space. Prof. Robert M. Fano (Huffman's professor) and Claude Shannon already envisioned such a compression strategy but couldn't find an efficient way to determine an encoding arrangement that would make it impossible to mistake one character for another.

REMEMBER

Prefix-free codes are necessary in order to avoid errors when decoding the message. It means that no previously used bit encoding should be used as the starting point for another bit encoding. Huffman found a simple and workable solution for implementing prefix-free codes using a greedy algorithm. The solution to the prefix-free problem found by Huffman is to transform the originally balanced tree (a data structure discussed in Chapter 6) containing the fixed-length encoding into an unbalanced tree, as shown in Figure 15-2.

An unbalanced tree has a special characteristic in that each node has only one branch that keeps on developing in other nodes and branches, whereas the other branch terminates with an encoded character. This characteristic assures that no previously used encoding sequence can start a new sequence (graphically, a branch terminating with an encoded character is a dead end).

Apart from graphically drafting the unbalanced structure, a greedy algorithm can also construct an unbalanced tree. The idea is to build the structure down from the root, starting with the least frequently used characters. The algorithm creates the lower levels of the tree by aggregating less frequent characters in sequence until there are no more characters and you reach the bottom.

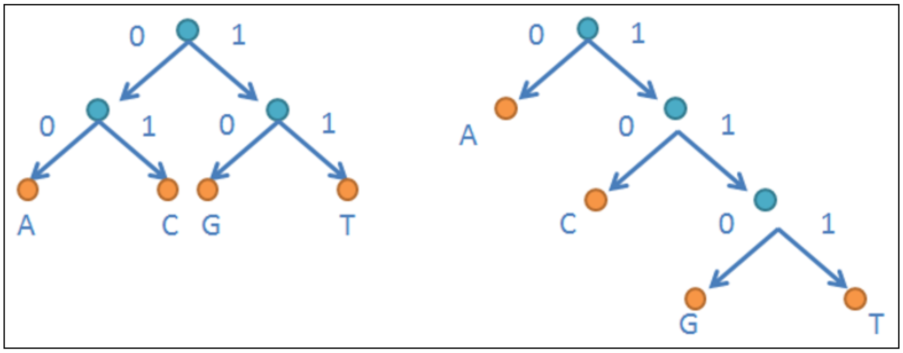


FIGURE 15-2: From a balanced tree (left) to an unbalanced tree (right).

To demonstrate the greedy recipe behind the algorithm, this section provides a Python code example based on DNA. DNA is represented as a sequence of the letters *A*, *C*, *T*, and *G* (the four nucleotides present in all living beings). A good trick is to use just two bits in order to represent each of the four letters, which is already a good memory-saving strategy when compared to using a full ASCII encoding (which is at least 7 bits).

The nucleotides aren't uniformly distributed. The distribution varies depending on what genes you study. The following table shows a gene with an uneven distribution, allowing for a predominance of *A* and *C* nucleotides.

Nucleotides	Percentage	Fixed Encoding	Huffman Encoding
A	40.5%	00	0
C	29.2%	01	10
G	14.5%	10	110
T	15.8%	11	111
Weighted bit average:		2.00	1.90

By multiplying the number of bits of the two encodings by their percentage and summing everything, you obtain the weighted average of bits used by each of them. In this case, the result is 1.9 for the Huffman encoding versus 2.0 for the fixed encoding. This means that you obtain a five percent bit saving in this example. You could save even more space when having genes with an even more unbalanced distribution in favor of some nucleotide.

The following example generates a random DNA sequence and shows how the code systematically generates the encoding. (If you change the seed value, the random generation of the DNA sequences may lead to a different result, both in the distribution of nucleotides and Huffman encoding.)

```
from random import shuffle, seed
from collections import defaultdict, Counter

generator = ["A"]*6+["C"]*4+["G"]*2+["T"]*2
text = ''
seed(4)
for i in range(1000):
    shuffle(generator)
    text += generator[0]

frequencies = Counter(list(text))
print(f"{text[:25]} ...\n{frequencies}")

CAACCCCGACACGCCTCCATAGCCA ...
Counter({'A': 405, 'C': 292, 'T': 158, 'G': 145})
```

After making the data inputs ready to compress, the code prepares a heap data structure (see the "Performing specialized searches using a binary heap" section of Chapter 7 for details) to arrange the results efficiently along the steps the algorithm takes. The elements in the heap contain the nucleotide characters and the frequency number of nucleotides. With a log-linear time complexity, O(n*log(n)), a heap is the right structure to use to order the results and allow the algorithm to draw the two smallest elements quickly.class BinaryHeap():

```
    def __init__(self):
        self.heap = []

    def swap(self, i, j):
        self.heap[i], self.heap[j] = self.heap[j], self.heap[i]

    def insert(self, key, value):
        index = len(self.heap)
        self.heap.append([key, value])
        while index!=0:
            parent = (index - 1) // 2
            if self.heap[parent][1] < self.heap[index][1]:
                self.swap(parent, index)
            index = parent

heap = BinaryHeap()
for key_value_pair in frequencies.items():
    heap.insert(*key_value_pair)
print(heap.heap)

[['A', 405], ['C', 292], ['G', 145], ['T', 158]]
```

When you run the algorithm, based on the sorting done by the binary heap, it picks the nucleotides with fewer frequencies from the heap (the greedy choice). It then aggregates these nucleotides into a new element, replacing the previous two. The process continues until the last aggregation reduces the number of elements left to extract from the heap to one.

```
encoding = {item[0]:'' for item in heap.heap}
for i in range(1, len(heap.heap)):
    aggregate = heap.heap[-i:]
    new = heap.heap[-i-1]
    # putting a 1 in front of previous element
    for item in aggregate:
        encoding[item[0]] = '1' + encoding[item[0]]
    # putting a 0 in front of following element
    encoding[new[0]] = '0' + encoding[new[0]]
    print(f"{aggregate} + {new} =\n{encoding}\n")

[['T', 158]] + ['G', 145] =
{'A': '', 'C': '', 'G': '0', 'T': '1'}
[['G', 145], ['T', 158]] + ['C', 292] =
{'A': '', 'C': '0', 'G': '10', 'T': '11'}
[['C', 292], ['G', 145], ['T', 158]] + ['A', 405] =
{'A': '0', 'C': '10', 'G': '110', 'T': '111'}
```

As the aggregations put the nucleotides together, constituting different levels of the unbalanced tree, their Huffman encoding is systematically modified; adding a zero in front of the encoding of the element next to enter the aggregate and adding one in front of the elements already in the aggregate. In this way, the algorithm efficiently replicates the unbalanced tree structure previously illustrated.

The final step is to print the result, showing how the aggregate built up and how the encodings changed. The last aggregation is presenting the final symbol table generated.

IN THIS CHAPTER

» Understanding what *dynamic* means when used with programming

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Chapter 16 Relying on Dynamic Programming

Instead of using brute force, which implies trying all possible solutions to a problem, greedy algorithms provide an answer that is quick and often satisfying. In fact, a greedy algorithm can potentially solve the problem fully. Yet, greedy algorithms are also limited because they make decisions that don't consider the consequences of their choices. Chapter 15 shows that you can't always solve a problem using a greedy algorithm.

This chapter presents dynamic programming. It explains how an algorithm may make an apparently optimal decision at a certain stage, which later appears limiting and suboptimal for achieving the best solution. A better algorithm, one that doesn't rely on the greedy approach, can revise past decisions or anticipate that an apparently good decision is not as promising as it might seem. This is the approach that dynamic programming takes.

This chapter offers you more than a simple definition of dynamic programming. In the first part, it also explains why dynamic programming has such a complicated name. In addition, you find out how to transform any algorithm (especially recursive ones) into dynamic programming using Python and its *function* *decorators* (powerful tools in Python that allow changing an existing function without rewriting its code). Practical applications explain dynamic programming better than theory, so the second half of the chapter shows dynamic programming applications that optimize resources and returns, create short tours between places, and compare strings in an approximate way. Dynamic programming provides a natural approach to dealing with many problems you encounter while journeying through the world of algorithms.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `\A4D2E\A4D2E; 16; Fibonacci.ipynb`, `\A4D2E\A4D2E; 16; Knapsack.ipynb`, `\A4D2E\A4D2E; 16; Levenshtein.ipynb`, and `\A4D2E\A4D2E; 16; TSP.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Explaining Dynamic Programming

Dynamic programming is an algorithm approach devised in the 1950s by Richard Ernest Bellman (an applied mathematician also known for other discoveries in the field of mathematics and algorithms; read more at `https://mathshistory.st-andrews.ac.uk/Biographies/Bellman/`) that tests more solutions than a corresponding greedy approach. Testing more solutions provides the ability to rethink and ponder the consequences of decisions. Dynamic programming avoids performing heavy computations thanks to a smart caching system called *memoization*, a term defined later in the chapter. (A *cache* is a storage system that collects data or information.)

Dynamic programming is as effective as an exhaustive algorithm — thus providing correct solutions — yet it is often as efficient as an approximate solution (the computational time of many dynamic programming algorithms is polynomial). It seems to work like magic because the solution you need often requires the algorithm to perform the same calculations many times. By modifying the algorithm and making it dynamic, you can record the computation results and reuse them when needed. Reusing takes little time when compared to recalculating, thus the algorithm finishes the steps quickly. The following sections discuss what dynamic programming involves in more detail.

Obtaining a historical basis

You can boil *dynamic programming* down to having an algorithm remember the previous problem results where you'd otherwise have to perform the same calculation repeatedly. Even though dynamic programming might appear to be quite complex, the implementation is actually straightforward. However, it does have some interesting historical origins.

Bellman described the name *dynamic programming* as being the result of necessity and convenience in his autobiography, *In the Eye of the Hurricane.* He writes that the name choice was a way to hide the true nature of his research at the RAND Corporation (a research and development institution funded by both the U.S. government and private financers) from Charles Erwin Wilson, the Secretary of Defense under the Eisenhower presidency. Cloaking the true nature of his research helped Bellman remain employed at the RAND Corporation. You can read his explanation in more detail in the excerpt at: `http://theory.cs.utah.edu/fall18/algorithms/dy_birth.pdf`. Some researchers don't agree about the name source. For example, Stuart Russell and Peter Norvig, in their book *Artificial Intelligence: A Modern Approach,* argue that Bellman actually used the term *dynamic programming* in a paper dating to 1952, which is before Wilson became Secretary in 1953 (and Wilson himself was CEO of General Motors before becoming an engineer involved in research and development).

Computer programming languages weren't widespread during the time that Bellman worked in operations research, a discipline that applies mathematics to make better decisions when approaching mainly production or logistic problems (but is also used for other practical problems). Computing was at the early stages and used mostly for planning. The basic approach of dynamic programming is the same as *linear programming,* another algorithmic technique (see Chapter 19) defined in those years when programming meant planning a specific process to find an optimal solution. The term *dynamic* reminds you that the algorithm moves and stores partial solutions. Dynamic programming is a complex name for a smart and effective technique to improve algorithm running times.

Making problems dynamic

Because dynamic programming takes advantage of repeated operations, it operates well on problems that have solutions built around solving subproblems that the algorithm later assembles to provide a complete answer. To work effectively, a dynamic programming approach uses subproblems nested in other subproblems. (This approach is akin to greedy algorithms, which also require an optimal substructure, as explained in Chapter 15.) Only when you can break a problem down into nested subproblems can dynamic programming beat brute-force approaches that repeatedly rework the same subproblems.

REMEMBER

As a concept, dynamic programming is a huge umbrella covering many different applications because it isn't really a specific algorithm for solving a specific problem. Rather, it's a general technique that supports problem solving. You can trace dynamic programming to two large families of solutions:

- **Bottom-up:** Builds an array of partial results that aggregate into a complete solution
- **Top-down:** Splits the problem into subproblems, starting from the complete solution (this approach is typical of recursive algorithms) and using memoization (defined in the next section) to avoid repeating computations

Typically, the top-down approach is more computationally efficient because it generates only the subproblems necessary for the complete solution. The bottom-up approach is more explorative and, using trial and error, often obtains partial results that you won't use later. On the other hand, bottom-up approaches better reflect the approach that you'd take in everyday life when facing a problem (thinking recursively, instead, requires abstraction and training before application). Both top-down and bottom-up approaches aren't all that easy to understand at times. That's because using dynamic programming transforms the way you solve problems, as detailed in these steps:

1. Create a working solution using brute force and possibly recursion. The solution works but it takes a long time or won't finish at all.
2. Store the results of subproblems to speed your computations and reach a solution in a reasonable time.
3. Change the way you approach the problem and gain even more speed.
4. Redefine the problem approach, in a less intuitive but more efficient way to obtain the greatest advantage from dynamic programming.

Transforming algorithms using dynamic programming to make them work efficiently generally makes them harder to understand. In fact, you might look at the solutions and think they work by magic. Becoming proficient in dynamic programming requires repeated observations of existing solutions and some practical exercise. This proficiency is worth the effort, however, because dynamic programming can help you solve problems for which you have to systematically compare or compute solutions.

TIP

Dynamic programming is especially known for helping solve (or at least make less time demanding) combinatorial optimization problems, which are problems that require obtaining combinations of input elements as a solution. Examples of such problems solved by dynamic programming are the traveling salesman and the knapsack problems, described later in the chapter.

Casting recursion dynamically

The basis of dynamic programming is to achieve something as effective as brute-force searching without actually spending all the time doing the computations required by a brute-force approach. You achieve the result by trading time for disk space or memory, which is usually done by creating a data structure (a hash table, an array, or a data matrix) to store previous results. Using lookup tables allows you to access results without having to perform a calculation a second time.

REMEMBER

The technique of storing previous function results and using them instead of the function is *memoization*, a term you shouldn't confuse with memorization. Memoization derives from *memorandum*, the Latin word for "to be remembered."

REMEMBER

Caching is another term that you find used when talking about memoization. *Caching* refers to using a special area of computer memory to serve data faster when required, which has more general uses than memoization.

To be effective, dynamic programming needs problems that repeat or retrace previous steps. A good example of a similar situation is using recursion, and the landmark of recursion is calculating Fibonacci numbers. The Fibonacci sequence is simply a sequence of numbers in which the next number is the sum of the previous two. The sequence starts with 0 followed by 1. After defining the first two elements, every following number in the sequence is the sum of the previous ones. Here are the first eleven numbers:

```
[0, 1, 1, 2, 3, 5, 8, 13, 21, 34, 55]
```

As with indexing in Python, counting starts from the zero position, and the last number in the sequence is the tenth position. The inventor of the sequence, the Italian mathematician Leonardo Pisano, known as Fibonacci, lived in 1200. Fibonacci thought that the fact that each number is the sum of the previous two should have made the numbers suitable for representing the growth patterns of a group of rabbits. The sequence didn't work great for rabbit demographics, but it offered unexpected insights into both mathematics and nature itself because the numbers appear in botany and zoology. For instance, you see this progression in the branching of trees and in the arrangements of leaves in a stem and of seeds in a sunflower (you can read about this arrangement at `https://www.goldennumber.net/spirals/`).

REMEMBER

Fibonacci was also the mathematician who introduced Hindu-Arabic numerals to Europe, the system we daily use today. He described both the numbers and the sequence in his masterpiece, the *Liber Abaci*, in 1202.

You can calculate a Fibonacci number sequence using recursion. When you input a number, the recursion splits the number into the sum of the previous two Fibonacci numbers in the sequence. After the first split, the recursion proceeds by performing the same task for each element of the split, splitting each of the two numbers into the previous two Fibonacci numbers. The recursion continues splitting numbers into their sums until it finally finds the roots of the sequence, the numbers 0 and 1. Reviewing the two types of dynamic programming algorithms described in the "Making problems dynamic" section, earlier in this chapter, this solution uses a top-down approach. The following code shows the recursive approach in Python. (You can find this code in the `A4D2E; 16; Fibonacci.ipynb` downloadable source code file; see the Introduction for details.)

```
def fib(n, tab = 0):
    if n == 0:
        return 0
    elif n == 1:
        return 1
    else:
        print(f"lvl {tab}", end = ': ')
        print(f"summing fib({n - 1}) and fib({n - 2})")
        return fib(n - 1, tab + 1) + fib(n - 2, tab + 1)
```

The code prints the splits generated by each recursion level. The following output shows what happens when you call `fib()` with an input value of `7`:

```
fib(7)

lvl 0: summing fib(6) and fib(5)
lvl 1: summing fib(5) and fib(4)
lvl 2: summing fib(4) and fib(3)
lvl 3: summing fib(3) and fib(2)
lvl 4: summing fib(2) and fib(1)
lvl 5: summing fib(1) and fib(0)
lvl 4: summing fib(1) and fib(0)
lvl 3: summing fib(2) and fib(1)
lvl 4: summing fib(1) and fib(0)
lvl 2: summing fib(3) and fib(2)
lvl 3: summing fib(2) and fib(1)
lvl 4: summing fib(1) and fib(0)
lvl 3: summing fib(1) and fib(0)
lvl 1: summing fib(4) and fib(3)
lvl 2: summing fib(3) and fib(2)
lvl 3: summing fib(2) and fib(1)
lvl 4: summing fib(1) and fib(0)
lvl 3: summing fib(1) and fib(0)
lvl 2: summing fib(2) and fib(1)
lvl 3: summing fib(1) and fib(0)

13
```

The output shows 20 splits. Some numbers appear more than once as part of the splits. It seems like an ideal case for applying dynamic programming. The following code adds a dictionary, called `memo`, which stores previous results. After the recursion splits a number, it checks whether the result already appears in the dictionary before starting the next recursive branch. If it finds the result, the code uses the precomputed result, as shown here:

```
memo = dict()
def fib_mem(n, tab = 0):
    if n == 0:
        return 0
    elif n == 1:
        return 1
    else:
        if (n-1, n-2) not in memo:
            print (f"lvl {tab}", end=': ')
            print (f"summing fib({n-1}) and fib({n-2})")
            memo[(n-1,n-2)] = fib_mem(n-1,tab+1
                              ) + fib_mem(n-2,tab+1)
        return memo[(n-1,n-2)]
```

Using memoization, the recursive function doesn't compute 20 additions but rather uses just six, the essential ones used as building blocks to solve the initial requirement for computing a certain number in the sequence:

```
fib_mem(7)

lvl 0: summing fib(6) and fib(5)
lvl 1: summing fib(5) and fib(4)
lvl 2: summing fib(4) and fib(3)
lvl 3: summing fib(3) and fib(2)
lvl 4: summing fib(2) and fib(1)
lvl 5: summing fib(1) and fib(0)

13
```

Looking inside the memo dictionary, you can find the sequence of sums that define the Fibonacci sequence starting from 1:

```
memo
{(1, 0): 1, (2, 1): 2, (3, 2): 3, (4, 3): 5, (5, 4): 8,
 (6, 5): 13}
```

Leveraging memoization

Memoization is the essence of dynamic programming. You often find the need to use it when scripting an algorithm yourself. When creating a function, whether recursive or not, you can easily transform it using a simple command, a *decorator*, which is a special Python function that transforms functions. To see how to work with a decorator, start with a recursive function, stripped of any print statement:

```
def fib(n):
    if n==0:
        return 0
    elif n == 1:
        return 1
    else:
        return fib(n-1) + fib(n-2)
```

When using Jupyter Notebook, you can use built-in magic commands, such as timeit, to measure the execution time of a command on your computer:

```
%timeit -n 1 -r 1 print(fib(36))

14930352
12.7 s ± 0 ns per loop (mean ± std. dev. of 1 run, 1 loop each)
```

The output shows that the function requires about 12.7 seconds to execute on the computer used for this test (a Windows system running on an Intel Core i3 processor). However, depending on your machine, function execution may require more or less time. No matter the speed of your computer, it will certainly take a few seconds to complete, because the Fibonacci number for 36 is quite huge: 14930352. Testing the same function for higher Fibonacci numbers takes even longer.

Now it's time to see the effect of decorating the function. Using the lru_cache() function from the functools package can radically reduce execution time. This function is available only when using Python 3. It transforms a function by automatically adding a cache to hold its results. You can also set the cache size by using the maxsize parameter (lru_cache() uses a cache with an optimal replacement strategy, as explained in Chapter 15). If you set `maxsize=None`, the cache uses all the available memory, without limits.

```
from functools import lru_cache

@lru_cache(maxsize=None)
def fib(n):
    if n==0:
        return 0
    elif n == 1:
        return 1
    else:
        return fib(n-1) + fib(n-2)
```

Note that the function is the same as before. The only addition is the imported `lru_cache()` function (`https://docs.python.org/3/library/functools.html`), which you call by putting an `@` symbol in front of it. Any call with the `@` symbol in front is an *annotation* and in this case calls the `lru_cache()` function as a decorator of the following function.

TECHNICAL STUFF

Using decorators is an advanced technique in Python. Decorators don't need to be explained in detail in this book, but you can still take advantage of them because they are so easy to use. (You can find additional information about decorators at `https://pythonbasics.org/decorators/` and `https://www.freecodecamp.org/news/python-decorators-explained-with-examples/`.) Just remember that you call them using annotations (`@` + *decorator function's name*) and that you put them in front of the function you want to transform. The original function is fed into the decorator and comes out transformed. In this example of a simple recursive function, the decorator outputs a recursion function enriched by memoization. It's time to test the function speed, as before:

```
%timeit -n 1 -r 1 print(fib(36))

14930352
707 µs ± 0 ns per loop (mean ± std. dev. of 1 run, 1 loop each)
```

Even if your execution time is different, it should decrease from seconds to milliseconds. Such is the power of memoization. You can also explore how your function uses its cache by calling the `cache_info()` method from the decorated function:

```
fib.cache_info()

CacheInfo(hits=34, misses=37, maxsize=None, currsize=37)
```

The output tells you that there are 37 function calls that didn't find an answer in the cache. However, 34 other calls did find a useful answer in the cache.

TIP

Just by importing `lru_cache()` from `functools` and using it in annotations in front of many heavy-duty algorithms in Python, you'll experience a great increase in performance (unless they are greedy algorithms).

If instead of using a pre-made function, you would like to write down a memoization function of your own, you can use the following function:

```
def memoize(fun):
    cache = dict()

    def memoized(*args):
        if args in cache:
            return cache[args]
        result = fun(*args)
        cache[args] = result
        return result

    return memoized
memoized_fib = memoize(fib)

%timeit -n 1 -r 1 print(memoized_fib(36))

14930352
956 µs ± 0 ns per loop (mean ± std. dev. of 1 run, 1 loop each)
```

In Python, when a function returns another function, the returned function gets associated with all the variables from the mother function. In this way, you can enrich the `fib()` function with a dictionary recording of all the previous results, which you can recall when the function is again required with the same parameters.

Discovering the Best Dynamic Recipes

Even dynamic programming has limitations. The biggest limitation of all relates to its main strength: If you keep track of too many partial solutions to improve running time, you may run out of memory. You may have too many partial solutions in store because the problem is complex, or simply because the order you use to produce partial solutions is not an optimal one and too many of the solutions don't fit the problem requirements.

The order used to solve subproblems is something you must track. The order you choose should make sense for the efficient progression of the algorithm (you solve something that you're going to reuse immediately) because the trick is in smart reuse of previously built building blocks. Therefore, using memoization may not provide enough benefit. Rearranging your problems in the right order can improve the results. You can learn how to correctly order your subproblems by learning directly from the best dynamic programming recipes available: knapsack, traveling salesman, and approximate string search, as described in the sections that follow.

Looking inside the knapsack

The knapsack problem has been around since at least 1897 and is likely the work of Tobias Dantzig (`https://www.britannica.com/biography/Tobias-Dantzig`). In this case, you have to pack up your knapsack with as many items as possible. Each item has a value, so you want maximize the total value of the items you carry. The knapsack has a threshold capacity, or you have a limit of weight you can carry, so you can't carry all the items.

The general situation fits any problem that involves a budget and resources, which you want to allocate in the smartest way possible. This problem setting is so common that many people consider the knapsack problem to be one of the most popular algorithmic problems. The knapsack problem finds applications in computer science, manufacturing, finance, logistics, and cryptography. For instance, real-world applications of the knapsack problem are how to best load a cargo ship with goods or how to optimally cut raw materials, thus creating the least waste possible.

REMEMBER

Even though it's such a popular problem, this book doesn't explore the knapsack problem again because the dynamic approach is incontestably one of the best solving approaches. It's important to remember, though, that in specific cases — for example, when the items are quantities — other approaches, such as using greedy algorithms, may work equally well (or even better).

This section shows how to solve the *0-1 knapsack problem.* In this case, you have a finite number of items and can put each of them into the knapsack (the one status) or not (the zero status). It's useful to know there are other possible variants of the problem:

- **Fractional knapsack problem:** Deals with quantities. For example, an item could be kilograms of flour, and you must pick the best quantity. You can solve this version using a greedy algorithm.
- **Bounded knapsack problem:** Puts one or more copies of the same item into the knapsack. In this case, you must deal with minimum and maximum number requirements for each item you pick.

» **Unbounded knapsack problem:** Puts one or more copies of the same item into the knapsack without constraints. The only limit is that you can't put a negative number of items into the knapsack.

The 0-1 knapsack problem relies on a dynamic programming solution and runs in pseudo-polynomial time (which is worse than just polynomial time) because the running time depends on the number of items `(n)` multiplied by the number of fractions of the knapsack capacity `(W)` that you use when building your partial solution. When using big-O notation, you can say that the running time is `O(nW)`. The brute-force version of the algorithm instead runs in $O(2^n)$. The algorithm works like this:

1. Given the knapsack capacity, test a range of smaller knapsacks (subproblems). In this case, given a knapsack capable of carrying 20 kilograms, the algorithm tests a range of knapsacks carrying from 0 kilograms to 20 kilograms.
2. For each item, test how it fits in each of the knapsacks, from the smallest knapsack to the largest. At each test, if the item can fit, choose the best value from the following:

   (a) The solution offered by the previous smaller knapsack

   (b) The test item, plus you fill the residual space with the best valued solution previously that filled that space

The example program solves the knapsack problem with the following set of six items of different weight and value combinations as well as a 20-kg knapsack:

Item	1	2	3	4	5	6
Weight in kg	2	3	4	4	5	9
Profit in 100 USD	3	4	3	5	8	10

Here is the code to execute the dynamic programming procedure described. (You can find this code in the `A4D2E; 16; Knapsack.ipynb` downloadable source code file; see the Introduction for details.)

```
values = [3, 4, 3, 5, 8, 10]
weights = [2, 3, 4, 4, 5, 9]
items = len(weights)
capacity = 20

memo = dict()
for size in range(0, capacity+1, 1):
    memo[(-1, size)] = ([], 0)
```

```
for item in range(items):
    for size in range(0, capacity+1, 1):
        # if the object doesn't fit in the knapsack
        if weights[item] > size:
            memo[item, size] = memo[item-1, size]
        else:
            # if the object fits, we check what can best fit
            # in the residual space
            previous_row, previous_row_value = memo[
                        item-1, size-weights[item]]
            if memo[item-1, size][1] > values[item
                            ] + previous_row_value:
                memo[item, size] = memo[item-1, size]
            else:
                memo[item, size] = (previous_row + [item
                    ], previous_row_value + values[item])
```

The best solution is the cached result when the code tests inserting the last item with the full capacity (20 kg) knapsack:

```
best_set, score = memo[items-1, capacity]
best_set_weights = [weights[item] for item in best_set]
print(f'The best set is {best_set}', end= ', ')
print(f'it weights {sum(best_set_weights)}', end= ' ')
print(f'and it values {score}')

The best set is [0, 3, 4, 5], it weights 20 and it values 26
```

You may be curious to know what happened inside the memoization dictionary:

```
print(len(memo))

147

print(memo[2, 10])

([0, 1, 2], 10)

knapsacks = len(range(0, capacity+1, 1))
print(f"tested {items} items, tested {knapsacks} knapsacks")

tested 6 items, tested 21 knapsacks
```

It contains 147 subproblems. In fact, six items multiplied by 21 knapsacks (with capacities ranging from 0 to 20) is 126 solutions, but you have to add another 21 naive solutions to allow the algorithm to work properly (*naive* means leaving the knapsack empty), which increases the number of subproblems to 147.

You may find solving 147 subproblems daunting (even though they're blazingly fast to solve). Using brute force alone to solve the problem means solving fewer subproblems in this particular case. Solving fewer subproblems requires less time, a fact you can test by solving the problem using Python and the `comb()` function:

```
from scipy.special import comb

objects = 6
print(sum([comb(objects,k+1) for k in range(objects)]))

63.0

objects = 20
print(sum([comb(objects,k+1) for k in range(objects)]))

1048575.0
```

It takes testing 63 combinations to solve this problem. However, if you try using more objects, say, 20, running times look much different because there are now 1,048,575 combinations to test. Contrast this huge number with dynamic programming, which requires solving just 20 * 21 + 21 = 441 subproblems (of course, this value holds true only for knapsacks that hold 20 items).

REMEMBER

The previous results show the difference between quasi-polynomial and exponential time. (As a reminder, the book discusses exponential complexity in Chapter 2 when illustrating the Big O Notation. In Chapter 15, you discover polynomial time as part of the discussion about NP complete problems.) Using dynamic programming becomes fruitful when your problems are complex. Toy problems are good for learning but they can't demonstrate the full extent of employing smart algorithm techniques such as dynamic programming. Each solution tests what happens after adding a certain item when the knapsack has a certain size. The preceding example adds item 2 (weight = 4, value = 3) and outputs a solution that puts items 0, 1, and 2 into the knapsack (total weight 9 kg) for a value of 10. This intermediate solution leverages previous solutions and is the basis for many of the following solutions before the algorithm reaches its end.

TIP

You may wonder whether the result offered by the script is really the best one achievable. Unfortunately, the only way to be sure is to know the right answer, which means running a brute-force algorithm (when feasible in terms of running time on your computer). This chapter doesn't use brute force for the knapsack problem, but you'll see a brute-force approach used in the traveling salesman problem that follows.

Touring around cities

The traveling salesman problem (TSP for short) is at least as widely known as the knapsack problem. You use it mostly in logistics and transportation; for example, for goods delivery by a single vehicle as well as a fleet of vehicles. The TSP problem asks a traveling salesperson to visit a certain number of cities and then come back to the initial starting city (because it's circular, it's called a tour) using the shortest path possible.

TSP is similar to graph problems, but without the edges because the cities are all interconnected. For this reason, TSP usually relies on a distance matrix as input, which is a table listing the cities on both rows and columns (a square matrix because the number of the rows is the same as the columns). The intersections contain the distance from a row city to a column city. TSP problem variants may provide a matrix containing time or fuel consumption instead of distances.

TSP is an NP-hard problem, but you can solve the problem using various approaches, some approximate (heuristic) and some exact (dynamic programming). The problem, as with any other NP-hard problem, is the running time. Although you can count on solutions that you hope are good enough to solve the problem (you can't be certain except when solving short tours), you can't know for sure with problems as complex as touring the world: `http://www.math.uwaterloo.ca/tsp/world/`. The following example tests various algorithms, such as brute force, greedy, and dynamic programming, on a simple tour of six cities, represented as a weighted graph (see Figure 16-1). (You can find this code in the `A4D2E; 16; TSP.ipynb` downloadable source code file; see the Introduction for details.)

```
import networkx as nx
import matplotlib.pyplot as plt
from random import seed

D = [[0,20,16,25,24],[20,0,12,12,27],
     [16,12,0,10,14],[25,12,10,0,20],
     [24,27,14,20,0]]

Graph = nx.Graph()
nodes = len(D[0])
Graph.add_nodes_from(range(nodes))
for i in range(nodes):
    for j in range(nodes):
        Graph.add_edge(i, j, weight=D[j][i])

seed(2)
pos=nx.shell_layout(Graph)
draw_params = {'with_labels':True,
               'node_color':'skyblue',
               'node_size':800, 'width':2,
               'font_size':14}
nx.draw(Graph, pos, **draw_params)
labels = nx.get_edge_attributes(Graph, 'weight')
nx.draw_networkx_edge_labels(Graph,pos,
                             edge_labels=labels)
plt.show()
```

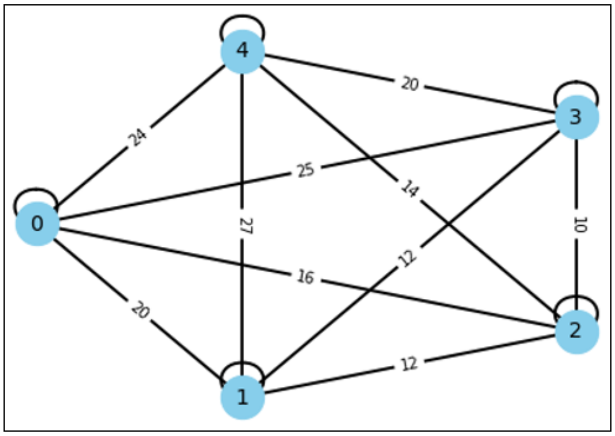


FIGURE 16-1: Cities represented as nodes in a weighted graph.

After defining the D (distance) matrix, the example tests the first, simplest solution to determine the shortest tour starting and ending from city zero. This solution relies on brute force, which generates all the possible order permutations between the cities, leaving out zero because it's the starting and stopping point. The distance from zero to the first city and from the last city of the tour to zero is added after the total distance of each solution is calculated. When all the solutions are available, you simply choose the shortest.

```
from itertools import permutations

best_solution = [None, sum([sum(row) for row in D])]
for solution in list(permutations(range(1, nodes))):
    start, distance = (0, 0)
    for next_one in solution:
        distance += D[next_one][start]
        start = next_one
    distance += D[0][start]
    if distance <= best_solution[1]:
        best_solution = [[0]+list(solution)+[0], distance]
        prt = str(best_solution)[1:-1]
        print(f'Best solution so far: {prt} kms')

Best solution so far: [0, 1, 2, 3, 4, 0], 86 kms
Best solution so far: [0, 1, 3, 2, 4, 0], 80 kms
Best solution so far: [0, 4, 2, 3, 1, 0], 80 kms
```

The brute-force algorithm quickly determines the best solution and its symmetrical path. However, as a result of the small problem size, you obtain a prompt answer because, given four cities, just 24 possible solutions exist. As the number of cities increases, the number of permutations to test becomes intractable, even after removing the symmetrical paths (which halves the permutations) and using a fast computer. For example, consider the number of computations when working with 13 cities plus the starting/ending point:

```
from scipy.special import perm

print(perm(13, 13) / 2)

3113510400.0
```

Dynamic programming can simplify the running time. The Held–Karp algorithm (also known as the Bellman–Held–Karp algorithm because Bellman published it in 1962, the same year as Michael Held and Richard Karp) can cut time complexity to `O(2`^{n}`)`. It's still exponential complexity, yet it requires less time than applying the exhaustive enumeration of all tours by brute force, which have a complexity of `O(n!)`.

TIP

Approximate and heuristic algorithms can provide fast and useful results. (Even though the result may not always reflect the optimal solution, it's usually good enough.) You see TSP again later in the book (see Chapters 18 and 20), when dealing with local search and heuristics.

To find the best TSP solution for *n* cities, starting and ending from city zero, the algorithm proceeds from city zero and keeps records of the shortest path possible, considering different settings. It always uses a different ending city and touches only a city subset. As the subsets become larger, the algorithm learns how to solve the problem efficiently. Therefore, when solving TSP for five cities, the algorithm first considers solutions involving two cities, then three cities, then four, and finally five. (Sets have dimensions 1 to *n*.) Here are the steps the algorithm uses:

1. Initialize a table to track the distances from city 0 to all other cities. These sets contain only the initial city and a destination city because they represent the initial step.
2. Consider every possible set size, from two to the number of tour cities. This is a first iteration, the outer loop.
3. Inside the outer loop, for each set size, consider every possible combination of cities of that size, with none containing the initial city. This is an inner iteration.
4. Inside the inner iteration (Step 3), for every available combination, consider each city inside the combination as the ending city. This is another inner iteration.
5. Inside the inner iteration (Step 4), given a different destination city, determine the shortest path connecting the cities in the set from the city that starts the tour (city 0). In finding the shortest path, use any useful, previously stored information, thus applying dynamic programming. This step saves computations and provides the rationale for working by growing subsets of cities. Reusing previously solved subproblems, you find the shorter tours by adding to a previous shortest path the distance necessary to reach the destination city. Given a certain set of cities, a specific initial city, and a specific destination city, the algorithm stores the best path and its length.
6. When all the iterations end, you have as many different shortest solutions as `n–1` cities, with each solution covering all the cities but ending at a different city. Add a closing point, the city 0, to each one to conclude the tour.
7. Determine the shortest solution and output it as the result.

TECHNICAL STUFF

The Python implementation of this algorithm isn't very simple because it involves some iterations and manipulating sets. It's an exhaustive search reinforced by dynamic programming, and it relies on an iterative approach, with subsets of cities and with candidates to add to them. The following commented Python example explores how this solution works. You can use it to calculate customized tours (possibly using cities in your region or county as entries in the distance matrix). The script uses advanced commands such as `frozenset()` (a command that makes a set usable as a dictionary key) and operators for sets in order to achieve the solution:

```
from itertools import combinations

memo = {(frozenset([0, idx+1]), idx+1): (dist, [0,idx+1])
```

```
        for idx,dist in enumerate(D[0][1:])}

cities = nodes
for subset_size in range(2, cities):
    # Here we define the size of the subset of cities
    new_memo = dict()
    for subset in [frozenset(comb) | {0} for comb in
                   combinations(range(1, cities),
                                subset_size)]:
        # We enumerate the subsets having a certain subset
        # size
        for ending in subset - {0}:
            # We consider every ending point in the subset
            all_paths = list()
            for k in subset:
                # We check the shortest path for every
                # element in the subset
                if k != 0 and k!=ending:
                    length = memo[(subset-{ending},k)][0
                                    ] + D[k][ending]
                    index  = memo[(subset-{ending},k)][1
                                        ] + [ending]
                    all_paths.append((length, index))
            new_memo[(subset, ending)] = min(all_paths)
    # In order to save memory, we just record the previous
    # subsets since we won't use shorter ones anymore
    memo = new_memo
# Now we close the cycle and get back to the tour start
# of the tour, city zero
tours = list()
for distance, path in memo.values():
    distance += D[0][path[-1]]
    tours.append((distance, path + [0]))
# We can now declare the shortest tour
distance, path = min(tours)
print('Shortest dynamic programming tour is:', end=' ')
print(f'{path}, {distance} kms')

Shortest dynamic programming tour is:
 [0, 1, 3, 2, 4, 0], 80 kms
```

Approximating string search

Determining when one word is similar to another isn't always simple. Words may differ slightly because of misspellings or different ways of writing the word itself, thus rendering any exact match impossible. This isn't just a problem that raises interesting issues during a spell check, though. For example, putting similar text strings together (such as names, addresses, or code identifiers) that refer to the same person may help create a one-customer view of a firm's customer base, or help a national security agency locate a dangerous criminal.

REMEMBER

Approximating string searches has many applications in machine translation, speech recognition, spell checking and text processing, computational biology, and information retrieval. Thinking about the manner in which sources input data into databases, you know there are many mismatches between data fields that a smart algorithm must solve. Matching a similar, but not precisely equal, series of letters is an ability that finds uses in fields such as genetics when comparing DNA sequences (expressed by letters representing nucleotides G,A,T, and C) to determine whether two sequences are similar and how they resemble each other.

Vladimir Levenshtein, a Russian scientist expert in information theory (see `http://ethw.org/Vladimir_I._Levenshtein` for details), devised a simple measure (named after him) in 1965 that computes the grade of similarity between two strings by counting how many transformations it takes to change the first string into the second. The Levenshtein distance (also known as edit distance) counts how many changes are necessary in a word:

- **Deletion:** Removing a letter from a word
- **Insertion:** Inserting a letter into a word and obtaining another word
- **Substitution:** Replacing one letter with another, such as changing the *p* letter into an *f* letter and obtaining *fan* from *pan*

TIP

Each edit has a cost, which Levenshtein defines as 1 for each transformation. However, depending on how you apply the algorithm, you could set the cost differently for deletion, insertion, and substitution. For example, when searching for similar street names, misspellings are more common than outright differences in lettering, so substitution might incur only a cost of 1, and deletion or insertion might incur a cost of 2. On the other hand, when looking for monetary amounts, similar values quite possibly will have different numbers of numbers. Someone could enter \$123 or \$123.00 into the database. The numbers are the same, but the number of numbers is different, so insertion and deletion might cost less than substitution. (A value of \$124 is not quite the same as a value of \$123, so substituting 3 for 4 should cost more.)

You can render the counting algorithm as a recursion or an iteration. However, it works much faster using a bottom-up dynamic programming solution, as described in the 1974 paper "The String-to-string Correction Problem," by Robert A. Wagner and Michael J. Fischer (`http://www.inrg.csie.ntu.edu.tw/algorithm2014/homework/Wagner-74.pdf`). The time complexity of this solution is `O(mn)`, where *n* and *m* are the lengths in letters of the two words being compared. The following code computes the number of changes required to turn the word *Saturday* into *Sunday* by using dynamic programming with a matrix (see Figure 16-2) to store previous results (the bottom-up approach). (You can find this code in the `A4D2E; 16; Levenshtein.ipynb` downloadable source code file; see the Introduction for details.)

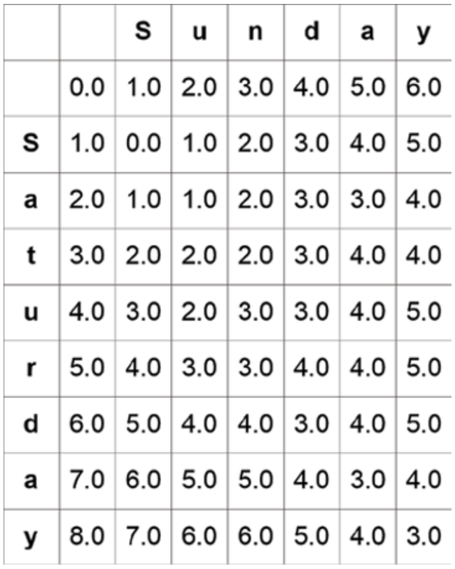
```
s1 = 'Saturday'
s2 = 'Sunday'
m = len(s1)
n = len(s2)
D = [list(range(n+1))]
for i in range(m):
        D.append([i+1] + [0] * n)

for j in range(1, n+1):
    for i in range(1, m+1):
        if s1[i-1] == s2[j-1]:
            D[i][j] = D[i-1][j-1]
        else:
            deletion = D[i-1][j] + 1
            insertion = D[i][j-1] + 1
            substitution = D[i-1][j-1] + 1
            D[i][j] = min(deletion,
                           insertion,
                          substitution)
print (f'Levenshtein distance is {D[-1][-1]}')

Levenshtein distance is 3
```

You can plot or print the result using Pandas (a package for data analysis and visualization). Pandas will print a nice header and row labels for the matrix represented by the list of lists `D`:

```
import pandas as pd
pd.DataFrame(D, columns=list(' '+s2), index=list(' '+s1))
```



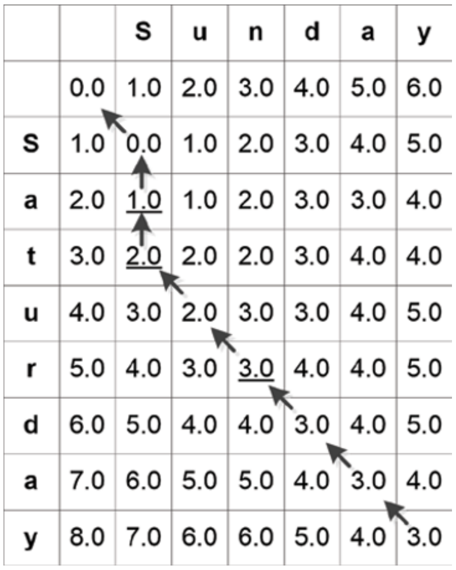
		S	u	n	d	a	y
	0.0	1.0	2.0	3.0	4.0	5.0	6.0
S	1.0	0.0	1.0	2.0	3.0	4.0	5.0
a	2.0	1.0	1.0	2.0	3.0	3.0	4.0
t	3.0	2.0	2.0	2.0	3.0	4.0	4.0
u	4.0	3.0	2.0	3.0	3.0	4.0	5.0
r	5.0	4.0	3.0	3.0	4.0	4.0	5.0
d	6.0	5.0	4.0	4.0	3.0	4.0	5.0
a	7.0	6.0	5.0	5.0	4.0	3.0	4.0
y	8.0	7.0	6.0	6.0	5.0	4.0	3.0

FIGURE 16-2: Transforming Saturday into Sunday.

Getting back to The algorithm builds the matrix, placing the best solution in the last cell. After building the matrix using the letters of the first string as rows and the letters of the second one as columns, it proceeds by columns, computing the differences between each letter in the rows compared to those in the columns. In this way, the algorithm makes a number of comparisons equivalent to the product of the number of the letters in the two strings. As the algorithm continues, it accounts for the result of previous comparisons and chooses the solution with the least number of edits.

When the matrix iteration completes, the resulting number represents the minimum number of edits necessary for the transformation to occur — the smaller the number, the more similar the two strings. Retracing from the last cell to the first one by moving to the previous cell with the least value (if more directions are available, it prefers to move diagonally) hints at what transformations to execute (see Figure 16-3). Note that the path isn't necessarily unique. The underlines show where two possible choices are available.

- A diagonal backward movement hints at a substitution in the first string if the letters on the row and column differ (otherwise, no edit needs to be done).
- An upward movement dictates a deletion of a letter in the first string.
- A left backward move indicates that an insertion of a new letter should be done on the first string.



		S	u	n	d	a	y
	0.0	1.0	2.0	3.0	4.0	5.0	6.0
S	1.0	0.0	1.0	2.0	3.0	4.0	5.0
a	2.0	1.0	1.0	2.0	3.0	3.0	4.0
t	3.0	2.0	2.0	2.0	3.0	4.0	4.0
u	4.0	3.0	2.0	3.0	3.0	4.0	5.0
r	5.0	4.0	3.0	3.0	4.0	4.0	5.0
d	6.0	5.0	4.0	4.0	3.0	4.0	5.0
a	7.0	6.0	5.0	5.0	4.0	3.0	4.0
y	8.0	7.0	6.0	6.0	5.0	4.0	3.0

FIGURE 16-3: Highlighting what transformations are applied.

In this example, the backtracking points out the following transformations (two deletions and one substitution):

Saturday => Sturday => Surday => Sunday

IN THIS CHAPTER

» Understanding how randomness can prove smarter than more reasoned ways

» Introducing key ideas about probability and its distributions

» Discovering how a Monte Carlo simulation works

» Learning about quick select and revisiting quick sort algorithms

Chapter 17 Using Randomized Algorithms

Random number generators are a key function in computing and play an important role in the algorithmic techniques discussed in this part of the book. As described in the first part of the chapter, randomization isn't just for gaming or gambling; people also employ it to solve a large variety of problems. Randomization sometimes proves more effective during optimization than other techniques, and in obtaining the right solution than more reasoned ways. It helps different techniques work better, for example local search, simulated annealing to heuristics, cryptography, and distributed computing (with cryptography for concealing information being the most critical).

The "Understanding how probability works" section illustrates the basic principles of probability and then explains how probability distribution can connect to randomization. Using examples from the game of cards and the quick select sorting algorithm, the last part of the chapter demonstrates how randomization can find shortcuts and reach a result in an easier way than other algorithms.

In fact, randomization makes finding a solution simpler, trading time for complexity. Simplifying tasks isn't its only advantage: Randomization saves resources and operates in a distributed way with a reduced need for communication and coordination. This chapter introduces you to the information needed to understand how enriching your algorithms with randomness can help solve problems (the chapter uses the term *injecting randomness,* as if it were a cure). Even more applications wait in the following chapters, so this chapter also discusses key topics such as probability basics, probability distributions, and Monte Carlo simulations.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 17; Probability.ipynb` and `A4D2E; 17; Quickselect.ipynb` files of the downloadable source. See the Introduction for details on how to find these source files.

Defining How Randomization Works

You can find randomization unexpectedly embedded into everyday tools. The first versions of the robot vacuum cleaner Roomba (designed by a company founded by people from the Massachusetts Institute of Technology [MIT]) cleaned rooms without having a precise plan or a blueprint of the place. The tool worked most of the time by wandering randomly around the room and, according to the original patent, after hitting an obstacle, it turned a random number of degrees and started in a new direction. Yet Roomba always completed its cleaning chores. (If you are curious about how it operated and how, over the years, it has improved its capabilities to navigate the house, check out `https://www.explainthatstuff.com/how-roomba-works.html`.)

From a historical perspective, randomized algorithms are a recent innovation because the first algorithm of this kind, the closest-pair algorithm was developed by Michael Rabin in 1976. The closest-pair algorithm determines the pair of points, among many on a geometric plane, that have the smallest distance between them, and does so without having to compare them all. The closest-pair algorithm was followed the next year by the randomized primality test (an algorithm for determining whether a number is a composite or a probable prime number), by Robert M. Solovay and Volker Strassen. Soon after, applications in cryptography and distributed computing made randomization more popular and the subject of intense research, although the field is still new and largely uncharted.

Randomization relies on the capability of your computer to generate random numbers, which means creating the number without a plan. Therefore, a random number is unpredictable, and as you generate subsequent random numbers, they shouldn't relate to each other.

REMEMBER

However, randomness is hard to achieve. Even when you throw dice, the result can't be completely unexpected because of the way you hold the dice, the way you throw them, and the fact that the dice aren't perfectly shaped. Computers aren't good at creating random numbers, either. They generate randomness by using algorithms or pseudorandom tables (which work by using a *seed* value as a starting point, a number equivalent to an index) because a computer can't create a truly random number. Computers are deterministic machines; everything inside them follows a well-defined response pattern, which means that it imitates randomness in some way.

Considering why randomization is needed

Even if a computer can't create true randomness, streams of *pseudorandom numbers* (numbers that appear as random but are somehow predetermined) can still make the difference in many computer science problems. Any algorithm that employs randomness in its logic can appear as a randomized algorithm, no matter whether randomness determines its results, improves performance, or mitigates the risk of failing by providing a solution in certain cases.

Usually you find randomness employed in selecting input data, the starting point of the optimization, or the number and kind of operations to apply to the data. When randomness is a core part of the algorithm logic and not just an aid to its performance, the expected running time of the algorithm and even its results may become uncertain and subject to randomness, too; for instance, an algorithm may provide different, though equally good, results during each run. It's therefore useful to distinguish between kinds of randomized solutions, each one named after iconic gambling locations:

- **Las Vegas:** These algorithms are notable for using random inputs or resources to provide the correct problem answer every time. Obtaining a result may take an uncertain amount of time because of its random procedures. An example is the quick sort algorithm.
- **Monte Carlo:** Because of their use of randomness, Monte Carlo algorithms may not provide a correct answer or even an answer at all, although these outcomes seldom happen. Because the result is uncertain, a maximum number of trials in their running time may bind them. Monte Carlo algorithms demonstrate that algorithms do not necessarily always successfully solve the problems they are supposed to. An example is the Solovay–Strassen primality test.
- **Atlantic City:** These algorithms run in polynomial time, providing a correct problem answer at least 75 percent of the time. Monte Carlo algorithms are always fast but not always correct, and Las Vegas algorithms are always correct but not always fast. People therefore think of Atlantic City algorithms as halfway between the two because they are usually both fast and correct.

This class of algorithms was introduced in 1982 by J. Finn in an unpublished manuscript entitled *Comparison of Probabilistic Test for Primality.* Created for theoretical reasons to test for prime numbers, this class comprises hard-to-design solutions, thus very few of them exist today.

Understanding how probability works

Probability tells you the likelihood of an event, which you normally express as a number. In this book, and generally in the field of probabilistic studies, the probability of an event is measured in the range between 0 (no probability that an event will occur) and 1 (certainty that an event will occur). Intermediate values, such as 0.25 or 0.75, indicate that the event will happen with a certain frequency under conditions that could lead to that event (referred to as *trials*). Even if a numeric range from 0 to 1 doesn't seem intuitive at first, working with probability over time makes the reason for using such a range easier to understand. When an event occurs with a probability of 0.25, you know that out of 100 trials, the event will more likely happen around 0.25 * 100 = 25 times.

For instance, when the probability of your favorite sports team winning is 0.75, you can use the number to determine the chances of success when your team plays a game against another team. You can even get more specific information, such as the probability of winning a certain tournament (your team has a 0.65 probability of winning a match in this tournament) or conditioned by another event (when a visitor, the probability of winning for your team decreases to 0.60).

Probabilities can tell you a lot about an event, and they're helpful for algorithms, too. In a randomized algorithmic approach, you may wonder when to stop an algorithm because it should have reached a solution. It's good to know how long to look for a solution before giving up. Probabilities can help you determine how many iterations you may need. The discussion of the 2-satisfiability (or 2-SAT) algorithm in Chapter 18 provides a working example of using probabilities as stopping rules for an algorithm.

REMEMBER

You commonly hear about probabilities as percentages in sports and economics, telling you that an event occurs a certain number of times after 100 trials. It's exactly the same probability no matter whether you express it as 0.25 or 25 percent. That's just a matter of conventions. In gambling, you even hear about odds, which is another way of expressing probability, where you compare the likelihood of an event (for example, having a certain horse win the race) against not having the event happen at all. In this case, you express 0.25 as 25 against 75, 25 to 75, or in any other way resulting in the same ratio.

You can multiply a probability for a number of trials and get an estimated number of occurrences of the event, but by doing the inverse, you can empirically estimate a probability. Perform a certain number of trials, observe each of them, and count the number of times an event occurs. The ratio between the number of occurrences and the number of trials is your probability estimate. For instance, the probability 0.25 is the probability of picking a certain suit when choosing a card randomly from a deck of cards. French playing cards (the most widely used deck; it also appears in America and Britain) provide a classic example for explaining probabilities. (The Italians, Germans, and Swiss, for example, use decks with different suits, which you can read about at `http://healthy.uwaterloo.ca/museum/VirtualExhibits/Playing%20Cards/decks/index.html`.) The deck contains 52 cards equally distributed into four suits: clubs and spades, which are black, and diamonds and hearts, which are red. If you want to determine the probability of picking an ace, you must consider that, by picking cards from a deck, you will observe four aces. Your trials at picking the cards are 52 (the number of cards), therefore the answer in terms of probability is 4/52 = 0.077.

TIP

You can get a more reliable estimate of an empirical probability by using a larger number of trials. When using a few trials, you may not get a correct estimate of the event probability because of the influence of chance. As the number of trials grows, event observations will get nearer to the true probability of the event itself. The principle there is a generating process behind events. To understand how the generating process works, you need many trials. Using trials in such a way is also known as *sampling* from a probabilistic distribution.

Understanding distributions

Probability distribution is another idea that is important for working out better algorithms. A *distribution* is a table of values or a mathematical function that links every possible value of an input to the probability that such values could occur. Probability distributions are usually (but not solely) represented in charts whose abscissa axis represents the possible values of an input and whose ordinal axis represents the probability of occurrence. Most statistical models rely on the normal distributions, a distribution which is symmetric and has a characteristic bell shape. Representing a normal distribution in Python (as shown in Figure 17-1) requires a few lines of code. (You can find this code in the `A4D2E; 17; Probability.ipynb` downloadable source code file; see the Introduction for details.) Note how the code forces the computer to draw the same casual numbers by using the command `seed(0)`, which recalls a specific sequence of random number that is stored into the computer memory. As mentioned previously, computers are deterministic, and randomness can only be mimicked in some way.

```
from random import seed, gauss, uniform
import matplotlib.pyplot as plt

seed(0)
normal_distribution = [gauss(mu=25, sigma=100)
```

```
                          for r in range(10_000)]
weights = [1./10_000] * 10_000

plt.figure(figsize=(12, 6))
plt.hist(normal_distribution, bins=20, weights=weights,
         color='lightblue', edgecolor='black',
         linewidth=1.2)
plt.xlabel("Value")
plt.ylabel("Probability")
plt.show()
```

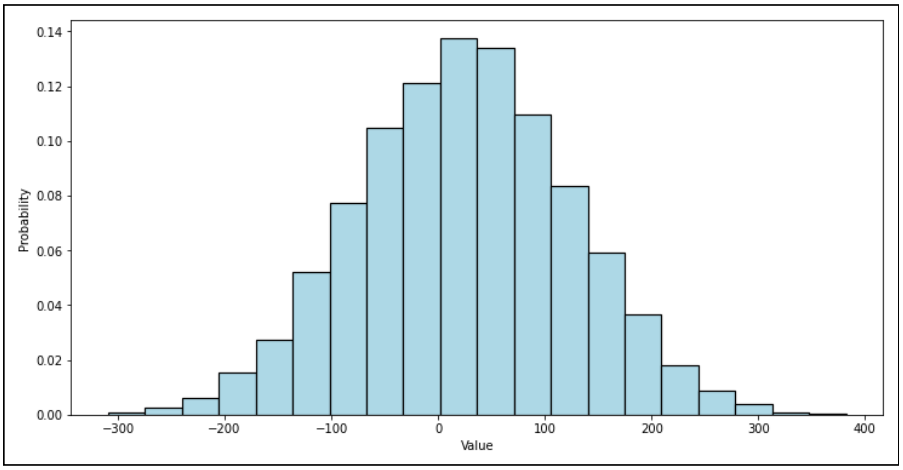


FIGURE 17-1: A histogram of a normal distribution.

The plotted distribution represents an input of 10,000 numbers whose average is about 100. Each bar in the histogram represents the probability that a certain range of values will appear in the input. If you sum all the bars, you obtain the value of 1, which comprises all the probabilities expressed by the distribution.

In a normal distribution, most of the values are around the mean value. Therefore, if you pick a random number from the input, you most likely get a number around the center of the distribution. You may also draw a number far from the center less often. If your algorithm works better by using the mean than it does with any other number, picking a number at random from a distribution centered on the mean makes sense and may be less trouble than devising a more sophisticated way to elaborate values for your input.

Another important distribution mentioned in this chapter is the uniform distribution. You can represent it using some Python code (the output appears in Figure 17-2), too:

```
seed(0)
uniform_distribution = [uniform(a=0, b=100)
                        for r in range(10_000)]
weights = [1./10_000] * 10_000

plt.figure(figsize=(12, 6))
plt.hist(uniform_distribution, bins=20, weights=weights,
         color='lightblue', edgecolor='black',
         linewidth=1.2)
plt.xlabel("Value")
plt.ylabel("Probability")
plt.show()
```

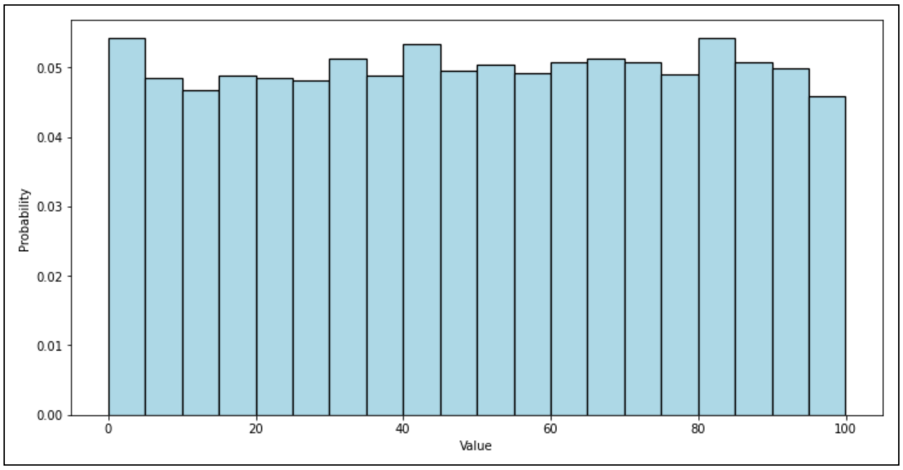


FIGURE 17-2: A histogram of a uniform distribution.

The uniform distribution is noticeably different from the normal distribution because each number has the same probability of being in the input as any other. Consequently, the histogram bars are all roughly of the same size, and picking a number in a uniform distribution means giving all the numbers the same chance to appear. It's a way to avoid systematically picking the same groups of numbers when your algorithm works better with varied inputs. For instance, uniform distributions work well when your algorithm works fine with certain numbers, so-so with most, and badly with a few others, and you prefer to pick numbers randomly to avoid picking a series of bad numbers. This is the strategy used by the quick select and randomized quick sort algorithms, described later in the chapter.

Because algorithms need numeric inputs, knowing their distribution can help make them work smarter. It's not just the initial distribution that counts. You can also take advantage of how data distribution changes as the algorithm proceeds.

As an example of how a changing distribution can improve your algorithm, the following code shows how to guess a card in a French deck by random choice:

```
numbers = ['Ace', '2', '3', '4', '5', '6', '7', '8', '9',
           '10', 'Jack', 'Queen', 'King']
seeds = ['Clubs','Spades','Diamonds','Hearts']
deck = [s+'_'+n for n in numbers for s in seeds]

from random import choice

seed(0)
my_cards = deck.copy()
guessed = 0
for card in deck:
    if card == choice(my_cards):
        guessed += 1
print('Guessed %i card(s)' % guessed)

Guessed 2 card(s)
```

The code begins by creating a `deck` using a combination of the potential card values: Ace through King, and the potential card suits: Clubs through Hearts with Python list comprehensions, so that the resulting `deck` contains values like `'Hearts_King'` and `'Clubs_Ace'`. The code then imports the `choice()` function, which can select an item from the `deck` at random. The call to `seed(0)` ensures you get the same result every time, but normally you wouldn't set a seed value in this manner to ensure that the result actually does look random. The next step is to create a copy of `deck`, `my_cards`, to use for comparison. The code then relies on a loop to go through each `card` in `deck` in order and obtains a random card from `my_cards` by calling `choice()`. When the two match, the value of `guessed` is incremented.

This strategy brings few results, and on average, you'll guess a single card in all 52 trials. In fact, for each trial, you have a 1/52 probability of guessing the correct card, which amounts to 1 after picking all the cards: (1/52) * 52 = 1. Instead, you can change this simple random algorithm by discarding the cards that you've seen from your possible choices:

```
seed(0)
my_cards = deck.copy()
guessed = 0
for card in deck:
    if card == choice(my_cards):
        guessed += 1
    else:
        my_cards.pop(my_cards.index(card))
print('Guessed %i card(s)' % guessed)

Guessed 3 card(s)
```

Now, on average, you'll guess the right card more often because as the deck decreases, your chances of guessing correctly increase, and you'll likely guess correctly more often when nearing the end of the game. (Your chances are 1 divided by the number of cards left in the deck.)

TIP

Counting cards can provide an advantage in card games. A team of MIT students used card counting and probability estimates to win huge amounts in Las Vegas until the practice was banned from Casinos. The story even inspired a 2008 film entitled *21*, starring Kevin Spacey. You can read more about the story at `https://www.bbc.com/news/magazine-27519748`.

Simulating the use of the Monte Carlo method

Calculating probabilities, apart from the operations discussed earlier in this chapter, is beyond the scope of this book. Understanding how an algorithm incorporating randomness works is not an easy task, even when you know how to compute probabilities, because it may be the result of blending many different probability distributions. However, a discussion of the Monte Carlo method casts light on the results of the most complex algorithms and helps you understand how they work. This method sees use in both mathematics and physics to solve many problems. For instance, scientists such as Enrico Fermi and Edward Teller used Monte Carlo simulations on specially devised supercomputers during the Manhattan project (which developed the atomic bomb during World War II) to accelerate their experiments. You can read more about this use at `https://www.atomicheritage.org/history/computing-and-manhattan-project`.

REMEMBER

Don't confuse the Monte Carlo method with a Monte Carlo algorithm. The Monte Carlo method is a way to understand how a probability distribution affects a problem, whereas, as discussed previously, a Monte Carlo algorithm is a randomized algorithm that isn't guaranteed to reach a solution.

In a Monte Carlo simulation, you repeatedly sample the algorithm results. You store a certain number of results and then calculate statistics, such as the mean, and visualize them as a distribution. For instance, if you want to understand better how reducing the size of the deck you're drawing from can help you achieve better results (as in the previous Python script), you iterate the algorithm a few times and record the success rate:

```
import numpy as np
seed(0)
samples = list()
for trial in range(10_000):
    my_cards = deck.copy()
    guessed = 0
    for card in deck:
        if card == choice(my_cards):
            guessed += 1
        else:
            my_cards.pop(my_cards.index(card))
    samples.append(guessed)
```

Running a Monte Carlo simulation may take a few seconds. The time required depends on the speed of the algorithm, the size of the problem, and the number of trials. However, when sampling from distributions, the more trials you make, the more stable the result. This example performs 10,000 trials. You can both estimate and visualize the expected result (see Figure 17-3) using the following code:

```
plt.figure(figsize=(12, 6))
plt.hist(samples, bins=8, color='lightblue',
         edgecolor='black', linewidth=1.2)
plt.xlabel("Guesses")
plt.ylabel("Frequency")
plt.show()
mean = round(sum(samples) / len(samples), 2)
print(f'On average you can expect {mean} guesses each run')

On average you can expect 3.13 guesses each run
```

Observing the resulting histogram, you can determine that you get a result of three in about 3,000 runs out of the 10,000 trials, which gives three the highest probability of happening. Interestingly, you never receive a result of zero, but it is also rare to score seven or more hits. Later examples in the chapter use Monte Carlo simulations to understand how more sophisticated randomized algorithms work.

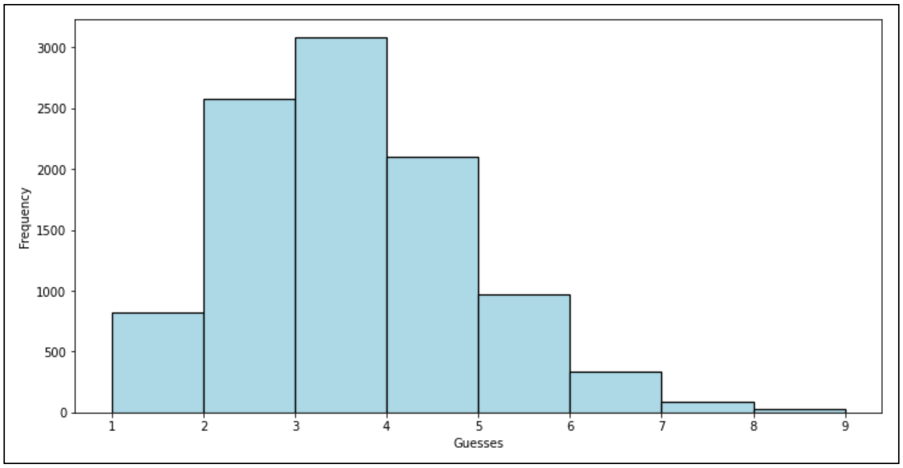


FIGURE 17-3: Displaying the results of a Monte Carlo simulation.

Putting Randomness into your Logic

Here are some of many reasons to include randomness in the logic of your algorithm:

- It makes algorithms work better and provide smarter solutions.
- It requires fewer resources, in terms of memory and computations.
- It creates algorithms that have a distributed output with little or no supervision.

In the next chapter, which is dedicated to local search, you see how randomization and probability can prove helpful when it's difficult to determine what direction your algorithm should take. The examples in the sections that follow demonstrate how randomization helps to quickly find values in a certain position in your data input, as well as how relying on randomness can speed up sorting.

Calculating a median using quick select

Calculating a statistical measure, the median, can prove challenging when you work on unsorted input lists. In fact, a median relies on the position of your data when it is ordered:

- If the data inputs have an odd number of elements, the median is exactly the middle value.
- If the data inputs have an even number of elements, the median is the average of the pair of middle numbers in the ordered input list.

REMEMBER

A median is like a mean, a single value that can represent a distribution of values. The median, based on the input vector element order, isn't influenced much by the values present in your list. It's simply the middle value. Instead, the values present at the head and tail of the input can influence the mean when they're extremely small or large. This robustness makes the median very helpful in many situations when using statistics. A simple example of a median calculation using Python functions helps you understand this measure. (You can find this code in the `A4D2E; 17; Quickselect.ipynb` downloadable source code file; see the Introduction for details.)

```
from random import randint, random
from random import choice, seed
import sys
sys.setrecursionlimit(1500)

n = 501
seed(0)
series = [randint(1,25) for i in range(n)]

from statistics import median
# https://docs.python.org/3/library/statistics.html
print(f'Median is {median(series)}')

Median is 12.0
```

The code creates a list of 501 elements and obtains the list median using the `median()` function from the NumPy package. The reported median is actually the middle point of the ordered list, which is the 251st element:

```
elem_251 = sorted(series)[250]
print(f'251st element of the ordered series is {elem_251}')

251st element of the ordered series is 12
```

Ordering the list and extracting the necessary element demonstrates how `median()` works. Because ordering is involved in calculating a median, you can expect a best running time of `O(n*log(n))`. By using randomization provided by the quick select algorithm, you can get an even better result, a running time of `O(n)`. Quick select works recursively, which is why you must set a higher recursion limit in Python, given a list and the position of the value needed from an ordered list. The value index is called *k*, and the algorithm is also known as the largest *kth value algorithm.* It uses the following steps to obtain a result:

1. Determine a pivot number in the data list and split the list into two parts, a left list whose numbers are less than the pivot number, and a right list whose numbers are higher.

2. Determine the length of each list. When the length of the left list is larger than the kth position, the median value is inside the left part. The algorithm applies itself recursively to just that list.
3. Compute the number of pivot number duplicates in the list (subtract from the length of the list the length of the left and right sides).
4. Determine whether the number of duplicates is more than k.

   (a) When this condition is true, it means that the algorithm has found the solution because the kth position is contained in the duplicates (it's the pivot number).

   (b) When this condition isn't true, remove the number of duplicates from k and apply the result recursively to the right side, which must contain the value of the kth position.

Now that you understand the process, you can look at some code. The following example shows how to implement a quick select algorithm:

```
def quickselect(series, k):
    pivot = choice(series)

    left, right = list(), list()
    for item in series:
        if item < pivot:
            left.append(item)
        if item > pivot:
            right.append(item)
    length_left = len(left)
    if length_left > k:
        return quickselect(left, k)
    k -= length_left

    duplicates = len(series) - (length_left + len(right))
    if duplicates > k:
        return float(pivot)
    k -= duplicates

    return quickselect(right, k)

quickselect(series, 250)

12.0
```

The algorithm works well because it keeps reducing the problem size. It works best when the random pivot number is drawn nearer to the kth position. (The stopping rule is that the pivot number is the value in the kth position.) Unfortunately, because you can't know the kth position in the unordered list, drawing randomly by using a uniform distribution (each element in the list has the same chance of being chosen) is the best solution because the algorithm eventually finds the right solution. Even when random chance doesn't work in the algorithm's favor, the algorithm keeps on reducing the problem, thus getting more chances to find the solution, as demonstrated earlier in the chapter when guessing the cards randomly picked from a deck. As the deck gets smaller, guessing the answer gets easier. The following code shows how to use quick select to determine the median of a list of numbers:

```
def my_median(series):
    if len(series) % 2 != 0:
        return quickselect(series, len(series)//2)
    else:
        left  = quickselect(series, (len(series)-1) // 2)
        right = quickselect(series, (len(series)+1) // 2)
        return (left + right) / 2

my_median(series)

12.0
```

Doing simulations using Monte Carlo

As part of understanding the quick select algorithm, it pays to know how it works internally. By setting a counter inside the `quickselect()` function, you can check performance under different conditions using a Monte Carlo simulation:

```
def quickselect(series, k, counter=0):
    pivot = choice(series)

    left, right = list(),list()
    for item in series:
        if item < pivot:
            left.append(item)
        if item > pivot:
            right.append(item)

    counter += len(series)
    length_left = len(left)
    if length_left > k:
        return quickselect(left, k, counter)
    k -= length_left

    duplicates = series.count(pivot)
    if duplicates > k:
        return float(pivot), counter
    k -= duplicates

    return quickselect(right, k, counter)
```

The first experiment tries to determine how many operations the algorithm needs, on average, to find the median of an input list of 10,001 numbers:

```
results = list()
n = 10_001
for run in range(1, n):
    series = [randint(1, 25) for i in range(n)]
    med, count = quickselect(series, n//2)
    assert(med==median(series))
    results.append(count)

avg_ops = sum(results) / len(results)
print(f"Mean operations: {avg_ops}")

Mean operations: 27564.3649
```

Displaying the results on a histogram (see Figure 17-4) reveals that the algorithm computes from two to four times the size of the input, with three times being the most likely number of processed computations.

```
import matplotlib.pyplot as plt

plt.figure(figsize=(12, 6))
plt.hist(results, bins=30, color='lightblue',
         edgecolor='black', linewidth=1.2)
plt.xlabel("Computations")
plt.ylabel("Frequency")
plt.show()
```

If on average it takes about three times the size of the input, quick select is providing good performance. However, you may wonder whether the proportion between inputs and computations will hold when the input size grows. As seen when studying NP-complete problems, many problems explode when the input size grows. You can prove this theory by using another Monte Carlo simulation on top of the previous one and plotting the output, as shown in Figure 17-5.

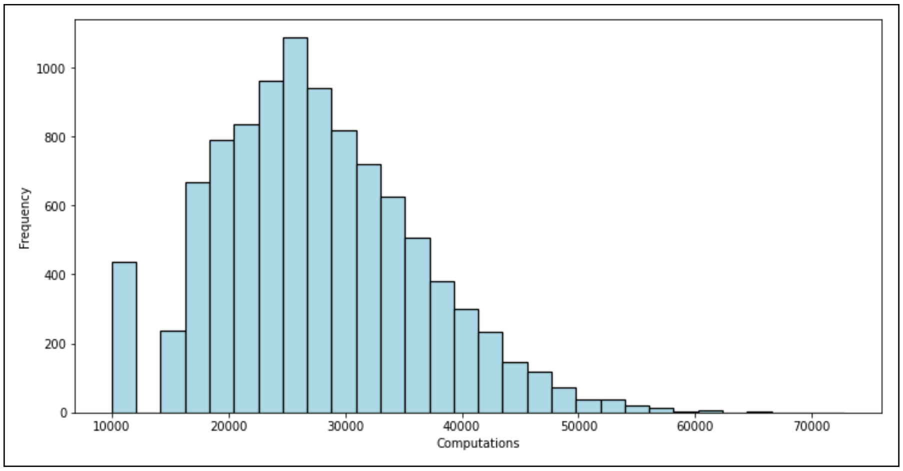


FIGURE 17-4: Displaying the results of a Monte Carlo simulation on quick select.

```
input_size = [501, 1001, 5001, 10001, 20001, 50001]
computations = list()
for n in input_size:
    results = list()
    for run in range(1000):
        series = [randint(1, 25) for i in range(n)]
        med, count = quickselect(series, n//2)
        assert(med==median(series))
        results.append(count)
    avg_ops = sum(results) / len(results)
    computations.append(avg_ops)

plt.figure(figsize=(12, 6))
plt.plot(input_size, computations, '-o')
plt.xlabel("Input size")
plt.ylabel("Number of computations")
plt.show()
```

WARNING

Completing the computations from this example may take up to ten minutes (some Monte Carlo simulations may be quite time consuming), but the result helps you visualize what it means to work with an algorithm that works with linear time. As the input grows (represented in abscissa), the computations (represented on the ordinal axis) grow proportionally, making the growth curve a perfect line.

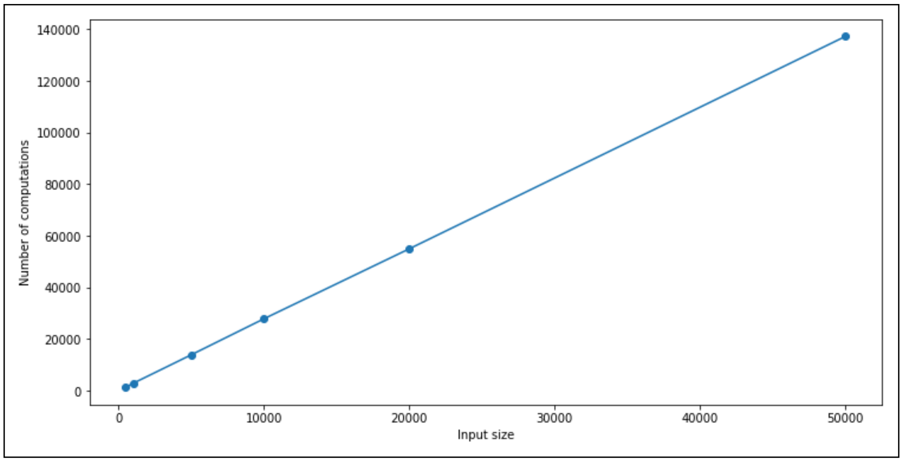


FIGURE 17-5: Displaying Monte Carlo simulations as input grows.

Ordering faster with quick sort

Chapter 7 explains ordering algorithms, the true foundation of all modern computer-based algorithmic knowledge. The quick sort algorithm, which can run in logarithmic time but sometimes fails and produces results in quadratic time under ill-conditioned inputs, will surely amaze you. This section explores the reasons why this algorithm may fail and provides an effective solution by injecting randomness into it. You start by examining the following code:

```
def quicksort(series, get):

    try:
        global operations
        operations += len(series)
    except:pass
    if len(series) <= 3:
        return sorted(series)

    pivot = get(series)
    duplicates = series.count(pivot)

    left, right = list(),list()
    for item in series:
        if item < pivot:
            left.append(item)
        if item > pivot:
            right.append(item)

    return quicksort(left, get) + [pivot
        ] * duplicates + quicksort(right, get)
```

This is another implementation of the algorithm from Chapter 7. However, this time the code extracts the function that decides the pivot the algorithm uses to recursively split the initial list. The algorithm decides the split by taking the first list value. It also tracks how many operations it takes to complete the ordering using the `operations` global variable, which is defined, reset, and accessed as a counter outside the function. The following code tests the algorithm, under unusual conditions, requiring it to process an already ordered list. Note its performance:

```
series = list(range(25))
operations = 0
sorted_list = quicksort(series, choose_leftmost)
print(f"Operations: {operations}" )
```

In this example, `choose_leftmost()` provides a basic output as shown here of selecting the leftmost item in a list:

```
def choose_leftmost(l): return l[0]
```

The output shows the number of operations.

```
Operations: 322
```

In this case, the algorithm takes 322 operations to order a list of 25 elements, which is horrid performance. Using an already ordered list causes the problem because the algorithm splits the list into two lists: an empty one and another one with the residual values. It has to repeat this unhelpful split for all the unique values present in the list. Usually the quick sort algorithm works fine because it works with unordered lists, and picking the leftmost element is equivalent to randomly drawing a number as the pivot. To avoid this problem, you can use a variation of the algorithm that provides a true random draw of the pivot value.

```
def choose_random(l): return choice(l)

seed(0)
series = [randint(1,25) for i in range(25)]
operations = 0
sorted_list = quicksort(series, choose_random)
print(f"Operations: {operations}" )

Operations: 92
```

Now the algorithm performs its task using a slightly higher number of operations, which is near the estimated running time of `n * log(n)`, that is, `25 * log(25) = 80.5`.

IN THIS CHAPTER

- » Determining how to perform a local search on an NP-hard problem
- » Working with heuristics and neighboring solutions
- » Discovering the many tricks to apply to a local search
- » Solving the 2-SAT problem with local search and randomization

Chapter 18 Performing Local Search

Previous chapters show how solving algorithms does not always correspond to finding an exact solution because of time and resource constraints, or because of the difficulty (or perhaps impossibility) of the problem you're facing. Such dire situations call for compromise, trading exact solutions for feasible approximations. This chapter discusses an approach, *local search* (a kind of optimization), that helps create a compromise with difficult problems and reach satisfying solutions. Local search is also sometimes called a *local improvement technique*.

The first part of the chapter introduces the principles under which local search works, and then analyzes the core ingredients of a local search solution. It also introduces the key concepts of heuristics and neighboring solutions, without which local search wouldn't exist. Finally, you explore a host of tricks for making local search algorithms work better. (Randomization is a really good match for most local search solutions.)

The concluding part delves deep into a problem, the 2-satisfiability (2-SAT) problem. This problem has deep implications in industrial production (for product personalization), air-traffic control planning, and sports-tournaments scheduling.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 18; Local Search.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Understanding Local Search

When dealing with an NP-hard problem, a problem for which no known solution has a running complexity less than exponential (see the NP-completeness theory discussion in Chapter 15), you have a few alternatives worth trying. Based on the idea that NP-class problems require some compromise (such as accepting partial or nonoptimal results), the following options offer a solution to this otherwise intractable problem:

- Identify special cases under which you can solve the problem efficiently in polynomial time using an exact method or a greedy algorithm. This approach simplifies the problem and limits the number of solution combinations to try.
- Employ dynamic programming techniques (described in Chapter 16) that improve on brute-force search and reduce the complexity of the problem.
- Compromise and sketch an approximate algorithm that finds a *partial,* close-to-optimal solution. When you're satisfied with a partial solution, you cut the algorithm's running time short. Approximate algorithms can be
  - Greedy algorithms (as discussed in Chapter 15)
  - Linear programming (the topic of Chapter 19)
  - Choose a heuristic or a *meta-heuristic* (a heuristic that helps you determine which heuristic to use) that works well for your problem in practice. However, it has no theoretical guarantee and tends to be empirical.
- Employ local search using randomization or some other heuristic technique.

Local search is a general problem=solving approach that comprises a large range of algorithms. Using local search helps you escape the exponential complexities of many NP problems. A local search starts from an imperfect problem solution and moves away from it, a step at a time. It determines the viability of nearby solutions, potentially leading to a perfect solution, based on random choice or an astute heuristic (no exact method is involved).

REMEMBER

A *heuristic* is an educated guess about a solution, such as a rule of thumb that points to the direction of a desired outcome, but can't tell exactly how to reach it. It's like being lost in an unknown city and having people tell you to go a certain way to reach your hotel (but without precise instructions) or just how far you are from it. Some local search solutions use heuristics, so you find some examples of them in this chapter. Chapter 20 delves into the full details of using heuristics to perform practical tasks.

You have no guarantee that a local search will arrive at a problem solution, but your chances do improve from the starting point when you provide enough time for the search to run its computations. It stops only after it can't find any further way to improve the solution it has reached.

Knowing the neighborhood

Local search algorithms iteratively improve from a starting solution, moving one step at a time through neighboring solutions until it isn't possible to improve the solution any further. Because local search algorithms are as simple and intuitive as greedy algorithms, designing a local search approach to an algorithmic problem is not difficult. The key is to define the correct procedure:

1. Start with an existing solution (usually a random solution or a solution from another algorithm).
2. Search for a set of possible new solutions within the current solution's neighborhood, which constitutes the *candidates' list.*
3. Determine which solution to use in place of the current solution based on the output of a heuristic that accepts the candidates' list as input.
4. Continue performing Steps 2 and 3 until you see no further improvement on the solution, which means that you have the best solution available in this neighborhood.

REMEMBER

Although easy to design, local search solutions may not find a solution in a reasonable time (you can stop the process after a while and use the current solution) or produce a minimum-quality solution. You can employ some tricks of the trade to ensure that you get the most out of this approach.

At the start of the local search, you pick an initial solution. If you decide on a random solution, it's helpful to wrap the search in repeated iterations in which you generate different random start solutions. Sometimes, arriving at a good final solution depends on the starting point. If you start from an existing solution that you want to refine, plugging the initial solution provided by a greedy algorithm may prove to be a good compromise because it won't take long to produce the greedy solution and to fit a local search solution directly from it. After choosing a starting point, define the neighborhood and determine its size. Defining a neighborhood requires figuring the smallest change you can impose on your solution. If a solution is a set of elements, all the neighboring solutions are the sets in which one of the elements mutates. For instance, in the traveling salesman problem (TSP), neighboring solutions could involve changing the ending cities of two (or more) trips, as shown in Figure 18-1.

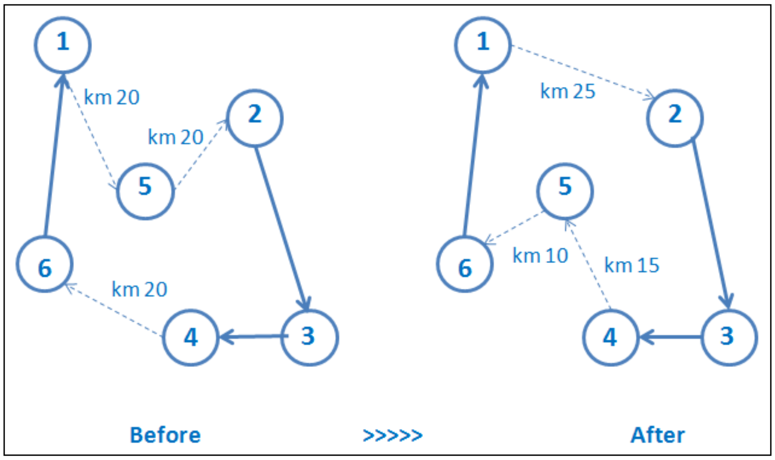


FIGURE 18-1: Switching ending trips in a TSP problem may bring better results.

Based on how you create the neighborhood, you may have a smaller or a larger candidates' list. Larger lists require more time and computations but, contrary to short lists, may offer more opportunities for the process to end earlier and better. List length involves a trade-off that you refine by using experimentation after each test to determine whether enlarging or shrinking the candidate list brings an advantage or a disadvantage in terms of time to complete and solution quality.

Base the choice of the new solution on a heuristic and, given the problem, decide on the best solution. For instance, in the TSP problem, use the trip switches that shorten the total tour length the most. In certain cases, you can use a random choice in place of a heuristic (as you discover in the SAT-2 problem, also called a 2-SAT problem, in this chapter). Even when you have a clear heuristic, the algorithm could find multiple best solutions. Injecting some randomness could make your local search more efficient. When faced with many solutions, you can safely choose one randomly.

TIP

Ideally, in a local search, you get the best results when you run multiple searches, injecting randomness as much as you can into the start solution and along the way as you decide the next process step. Let the heuristic decide only when you see a clear advantage to doing so. Local search and randomness are good friends.

Your search has to stop at a certain point, so you need to choose stopping rules for the local search. When your heuristic can't find good neighbors anymore, or it can't improve solution quality (for instance, computing a cost function, as it happens in TSP, by measuring the total length of the tour). Depending on the problem, if you don't create a stopping rule, your search may go on forever or take an unacceptably long time. In case you can't define a stopping point, limit the time spent looking for solutions or count the number of trials. However, when watching the clock or counting trials, you're basing decisions on the algorithm's probability of success at a certain point of the process. Although this is a convenient approach, basing the process on time or trials may lead to less-than-acceptable solutions.

Presenting local search tricks

Local search tracks the current solution and moves to neighboring solutions one at a time until it finds a perfect solution (or can't improve on the present solution). It presents some key advantages when working on NP-hard problems because it

- Is simple to devise and execute
- Uses little memory and computer resources (but searches require running time)
- Finds acceptable or even good problem solutions when starting from a less-than-perfect solution (neighboring solutions should create a path to the perfect solution)

TIP

You can see the problems that a local search can solve as a graph of interconnected solutions. The algorithm traverses the graph, moving from node to node looking for the node that satisfies the task requirements. Using this perspective, a local search takes advantage of graph-exploration algorithms such as depth-first search (DFS) or breadth-first search (BFS), both discussed in Chapter 9.

Local search provides a viable way to find acceptable solutions to NP-hard problems. However, local search can't work properly without the right heuristic. Randomization can provide a good match with local search, and it helps by using

- **Random sampling:** Generating solutions to start
- **Random walk:** Picking a random solution that neighbors the current one (You find more on random walks in the "Solving 2-SAT using randomization" section, later in this chapter.)

Randomization isn't the only heuristic available. A local search can rely on a more reasoned exploration of solutions using an objective function to get directions (as in *hill-climbing* optimization) and avoid the trap of so-so solutions (as in *simulated annealing* and *Tabu Search*). An *objective function* is a computation that can assess the quality of your solution by outputting a score number. If you need higher scores in hill climbing, you have a maximization problem; if you are looking for smaller score numbers, you have a problem of minimization.

Explaining hill climbing with n-queens

You can easily find analogies of the techniques employed by local search because many phenomena imply a gradual transition from one situation to another. Local search isn't just a technique devised by experts on algorithms but is actually a process that you see in both nature and human society. In society and science, for instance, you can view innovation as a local search of the next step among the currently available technologies: `https://www.technologyreview.com/2017/01/13/154580/mathematical-model-reveals-the-patterns-of-how-innovations-arise/`. Many heuristics derive from the physical world, taking inspiration from the force of gravity, the fusion of metals, the evolution of DNA in animals, and the behavior of swarms of ants, bees, and fireflies (the paper at `https://arxiv.org/pdf/1003.1464.pdf` explains the Lévy-Flight Firefly algorithm and other nature-inspired algorithms).

Hill climbing takes inspiration from the force of gravity. It relies on the observation that as a ball rolls down a valley, it takes the steepest descent; then, when it encounters a hill, it tends to take the most direct upward direction to reach the top. Gradually, one step after the other, no matter whether it's climbing up or down, the ball arrives at its destination, where proceeding higher or lower isn't possible.

In local search, you can mimic the same procedure successfully using an *objective function,* a measurement that evaluates the neighboring solutions and determines which one improves on the current one. Using the hill-climbing analogy, having an objective function is like feeling the inclination of the terrain and determining the next best move. From the current position, a hiker evaluates each direction to determine the terrain's slope. When the goal is to reach the top, the hiker chooses the direction with the greatest upward slope to reach the top. However, that's just the ideal situation; hikers often encounter problems during a climb and must use other solutions to circumnavigate them.

An objective function is similar to a greedy criterion (see Chapter 5). It's blind with respect to its final destination, so it can determine direction but not detect obstacles. Think about the effect of blindness when climbing the mountains — it's difficult to say when a hiker reaches the top. Flat terrain that lacks any opportunities for upward movement could indicate that the hiker reached the top. Unfortunately, a flat spot can also be a plain, a depression, or even a hole the hiker happened to fall into. You can't be sure because the hiker can't see.

The same problem happens when using a local search guided by a hill-climbing heuristic: It pursues progressively better neighbor solutions until it can't find a better solution by checking the solutions that exist around the current one. At this point, the algorithm declares it found a solution. It also says that it has found a global solution, even though, as illustrated in Figure 18-2, it may have simply found a local *maximum*, a solution that's the best around because it's surrounded by worse solutions. It's still possible to find a better solution through further exploration.

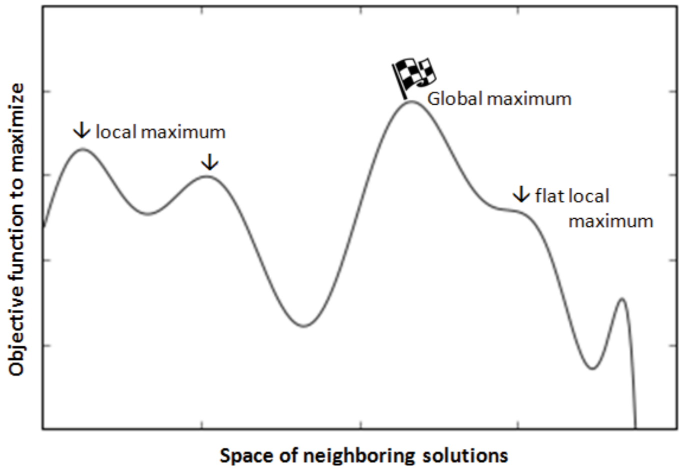


FIGURE 18-2: Local search explores the landscape by hill climbing.

An example of hill climbing in action (and of the risks of getting stuck in a local maximum or local minimum when you're descending, as in this example) is the n-queens puzzle, first created by the chess expert Max Bezzel, in 1848, as a challenge for chess lovers. In this problem, you have a number of queens (this number is *n*) to place on a chessboard of *n* x *n* dimensions. You must place them so that no queen is threatened by any other. (In chess, a queen can attack by any direction by row, column, or diagonal.)

TIP

This is really a NP-hard problem. If you have eight queens to place on a 8-x-8 chessboard, there are 4,426,165,368 different ways to place them but only 92 configurations to solve the problem. Clearly, you can't solve this problem using brute force or luck alone. Local search solves this problem in a very simple way by using hill climbing:

1. Place the *n* queens randomly on the chessboard so that each one is on a different column (no two queens on the same column).
2. Evaluate the next set of solutions by moving each queen one square up or down in its column. This step requires 2 * *n* moves.
3. Determine how many queens are attacking each other after each move.
4. Determine which solution has the fewest queens attacking each other and use that solution as the starting point for the next iteration.
5. Perform Steps 2 through 4 until you find a solution.

Unfortunately, this approach works only about 14 percent of the time using a standard 8 x 8 board because it often gets stuck in a chessboard configuration that won't allow any further improvement 86 percent of the time. (The number of queens under attack won't diminish for all 2 * *n* moves available as next solutions.) The only way you get away from such a block is to restart the local search from scratch by choosing another random starting configuration of the queens on the chessboard. On average, perseverance will be rewarded one in ten attempts, a less rewarding result than trying all possible solutions systematically. Figure 18-3 shows a successful solution.

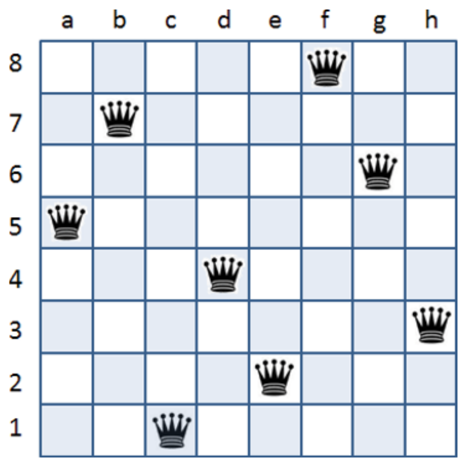


FIGURE 18-3: An 8-queen puzzle solved.

In spite of their weakness in finding a best solution (or a solution at all) on the first attempt, hill-climbing algorithms are used everywhere, especially in artificial intelligence and machine learning. Neural networks that recognize sounds or images, power mobile phones, and motivate self-driving cars mostly rely on a hill-climbing optimization called *gradient descent.* Randomized starts and random injections in the hill-climbing procedure make it possible to escape any local solution and reach the global maximum. Both simulated annealing and Tabu Search are smart ways to use random decisions in hill climbing.

Discovering simulated annealing

At a certain point in the search, if your objective function stops giving you the right indications, you can use another heuristic to control the situation and try to find a better path to a better task solution. This is how both simulated annealing and Tabu Search work: They provide you with an emergency exit when needed.

Simulated annealing takes its name from a technique in metallurgy, which heats the metal to a high temperature and then slowly cools it to soften the metal for cold working and to remove internal crystalline defects (see `https://www.azom.com/article.aspx?ArticleID=20195` for details on this metal-working process). Local search replicates this idea by viewing the solution search as an atomic structure that changes to improve its workability. The temperature is the game changer in the optimization process. Just as high temperatures make the structure of a material relax (solids melt and liquids evaporate at high temperatures), so high temperatures in a local search algorithm induce relaxation of the objective function, allowing it to prefer worse solutions to better ones. Simulated annealing modifies the hill-climbing procedure, keeping the objective function for neighbor solution evaluation but allowing it to determine the search solution choice in a different way:

1. Obtain a temperature expressed as probability. (The Gibbs-Boltzmann physics function is a formula that converts temperature to probability, but you can also use simpler approaches that map temperature to probability.)
2. Set a temperature schedule. The temperature decreases at a certain rate as time passes and the search runs.
3. Define a starting solution (using random sampling or another algorithm) and start a loop. As the loop proceeds, the temperature decreases.
4. Stop the optimization when the temperature is zero.
5. Propose the current result as the solution.

At this point, you must iterate the search for solutions. For each step in the previous iteration, between the preceding Steps 3 and 4, do the following:

1. List the neighboring solutions and choose one at random.
2. Set the neighboring solution as the current solution when the neighboring solution is better than the current one.
3. Otherwise, pick a random number between 0 and 1 based on a threshold probability associated with the actual temperature, and determine whether it's less than the threshold probability:
   - If it's less, set the neighboring solution as the current solution (even if it's worse than the current solution, according to the objective function).
   - If it's more, keep the current solution.

Simulated annealing is a smart way to improve hill climbing because it avoids having the search stopped at a local solution. When the temperature is high enough, the search might use a random solution and find another way to a better optimization. Because the temperature is higher at the beginning of the search, the algorithm has a chance of injecting randomness into the optimization. As the temperature cools to zero, less and less chance exists for picking a random solution, and the local search proceeds as in hill climbing. In TSP, for instance, the algorithm achieves simulated annealing by challenging the present solution at high temperatures by

- Choosing a segment of the tour randomly and traversing it in the opposite direction
- Visiting a city earlier or later in the tour, leaving the order of visit to the other cities the same

If the resulting adjustments worsen the tour's length, the algorithm keeps or rejects them according to the temperature in the simulated annealing process.

Avoiding repeats using Tabu Search

Tabu is an ancient word from Polynesian Tongan that says certain things can't be touched because they're sacred. The word *tabu* (which is spelled as taboo in English) passed from anthropological studies to the everyday language to indicate something that is prohibited. In local search optimization, it's common to become stuck in a neighborhood of solutions that don't offer any improvement; that is, it's a local solution that appears as the best solution but is far from being the solution you want. Tabu Search relaxes some rules and enforces others to offer a way out of local minima and help you reach better solutions.

The Tabu Search heuristics wraps objective functions and works its way along many neighboring solutions. It intervenes when you can't proceed because the next solutions don't improve on your objective. When such happens, Tabu Search does the following:

- Allows use of a pejorative solution for a few times to see whether moving away from the local solution can help the search find a better path to the best solution.
- Remembers the solutions that the search tries and forbids it from using them anymore, thus assuring that the search doesn't loop between the same solutions around the local solution without finding an escape route.
- Creates a long-term or short-term memory of Tabu solutions by modifying the length of the queue used to store past solutions. When the queue is full, the heuristic drops the oldest Tabu to make space for the new one.

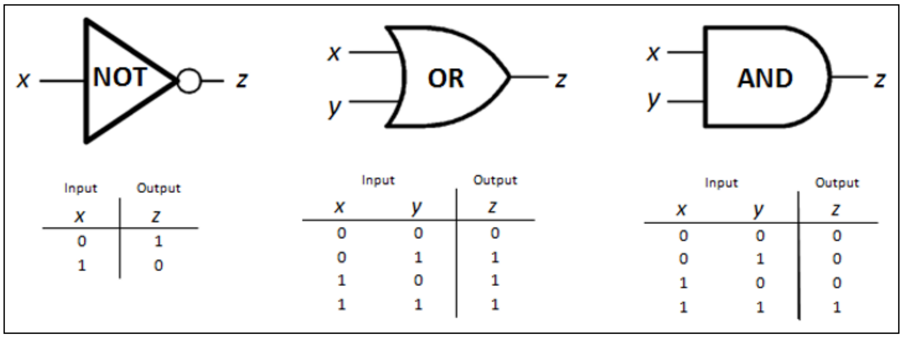
You can relate Tabu Search to caching and memoization (see Chapter 16) because it requires the algorithm to track its steps to save time and avoid retracing previously used solutions. In the TSP, it can help when you try optimizing your solution by swapping the visit order of two or more cities to avoid repeat solution sets.

Solving Satisfiability of Boolean Circuits

As a practical view of how a local search works, the example in this section delves into circuit satisfiability, a classic NP-complete problem with quite a few applications in the real world, including industrial planning, sports scheduling, and air traffic control. The algorithm is also used for testing how electronic circuits work, optimizing them by removing circuits that won't transport electrical signals (they're redundant). Moreover, the solving algorithm sees use in quite a few other applications: automatic labeling on maps and charts; discrete tomography; scheduling with constraints; data clustering into groups; and other problems for which you have to make conflicting choices. It uses a randomization and Monte Carlo algorithm approach. As seen in Chapter 17, a Monte Carlo algorithm relies on random choices during its optimization process and isn't guaranteed to succeed in its task, although it has a high likelihood of completing the task successfully.

The example revolves around computer circuit testing. Computer circuits are composed of a series of connected components, each one opening or closing a circuit based on its inputs. Such elements are called *logic gates* (physically, their role is played by transistors) and if you build a circuit with many logic gates, you need to understand whether electricity can pass through it and under what circumstances.

Chapter 14 discusses the internal representation of a computer, based on zeros (absence of electricity in the circuit) or ones (presence of electricity). You can render this 0/1 representation from a logical perspective, turning signals into `False` (there isn't electricity in the circuit) or `True` (there is indeed electricity) conditions. Chapter 4 examines the Boolean operators (`AND`, `OR`, and `NOT`), as shown in Figure 18-4, which will interact with `True` and `False` inputs to transform them into different outputs. All these concepts help you represent a physical electric circuit as a sequence of Boolean operators defining logic gates. The combination of all their conditions determines whether the circuit can carry electricity.



Input	Output
x	z
0	1
1	0

Input		Output
x	y	z
0	0	0
0	1	1
1	0	1
1	1	1

Input		Output
x	y	z
0	0	0
0	1	0
1	0	0
1	1	1

FIGURE 18-4: Symbols and truth tables of logic operators `AND`, `OR`, and `NOT`.

This logic representation is a *Boolean combinational circuit,* and the test to verify its functionality is the *circuit satisfiability problem.* In the easiest scenario, the circuit consists of only `NOT` conditions (called *inverters*) that accept one wire input, and `OR` conditions that accept two wires as inputs. This is a 2-satisfiability (2-SAT) scenario, and if the algorithm were to go through it using an exhaustive search, it would take at worst `2k` trials (having *k* as the number of input wires) to find a set of conditions that makes electricity pass through the whole circuit, if one exists. There are even more complex versions of the problem, which accept more inputs for each `OR` logic gate and use `AND` gates, but they are beyond the scope of this book.

Solving 2-SAT using randomization

No matter the electronic circuit you have to test using a Boolean representation, you can render it as a vector of Boolean variables. You can also create another vector to contain the *clauses,* the set of conditions the circuit needs to satisfy (for example, that wire A and wire B should both be `True`). This isn't the only way to represent the problem; in fact, there are other solutions involving the use of graphs. However, for this example, these two vectors are enough.

You can solve the problem using a randomized local search in polynomial time. Professor Christos H. Papadimitriou, teaching at the University of California at

Berkeley (`https://www.engineering.columbia.edu/faculty/christos-papadimitriou`), devised this algorithm, called *RandomWalkSAT*. He presented it in his paper "On Selecting a Satisfying Truth Assignment," published in 1991 by the Proceedings of the 32nd IEEE Symposium on the Foundations of Computer Science. The algorithm is competitive when compared to more reasoned ways, and it is an exemplary local search approach because it makes just one change at a time on the current solution. It uses two nested loops, one for trying the starting solution multiple times and one for randomly amending the initial random solution. Repeat the outer loop `log2(k)` times (where *k* is the number of wires). The inner loop uses the following steps:

1. Pick a random problem solution.
2. Repeat the following steps `2*k`^{2} times:
   - **(a)** Determine whether the current solution is the right one. When it is the correct solution, break free of all the loops and report the solution.
   - **(b)** Pick an unsatisfied clause at random. Choose one of the conditions in it at random and amend it.

Implementing the Python code

To solve the 2-SAT problem using Python and the RandomWalkSAT algorithm, you need to set a few helpful functions. The `create_clauses()` and `signed()` functions help generate a circuit problem to solve by handling the `OR` and `NOT` gates, respectively. Using these functions, you specify the number of `OR` gates and provide a seed number that guarantees that you can recreate the resulting problem later (allowing you to try the problem multiple times and on different computers).

The `create_random_solutions()` function provides a cold problem start by giving a random solution that sets the inputs. The chances of finding the right solution using random luck is slim (one out of the power of two to the number of gates), but on average, you can expect that three quarters of the gates are correctly set (because, as seen using the truth table for the `OR` function, three inputs out of four possible are `True`). The `check_solution()` function determines when the circuit is satisfied (indicating a correct solution). Otherwise, it outputs what conditions aren't satisfied. (You can find this code in the `A4D2E; 18; Local Search.ipynb` downloadable source code file; see the Introduction for details.)

```
import random
from math import log2

def signed(v):
    return v if random.random() < 0.5 else -v

def create_clauses(i, seed=1):
    random.seed(seed)
    return [(signed(random.randint(0, i-1)),
             signed(random.randint(0, i-1)))
            for j in range(i)]

def create_random_solution(i, *kwargs):
    return {j:signed(1)==1 for j in range(i)}

def check_solution(solution, clauses):
    violations = list()
    for k,(a,b) in enumerate(clauses):
        if not (((solution[abs(a)]) == (a > 0)) |
                ((solution[abs(b)]) == (b > 0))):
            violations.append(k)
    return violations
```

After setting these functions, you have all the building blocks for a `sat2()` function to solve the problem. This solution uses two nested iterations: The first replicates many starts; the second picks unsatisfied conditions at random and makes them `True`. The solution runs in polynomial time. The function isn't guaranteed to find a solution, if one exists, but chances are, it will provide a solution when one exists. In fact, the internal iteration loop makes $2*k^2$ random attempts to solve the circuit, which usually proves enough for a random walk on a line to reach its destination.

REMEMBER

A random walk is a series of computations representing an object that moves away from its initial position by taking a random direction at every step. You might imagine a random walk as the journey of a drunken person from one light pole to the next. Random walks are useful for representing a mathematical model of many real-world aspects. They find applications in biology, physics, chemistry, computer science, and economics, especially in stock market analysis. If you want to know more about random walks, go to `http://www.mit.edu/~kardar/teaching/projects/chemotaxis(AndreaSchmidt)/random.htm`.

A random walk on a line is the easiest example of a random walk. On average, k^2 steps of a random walk are required to arrive at a *k* distance from the starting point. This expected effort explains why RandomWalkSAT requires $2*k^2$ random chances to amend the starting solution. The number of chances provides a high probability that the algorithm will fix the *k* clauses. Moreover, it works in the same manner as the random card guessing game discussed in the previous chapter. As the algorithm proceeds, choosing the right answer becomes easier. The external replications guarantee an escape from unfortunate internal-loop random choices that may stop the process in a local solution.

```
def sat2(clauses, n, start=create_random_solution):
    not_solved = True
    for external_loop in range(round(log2(n))):
        solution = start(n, clauses)
        history = list()
        for internal_loop in range(2 * n**2):
            response = check_solution(solution, clauses)
            unsatisfied = len(response)
            history.append(unsatisfied)
            if unsatisfied==0:
                print ("Solution in %i external loops," %
                       (external_loop + 1), end=" ")
                print ("%i internal loops" %
                       (internal_loop + 1))
                not_solved = False
                break
            else:
                r1 = random.choice(response)
                r2 = random.randint(0, 1)
                clause_to_fix = clauses[r1][r2]
                solution[abs(clause_to_fix)] = (
                    clause_to_fix>0)
        else:
            continue
        break
    if not_solved is True:
        print("Not solvable")
    return history, solution
```

Now that all the functions are correctly set, you can run the code to solve a problem. Here's the first example, which tries the circuit created by seed 0 and uses 1,000 logic gates:

```
n = 1000
clauses = create_clauses(n, seed=0)
history, solution = sat2(clauses, n,
        start=create_random_solution)

Found solution in 1 external loops, 674 internal loops
```

Plotting the solution as a chart representing the number of steps on the abscissa (random emendations of the solution) and the clauses left to fix on the ordinal axis, you can verify that the algorithm tends to find the correct solution in the long run, as shown in Figure 18-5.

```
import matplotlib.pyplot as plt

plt.figure(figsize=(12, 6))
plt.plot(history, 'b-')
plt.xlabel("Random adjustments")
plt.ylabel("Unsatisfied clauses")
plt.grid(True)
plt.show()
```

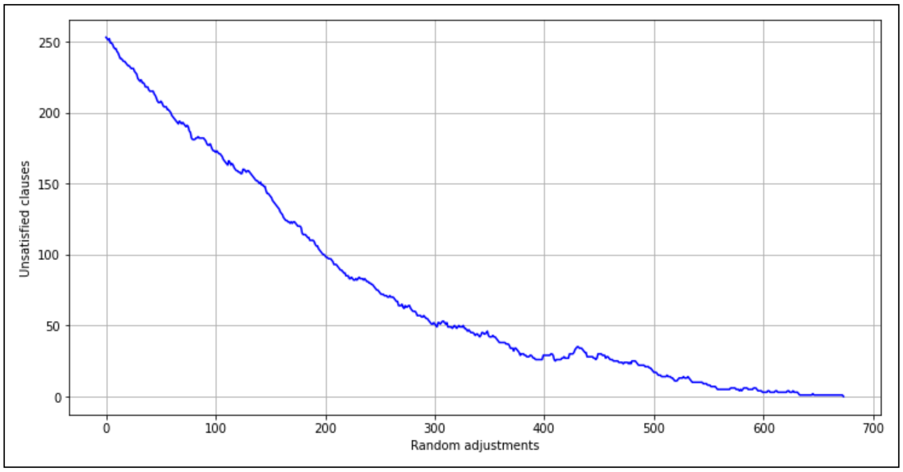


FIGURE 18-5: The number of unsatisfiable clauses decreases after random adjustments.

Not all clauses are actually solvable. You can try different seeds and find some that take a long time to process, such as the circuit with 1,000 gates that you can create by setting the seed equal to 12. When you create an unsolvable circuit the script returns a message telling you that the circuit is not solvable after it has performed the correct number of trials. It takes more time when an unsolvable set of clauses is met. It happens because of the external loop that needs to exhaust the equivalent of `log`$_2$`(k)` the number of clauses in order to have a statistical assurance that you're not finding a solution because the circuit is not working, and not because you are just unlucky in the randomized local search.

Realizing that the starting point is important

Even though the RandomWalkSAT algorithm has a runtime complexity of $O(\log_2 k * k^2)$ at worst, with *k* the number of inputs, you can speed it up by hacking the starting point. In fact, even though starting with a random configuration means that a quarter of the clauses remain unsatisfied at the start on average, you can fix many of them by performing a pass over the data.

The problem with clauses is that many require a `True` input, and simultaneously, many others require a `False` input. When all clauses require an input to be `True` or `False`, you can set it to the required condition, which satisfies a large number of clauses and makes solving the residual ones easier. The following new RandomWalkSAT implementation includes a start phase that immediately solves the situations in which an input requires a specific `True` or `False` setting by all the clauses they interact with:

```
def better_start(n, clauses):
    clause_dict = dict()
    for pair in clauses:
        for clause in pair:
            if abs(clause) in clause_dict:
                clause_dict[abs(clause)].add(clause)
            else:
                clause_dict[abs(clause)] = {clause}

    solution = create_random_solution(n)

    for clause, value in clause_dict.items():
        if len(value) == 1:
            solution[clause] = value.pop() > 0
    return solution
```

The code defines a new function for the cold start, where it scans through the solution and finds all the inputs associated with a single state (`True` or `False`) after generating a random solution. By setting them immediately to the required state, you can reduce the number of clauses requiring amendment, and have the local search do less work and complete earlier:

```
n = 1000
clauses = create_clauses(n, seed=0)
history, solution = sat2(clauses, n, start=better_start)

Found solution in 1 external loops, 400 internal loops
```

By providing this new, simplified starting point, you can immediately see an improvement after charting the results. On average, fewer operations are needed to complete the task.

TIP

In a local search, always consider that the starting point is important to allow the algorithm to complete earlier and more successfully, as shown in Figure 18-6. In sum, try to provide the best-quality start for your search as possible.

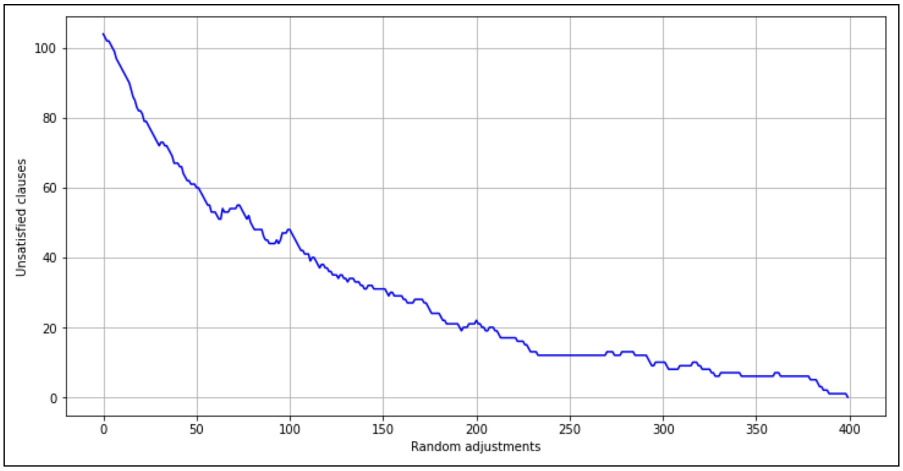


FIGURE 18-6: Execution is speedier because the starting point is better.

IN THIS CHAPTER

» Discovering how optimization happens using linear programming

» Transforming real-world problems into math and geometry ones

» Learning how to use Python to solve linear programming problems

Chapter 19 Employing Linear Programming

Linear programming (LP) is also called linear optimization and is a method for finding the maximum or minimum value of a function called the objective function. The objective function is constrained by some bounds, also called constraints. As the name hints, LP works by relying on functions and bounds based on linearity, in which everything can be represented as a line in a graph; no curves admitted. Despite such limitations, if you can simplify and define your problem based on linear functions, LP is powerful. Commonly, its applications are vast and important, touching everyday problems in production and logistics.

This chapter helps you understand linear programming. The first part provides you with the concepts needed to know how to use linear programming effectively. It includes the basic math you can't avoid when implementing it. This first part also shows how simpler problems can be visually represented graphically by a chart.

In the second part you see how to apply linear programming to real-world problems by using Python as the tool to express those problems in code. It introduces you to the PuLP Python package, which is both easy to run and to apply to your own problems. Using this package gives you the chance to solve problems that, though still linear, are so complex that you can't represent them with paper and pencil on a chart.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 19; Linear Programming.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Using Linear Functions as a Tool

LP made a first appearance during World War II, when logistics proved critical in maneuvering armies of millions of soldiers, weapons, and supplies across geographically variegated battlefields. Tanks and airplanes needed to refuel and rearm, which required a massive organizational effort to succeed in spite of limitations in time, resources, and actions from the enemy.

You can express most of these military problems in mathematical form. Mathematician George Bernard Dantzig, who was employed in the U.S. Air Force Office of Statistical Control, devised a smart way to solve these problems using the *simplex* algorithm. Simplex is the core idea that created interest in numerical optimization after the war and gave birth to the promising field of linear programming. The availability of the first useful computers of the time also increased interest, rendering complex computations solvable in a new and fast way. You can view the early history of computing in the 1950s and 1960s as a quest to optimize logistical problems using the simplex method and applying both high-speed computers and specialized programming languages.

Dantzig died in 2005, and the field he inaugurated is still under constant development. In the recent years, fresh ideas and methods related to linear programming continue to make successful appearances, such as the following:

- **Constraint programming:** Expresses the relationships between the variables in a computer program as constraints in linear programming.
- **Genetic algorithms:** Considers the idea that math formulas can replicate and mutate in order to solve problems in the same manner as DNA does in nature by evolution. Genetic algorithms also appear in Chapter 20 because of their heuristic approach to optimization.

To start working with LP, you first need to grasp its different approach and terminology to the solutions explored so far. This section shows how to address a problem whose objective and constraints have been transformed into linear functions. The *objective* of a problem is the representation of cost, profit, or some other quantity to maximize or minimize, subject to the constraints. The *constraints* are linear inequalities derived from the application, such as the limit of a 40-hour work week. The purpose of LP is to provide an optimum numeric solution, which could be a maximum or a minimum value, and the set of conditions to obtain it.

This definition of linear programming may sound a little bit tricky because both math and some abstraction is involved (objective and constraints as linear functions), but things become clearer after considering what a function is and when you can determine whether a function is linear. Beyond the math jargon, linear programming is just a different point of view when dealing with algorithmic problems: You trade operations and manipulations of data inputs with mathematical functions, and you perform calculations using a software program called an *optimizer*.

You can't use linear programming to solve all problems, but a large number of them fit linear programming requirements, especially problems requiring optimization using previously defined limits. Previous chapters discuss how dynamic programming is the best approach when you need to optimize problems subject to constraints. Dynamic programming works with problems that are discrete; that is, the numbers you work with are whole numbers. Linear programming mainly works with decimal numbers, although special optimization algorithms are available that provide solutions as integer numbers; for example, you can solve the traveling salesman problem using integer linear programming. Linear programming has a wider scope, because it can cope with almost any polynomial time problem.

Linear programming sees use in manufacturing, logistics, transportation (especially for airlines, for defining routes, timetables, and the cost of tickets), marketing, finance, and telecommunications. All these applications require that you obtain a maximum economic result at a minimum cost while optimizing available resource allocation and satisfying all constraints and limitations. In addition, you can apply linear programming to common applications such as video games and computer visualization, because games rely on bidimensional and tridimensional complex shapes, and you need to determine whether any shapes collide as well as ensure that they respect the rules of the game. You achieve these aims via the convex hull algorithm powered by linear programming (see `https://0fps.net/category/programming/video-games/`). Finally, linear programming is at work in search engines for document-retrieval problems; you can transform words, phrases, and documents into functions and determine how to maximize your search result (getting the documents you need to answer your query) when you look for documents with certain mathematical characteristics.

Grasping the basic math you need

In computer programming, functions provide the means for packaging code that you intend to use more than once. Functions turn code into a black box, an entity to which you provide inputs and expect certain outputs. (Chapter 4 discusses how to create functions in Python.) Mathematics uses functions in a similar manner to programming; they are a set of mathematical operations that transform some input into an output. The input can include one or more variables, resulting in a unique output based on the input. Usually a function has this form:

```
f(x) = x * 2
```

- **f:** Determines the function name. It can be anything; you can use any letter of the alphabet or even a word.
- **(x):** Specifies the input. In this example, the input is the variable x, but you can use more inputs and of any complexity, including multiple variables or matrices.
- **x * 2:** Defines the set of operations that the function performs after receiving the input. The result is the function output in the form of a number.

If you plug the input 2 as x in this example, you obtain:

```
f(2) = 4
```

In math terms, by calling this function, you mapped the input 2 to the output 4.

REMEMBER

Functions can be simple or complex, but every function has one and only one result (even if that result is a tuple) for every set of inputs that you provide (even when the input is made of multiple variables).

Linear programming leverages functions to render the objectives it has to reach in a mathematical way to solve the problem at hand. When you turn objectives into a math function, the problem translates into determining the input to the function that maps the maximum output (or the minimum, depending on what you want to achieve). The function representing the optimization objective is the *objective function.* In addition, linear programming uses functions and inequalities to express constraints or bounds that keep you from plugging just any input you want into the objective function. For instance, inequalities are

```
0 >= x <= 4
y + x < 10
```

The first of these inequalities translates into limiting the input of the objective function to values between 0 and 4. Inequalities can involve more than one input variable at a time. The second of these inequalities ties the values of an input to other values because their sum can't exceed 10.

REMEMBER

Bounds imply an input limitation on a value, as in the first example. *Constraints* always involve a math expression comprising more than one variable, as in the second example.

The final linear programming requirement is for both the objective function and the inequalities to be linear expressions. This means that the objective function and inequalities can't contain variables that multiply each other, or contain variables raised to a power (squared or cubed, for instance).

TECHNICAL STUFF

All the functions in an optimization should be linear expressions because the procedure represents them as lines in a Cartesian space. (If you need to review the concept of a Cartesian space, you can find useful information at `https://www.mathsisfun.com/data/cartesian-coordinates.html`.) As explained in the "Using Linear Programming in Practice" section, later in this chapter, you can imagine working with linear programming more as solving a geometric problem than a mathematical one.

Learning to simplify when planning

The problems that the original simplex algorithm solved were all of the kind that you usually read as word problems in a textbook. In such problems, all the data, information, and limitations are stated clearly; there is no irrelevant or redundant information; and you clearly have to apply a math formula (and most likely the one you just studied) to solve the problem.

In the real world, solutions to problems are never so nicely laid out. Instead, they often appear in a confused way, and some necessary information isn't readily available for you to process. Yet, you can analyze the problem and locate required data and other information. In addition, you can discover limitations such as money, time, or some rule or order that you must consider. When solving the problem, you gather the information and devise the means to simplify it.

Simplification implies some loss of realism but renders the problem description simpler, which can highlight the underlying processes that make things move, thereby helping you decide what happens. A simpler problem allows you to develop a model representing the reality. A model can approximate what happens in reality, and you can use it for both managing simulations and linear programming.

For instance, if you work in a factory and have to plan a production schedule, you know that the more people you add, the speedier production will be. However, you won't always obtain the same gain with the same addition of people. For example, the skills of the operators you add to the job affects results. In addition, you may find that adding more people to the job brings decreasing results when those people spend more time communicating and coordinating among themselves than performing useful work. Yet, you can make the model easier by pretending that every person you add to the task will produce a certain amount of final or intermediate goods.

Working with geometry using simplex

Classic examples of linear programming problems imply production of goods using limited resources (time, workers, or materials). For an example of depicting how linear programming approaches such challenges, imagine a factory that assembles two or more products that it must deliver in a certain time. The factory workers produce two products, x and y, during an eight-hour shift. For each product, they get a different profit (that you compute by subtracting costs from revenue), different hourly production rates, and different daily demands from the market:

- **Revenue in USD for each product:** x = 15, y = 25
- **Production rate per hour:** x = 50, y = 40
- **Daily demand per product:** x = 300, y = 200

In essence, the business problem is to decide whether to produce more x, which is easier to assemble but pays less, or y, which guarantees more revenue but less production. To solve the problem, first determine the objective function. Express it as the sum of the quantities of the two products, multiplied by their expected unit revenue, which you know you have to maximize (only if the problem is about costs do you have to minimize the objective function):

```
f(x, y) = 15 * x + 25 * y
```

This problem has inequalities, which are bounded by x and y values that have to hold true to obtain a valid result from the optimization:

```
0 <= x <= 300
0 <= y <= 200
```

In fact, you can't produce a negative number of products, nor does it make sense to produce more products than the market demands. Another important limitation is available time, because you can't exceed eight hours for each work shift. This means calculating the time to produce both x and y products and constraining the total time to less than or equal to eight hours.

```
x / 40 + y / 50 <= 8
```

You can represent functions on a Cartesian plane. (For a refresher on plotting functions, consult `https://www.mathplanet.com/education/pre-algebra/graphing-and-functions/linear-equations-in-the-coordinate-plane`.) Because you can express everything using functions in this problem, you can also solve the linear programming problems as geometry problems on a Cartesian coordinate space. If the problem doesn't involve more than two variables, you can plot the two variables and their constraints as lines on a plane, and determine how they delimit a geometric shape. You'll discover that the lines delimit an area, shaped as a polygon, called the *feasible region*. This region is where you find the solution, which contains all the valid (according to constraints) inputs for the problem.

When the problem deals with more than two variables, you can still imagine it using lines intersecting in a space, but you can't represent this visually because each input variable needs a dimension in the graph, and graphs are bound to the three dimensions of the world we live in.

At this point, the linear programming algorithm explores the delimited feasible region in a smart way and reports back with the solution. In fact, you don't need to check every point in the delimited area to determine the best problem solution. Imagine the objective function as another line that you represent on the plane (after all, even the objective function is a linear function). You can see that the solution you are looking for is the coordinate points where the feasible area and the objective function line first touch each other (see Figure 19-1). When the objective function line descends from above (arriving from outside the feasible region, where results occur that you can't accept because of the constraints), at a certain point it will touch the area. This contact point is usually a vertex of the area, but it could be an entire side of the polygon (in which case, each point on that side is an optimal solution).

As a practical matter, the simplex algorithm can't make lines visually descend, as in this example. Instead, it walks along the border of the feasible area (by enumerating the vertexes) and tests the resulting objective function values at each vertex until it finds the solution. Consequently, the effective running time depends on the number of vertexes, which for its part depends on the number of constraints and variables involved in the solution. (More variables mean more dimensions and more vertexes.)

Understanding the limitations

As you gain more confidence with linear programming and the problems become more challenging, you require more complex approaches than the basic simplex algorithm presented in this chapter. In fact, the original simplex isn't used anymore because more sophisticated algorithms have replaced it — algorithms that geometrically cut through the interior of the feasible region instead of walking along it. These newer algorithms take a shortcut when the algorithm is clearly looking for the solution at the wrong side of the region.

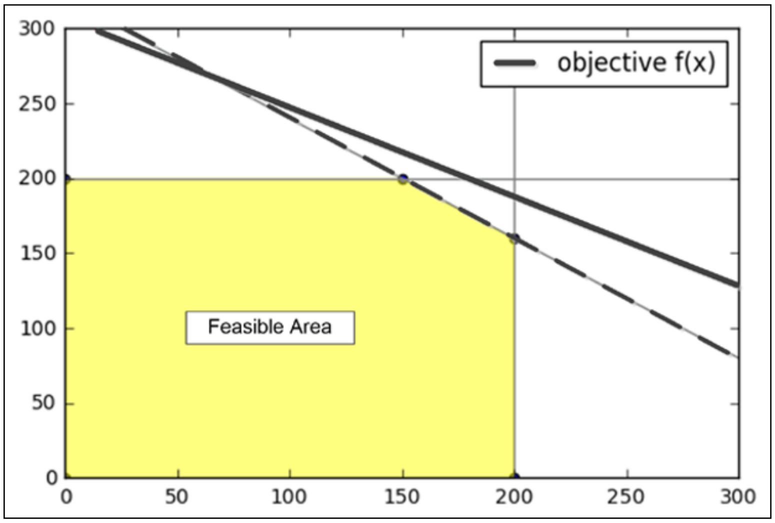


FIGURE 19-1: Looking where the objective function is going to touch the feasible area.

You can also find working with floating-point numbers limiting because many problems require a binary (1/0) or integer answer. (In the two products example, you can't make fractional numbers of the products. The values x and y must be integers.) Moreover, other problems may require using curves, not lines, to represent the problem space and feasible region correctly. You find integer linear programming and nonlinear programming algorithms implemented in commercial software. Just be aware that both integer and nonlinear programming are NP-complete problems and may require as much time as, if not more time than, other algorithms you know.

Using Linear Programming in Practice

The best way to start in linear programming is to use predefined solutions, rather than create custom applications on your own. The first section that follows helps you install a predefined solution used for the examples that follow.

WARNING

When working with a software product, you may find significant differences between open source software and commercial packages. Although open source software offers a wide spectrum of algorithms, performance could be disappointing on large and complex problems. Much art is still involved in implementing linear programming algorithms as part of working software, and you can't expect open source software to run as fast and smoothly as commercial offerings.

Even so, open source provides some nice options for learning linear program. The following sections use an open source Python solution named PuLP that allows you to create linear programming optimizations after defining a cost function and constraints as Python functions. It's mostly a didactic solution, suitable to help you test how linear programming works on some problems and get insight on formulating problems in math terms.

TECHNICAL STUFF

PuLP provides an interface to the underlying solver programs. Python comes with a default, open source, solver program that PuLP helps you access. The performance (speed, accuracy, and scalability) that PuLP provides depends almost entirely on the solver and optimizer that the user chooses. The best solvers are commercial products, such as CPLEX (`https://www.ibm.com/analytics/cplex-optimizer`), XPRESS (`https://www.fico.com/fico-xpress-optimization/docs/latest/overview.html`), and GuRoBi (`https://www.gurobi.com/`), which provide a huge speed advantage when compared to open source solvers.

Setting up PuLP at home

PuLP is a Python open source project created by Jean-Sebastien Roy, later modified and maintained by Stuart Antony Mitchell. The PuLP package helps you define linear programming problems and solve them using the internal solver (which relies on the simplex algorithm). You can also use other solvers that are available on public domain repositories or by paying for a license. The project repository (containing all the source code and many examples) is at `https://github.com/coin-or/pulp`. The complete documentation is located at `https://coin-or.github.io/pulp/`.

PuLP isn't readily available as part of the Anaconda distribution, thus you have to install it yourself. You must use the Anaconda3 (or above) command prompt to install PuLP because the older versions of the Anaconda command prompt won't work. Open a command-line shell, type **pip install pulp**, and press Enter. If you have Internet access, the pip command downloads the PuLP package and installs it in Python. (The version used by the examples in this chapter is PuLP 1.6.1, but later versions should provide the same functionality.) The example will need to operate on some vectors of values, so you also need to have the NumPy available (just type **pip install numpy** if it's not present in your Python environment).

Optimizing production and revenue

The problem in this section is another optimization related to production. You work with two products (because this implies just two variables that you can represent on a bidimensional chart), product A and B, which have to undergo a series of transformations through three stages. Each stage requires a number of operators (the value *n*), which could be workers or robots, and each stage is operative at most for a number of days in the month (represented by the value *t*). Each stage operates differently on each product, requiring a different number of days before completion. For instance, a worker in the first stage (called 'res_1') takes two days to finish product A but three days for product B. Finally, each product has a different profit: product A brings $3,000 USD each and product B $2,500 USD each. The following table summarizes the problem:

Production Stage	Time for Product A per Worker (Days)	Time for Product B per Worker (Days)	Uptime (Days)	Workers
res_1	2	3	30	2
res_2	3	2	30	2
res_3	3	3	22	3

To find the objective function, compute the sum of each product quantity multiplied by its profit. It has to be maximized. Although not stated explicitly by the problem, some constraints exist. First is the fact that uptime limits productivity at each stage. Second is the number of workers. Third is productivity relative to the processed product type. You can restate the problem as the sum of the time used to process each product at each stage, which can't exceed the uptime multiplied by the number of workers available. The number of workers multiplied by the number of working days provides you with the time resources you can use. These resources can't be less than the time it takes to produce all the products you plan to deliver. Here are the resulting formulations, with constraints for each stage:

```
objective = 3000 * qty_A + 2500 * qty_B
   production_rate_A * qty_A + production_rate_B * qty_B
     <=  uptime_days * workers
```

You can express each constraint using the quantity of one product to determine the other (in fact, if you produce A, you can't produce B when A's production leaves no time):

```
qty_B  <= ((uptime_days * workers) -
   (production_rate_A * qty_A) ) / production_rate_B
```

You can record all the values relative to each stage for production_rate_A, production_rate_B, uptime_days, and workers for easier access into a Python dictionary. Keep profits in variables instead. (You can find this code in the A4D2E; 19; Linear Programming.ipynb downloadable source code file; see the Introduction for details.)

```
import numpy as np
import matplotlib.pyplot as plt
import pulp



res_1 = {'A':2, 'B':3, 't':30, 'n':2}
res_2 = {'A':3, 'B':2, 't':30, 'n':2}
res_3 = {'A':3, 'B':3, 't':22, 'n':3}
res = {'res_1':res_1, 'res_2':res_2, 'res_3':res_3}
profit_A = 3000
profit_B = 2500
```

Having framed the problem in a suitable data structure, try to visualize it using the Python plotting functions. Set product A as the abscissa and, because you don't know the solution, represent the production of product A as a vector of quantities ranging from 0 to 30 (quantities can't be negative). As for product B (as seen in the formulations above), derive it from the production remaining after A is done. Formulate three functions, one for each stage, so that as you decide the quantity for A, you get the consequent quantity of B — considering the constraints:

```
a = np.linspace(0, 30, 30)
c1 = ((res['res_1']['t'] * res['res_1']['n'])-
      res['res_1']['A']*a) / res['res_1']['B']
c2 = ((res['res_2']['t'] * res['res_2']['n'])-
      res['res_2']['A']*a) / res['res_2']['B']
c3 = ((res['res_3']['t'] * res['res_3']['n'])-
      res['res_3']['A']*a) / res['res_3']['B']

plt.figure(figsize=(12, 6))
plt.plot(a, c1, label='constrain #1')
plt.plot(a, c2, label='constrain #2')
plt.plot(a, c3, label='constrain #3')

axes = plt.gca()
axes.set_xlim([0,30])
axes.set_ylim([0,30])
plt.xlabel('qty model A')
plt.ylabel('qty model B')

border = np.array((c1,c2,c3)).min(axis=0)

plt.fill_between(a, border, color='yellow', alpha=0.5)
plt.scatter(*zip(*[(0,0), (20,0),
                   (0,20), (16,6), (6,16)]))
plt.legend()
plt.show()
```

The constraints turn into three lines on a chart, as shown in Figure 19-2. The lines intersect among themselves, showing the feasible area. This is the area delimited by the three lines whose A and B values are always inferior or equal compared to the values on any of the constraint lines. (The constraints represent a frontier; you can't have A or B values beyond them.)

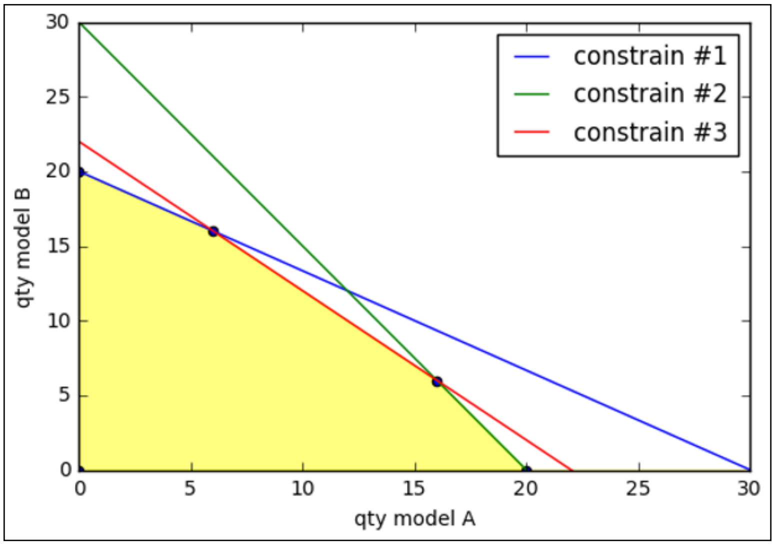


FIGURE 19-2: Wondering which vertex is the right one.

According to the simplex method, the optimal solution is one of the five vertexes of the polygon (which are (0,0), (20,0), (0,20), (16,6), and (6,16)). You can discover which one is the solution by setting the necessary functions from the PuLP package. First, define the problem and call it *model.* By doing so, you determine that it's a maximization problem and that both A and B should be positive:

```
model = pulp.LpProblem("max_profit", pulp.LpMaximize)
A = pulp.LpVariable('A', lowBound=0)
B = pulp.LpVariable('B', lowBound=0)
```

TIP

The PuLP solver can also look for integer solutions, something the original simplex can't do. Just add `cat='Integer'` as a parameter when defining a variable: `A = pulp.LpVariable('A', lowBound=0, cat='Integer')`, and you get only whole numbers as a solution. Be aware that in certain problems, integer number results may prove less optimal than the decimal number results; therefore, use an integer solution only if it makes sense for your problem (for instance, you can't produce a fraction of a product).

Next, add the objective function by summing the sum of the two variables defined by `pulp.LpVariable` and representing the ideal quantities of products A and B, multiplied by each unit profit value:

```
model += profit_A * A + profit_B * B
```

Finally, add the constraints, in exactly the same way as the objective function. You create the formulation by using the appropriate values (taken from the data dictionary) and the predefined A and B variables:

```
model += res['res_1']['A'] * A + res['res_1']['B'
            ] * B <= res['res_1']['t'] * res['res_1']['n']
model += res['res_2']['A'] * A + res['res_2']['B'
            ] * B <= res['res_2']['t'] * res['res_2']['n']
model += res['res_3']['A'] * A + res['res_3']['B'
            ] * B <= res['res_3']['t'] * res['res_3']['n']
```

The model is ready to optimize (it has ingested both the objective function and the constraints). Call the solve method and then check its status. (Sometimes a solution may prove impossible to find or may not be optimal.)

```
model.solve()
print(f"Completion status: {pulp.LpStatus[model.status]}")

Completion status: Optimal
```

Having received confirmation that the optimizer found the optimal solution, you print the related quantities of product A and B:

```
print(f"Production of model A = {A.varValue:0.1f}")
print(f"Production of model B = {B.varValue:0.1f}")

Production of model A = 16.0
Production of model B = 6.0
```

In addition, you print the resulting total profit achievable by this solution.

```
print(f"Maximum profit achieved: {pulp.value(model.
  objective):0.1f}")

Maximum profit achieved: 63000.0
```

IN THIS CHAPTER

- » **Understanding when heuristics are useful to algorithms**
- » **Discovering how pathfinding can be difficult for a robot**
- » **Getting a fast start using the best-first search**
- » **Improving on Dijkstra's algorithm and taking the best heuristic route using A***

Chapter 20 Considering Heuristics

As a concluding algorithm topic, this chapter completes the overview of heuristics started in Chapter 18 that describes heuristics as an effective means of using a local search to navigate neighboring solutions. Chapter 18 defines heuristics as educated guesses about a solution — that is, they are sets of rules of thumb pointing to the desired outcome, thus helping algorithms take the right steps toward it; however, heuristics alone can't tell you exactly how to reach the solution.

The chapter starts by examining the different flavors of heuristics, some of which are quite popular now because of AI and robotics applications: swarm heuristics, metaheuristics; machine learning–based modeling; and heuristic routing. Next, the chapter discusses how heuristics are used by mobile robots to safely and effectively navigate known and unknown territories to accomplish their tasks. All such heuristics are based on distance, and the section "Using distance measures as heuristics" presents how two of the most common distance measures, Euclidean distance and Manhattan distance, are calculated and can help in different problem settings.

The chapter closes by demonstrating two powerful pathfinding algorithms to help robots reach their destinations safely: the *best-first search* algorithm and the *A** (pronounced A-star) algorithm. The A* algorithm is famous because it powered Shakey the robot, as explained in the chapter. Before showing the Python code that explains how the algorithms work, the chapter also discusses how to create a maze in an effectively manner (which is an algorithm in itself) to simulate an environment with some challenges (obstacles) for the heuristic-based pathfinding algorithms to navigate.

REMEMBER

You don't have to type the source code for this chapter manually. In fact, using the downloadable source is a lot easier. You can find the source for this chapter in the `A4D2E; 20; Heuristic Algorithms.ipynb` file of the downloadable source. See the Introduction for details on how to find this source file.

Differentiating Heuristics

The word *heuristic* comes from the ancient Greek *heuriskein,* which meant to invent or discover. Its original meaning underlines the fact that employing heuristics is a practical means of finding a solution that isn't well defined, but that is found through exploration and an intuitive grasp of the general direction to take. Heuristics rely on the lucky guess or a trial-and-error approach of trying different solutions. A *heuristic algorithm,* which is an algorithm powered by heuristics, solves a problem faster and more efficiently in terms of computational resources by sacrificing solution precision and completeness. These solutions are in contrast to most of the algorithms discussed so far in the book, which have certain output guarantees. When a problem becomes too complex, a heuristic algorithm can represent the only way to obtain a solution.

You have to consider that there are shades of heuristics, just as there can be shades to the truth. Heuristics touch the fringes of algorithm development today. The AI revolution builds on the algorithms presented so far in the book that order, arrange, search, and manipulate data inputs. At the top of the hierarchy are heuristic algorithms that power optimization, as well as searches that determine how machines learn from data and become capable of solving problems autonomously from direct intervention.

Heuristics aren't silver bullets; no solution solves every problem. Heuristic algorithms have serious drawbacks, and you need to know when to use them. In addition, heuristics can lead to wrong conclusions for both computers and humans.

In fact, for humans, everyday heuristics that save time can often prove wrong, such as when evaluating a person or situation at first glance in a prejudiced manner. Even more reasoned rules of conduct taken from experience obtain the right solution only under certain circumstances. For instance, consider the habit of hitting electric appliances when they don't work. If the problem is a loose connection, hitting the appliance may prove beneficial by reestablishing the electric connection, but you can’t make hitting appliances a general heuristic because in other cases, that “solution” may prove ineffective or even cause serious damage to the appliance.

Considering the goals of heuristics

Heuristics can speed the long, exhaustive searches performed by other solutions, especially with NP-hard problems that require an exponential number of attempts based on the number of their inputs. For example, consider the traveling salesman problem or variants of the SAT problem (2-SAT appears in Chapter 18), such as the MAX-3SAT (see `https://people.maths.bris.ac.uk/~csxam/bccs/approx.pdf` for additional details). Heuristics determine the search direction using an estimation, which eliminates a large number of the combinations it would have to test otherwise.

Because a heuristic is an estimate or a guess, it can lead the algorithm that relies on it to a wrong conclusion, which could be an inexact solution or just a suboptimal solution. A *suboptimal solution* is a solution that works, but is not the best possible. For example, in a numerical estimation, a heuristic might provide a solution that is a few numbers off the correct answer. This suboptimal solution might be acceptable for many situations, but some situations require an exact solution. Other problems often associated with heuristics are the impossibility of finding all the best solutions as well as the variability of time and computations required to reach a solution. A heuristic provides a perfect match when working with algorithms that would otherwise incur a high cost when interacting with other algorithmic techniques. For instance, you can’t solve certain problems without heuristics because of the poor quality and overwhelming number of data inputs. The traveling salesman problem (TSP) is one of these: If you have to tour a large number of cities, you can’t use any exact method. TSP and other problems exclude any exact solution. AI applications fall into this category because many AI problems, such as recognizing spoken words or the content of an image, aren’t solvable in an exact sequence of steps and rules.

Going from genetic to AI

The Chapter 18 local search discussion presents heuristics such as simulated annealing and Tabu Search. You use these heuristics to help with hill-climbing optimization (an optimization that helps by not getting stuck with solutions that are less than ideal). Apart from these, the family of heuristics comprises many different applications, among which are the following:

- **Swarm intelligence:** A set of heuristics based on the study of the behavior of insect swarms (such as bees, ants, or fireflies) or particles. The method uses multiple attempts to find a solution using agents that interact cooperatively between themselves and the problem setting. An *agent* is an independent computational unit, such as when running several independent instances of the same algorithm, with each one working on a different piece of the problem. Professor Marco Dorigo, one of the top experts and contributors on the study of swarm intelligence algorithms, provides more information on this topic at `https://scholar.google.com/citations?user=PwYT6EMAAAAJ` (which contains a listing of his various works).

- **Metaheuristics:** Heuristics that help you determine (or even generate) the right heuristic for your problem. Among metaheuristics, the most widely known are *genetic algorithms,* inspired by natural evolution. Genetic algorithms start with a pool of possible problem solutions and then generate new solutions using mutation (they add or remove something in the solution) and cross-over (they mix parts of different solutions when a solution is divisible). For instance, in the n-queens problem (Chapter 18), you see that you can split a chessboard vertically into parts because the queens don't move horizontally as part of the problem solution, making it a problem suitable for cross-over. When the pool is large enough, genetic algorithms select the surviving solutions by ruling out those that don't work or lack promise. The selected pool then undergoes another iteration of mutation, cross-over, and selection. After enough time and iterations, genetic algorithms can find solutions that perform better and are completely different from the initial ones.
- **Machine learning:** Approaches such as neuro-fuzzy systems, support vector machines, and neural networks are the foundation of how a computer learns to estimate and classify from training examples that are provided as part of sets of data. Similarly to how a child learns by experience, machine learning algorithms determine how to deliver the most plausible answer without using precise rules and detailed rules of conduct. (See *Machine Learning For Dummies,* 2nd Edition, by John Paul Mueller and Luca Massaron [Wiley], for details on how machine learning works.)
- **Heuristic routing:** A set of heuristics that helps robots (but is also found in network telecommunications and transportation logistics) to choose the best path to avoid obstacles when moving around.

Routing Robots Using Heuristics

Guiding a robot in an unknown environment means avoiding obstacles and finding a way to reach a specific target. It's both a fundamental and challenging task in artificial intelligence. Robots can rely on different sensors such as *laser rangefinder*, *lidar* (devices that allow you to determine the distance to an object by means of a laser ray), or *sonar arrays* (devices that use sounds to see their environment) to navigate their surroundings. Yet, the sophistication of the hardware used to equip robots doesn't matter; robots still need proper algorithms to:

- Find the shortest path to a destination (or at least a reasonably short one)
- Avoid obstacles on the way
- Perform custom behaviors such as minimizing turning or braking

A *pathfinding* (also called *path planning* or simply *pathing*) algorithm helps a robot start in one location and reach a goal using the shortest path between the two, anticipating and avoiding obstacles along the way. (It isn't enough to react after hitting a wall.) Pathfinding is also useful when moving any other device to a target in space, even a virtual one, such as in a video game or the pages on websites.

REMEMBER

Routing autonomously is a key capability of self-driving cars (SDC), which are vehicles that can sense the road environment and drive to the destination without any human intervention. (You still need to tell the car where to go; it can't read minds.) This recent article from *Automotive World Magazine* offers a good overview about the developments and expectations for self-driving cars: `https://www.automotiveworld.com/articles/the-future-of-driving-what-to-expect-in-2021/`.

Scouting in unknown territories

Pathfinding algorithms accomplish all the previously discussed tasks to achieve shortest routing, obstacle avoidance, and other desired behaviors. Algorithms work by using basic schematic maps of their surroundings. These maps are of two kinds:

- **Topological maps:** Simplified diagrams that remove every unnecessary detail. The maps retain key landmarks, correct directions, and some scale proportions for distances. Real-life examples of topological maps include subway maps of Tokyo (`https://www.tokyometro.jp/en/subwaymap/`) and London (`https://tfl.gov.uk/maps/track/tube`).
- **Occupancy grid maps:** These maps divide the surroundings into small, empty squares or hexagons, filling them in when the robot's sensors find an obstacle on the spot they represent. You can see an example of such a map at the Czech Technical University in Prague: `http://cmp.felk.cvut.cz/cmp/demos/Omni/mobil/`. In addition, check out the videos showing how a robot builds and visualizes such a map at `https://www.youtube.com/watch?v=zjl7NmutMIc` and `https://www.youtube.com/watch?v=RhPlzIyTT58`.

You can visualize both topological and occupancy grid maps as graphic diagrams. However, they're best understood by algorithms when rendered into an appropriate data structure. The best data structure for this purpose is the graph because vertexes can easily represent squares, hexagons, landmarks, and waypoints. Edges can connect vertexes in the same way that roads, passages, and paths do.

REMEMBER

Your GPS navigation device operates using graphs. Underlying the continuous, detailed, colorful map that the device displays on screen, road maps are elaborated behind the scenes as sets of vertexes and edges traversed by algorithms helping you find the way while avoiding traffic jams.

Representing the robot's territory as a graph re-introduces problems discussed in Chapter 9, which examines how to travel from one vertex to another using the shortest path. The shortest path can be the path that touches the fewest vertexes or the path that costs less (given the sum of the cost of the crossed edge weights, which may represent the length of the edge or some other cost). As when driving your car, you choose a route based not only on the distance driven to reach your destination but also on traffic (roads crowded with traffic or blocked by traffic jams), road conditions, and speed limits that may influence the quality of your journey.

When finding the shortest path to a destination in a graph, the simplest and most basic algorithms in graph theory are depth-first search and Dijkstra's algorithm (described in Chapter 9). Depth-first search explores the graph by going as far as possible from the start and then retracing its steps to explore other paths until it finds the destination. Dijkstra's algorithm explores the graph in a smart and greedy way, considering only the shortest paths. Despite their simplicity, both algorithms are extremely effective when evaluating a simple graph, as in a bird's-eye view, with complete knowledge of the directions you must take to reach the destination and little cost in evaluating the various possible paths.

The situation with a robot is slightly different because it can't perceive all the possible paths at one time, being limited in both visibility and range of sight (obstacles may hide the path or the target may be too far). A robot discovers its environment as it moves and, at best, can assess the distance and direction of its final destination. It's like solving a maze, though not as when playing in a puzzle maze but more akin to immersion in a hedge maze, where you can feel the direction you are taking or you can spot the destination in the distance.

TIP

Hedge mazes are found everywhere in the world. Some of the most famous were built in Europe from the mid-16th century to eighteenth century. In a hedge maze, you can't see where you're going because the hedges are too high. You can perceive direction (if you can see the sun) and even spot the target (see `https://www.venetoinside.com/hidden-treasures/post/maze-of-villa-pisani-in-stra-venice/` as an example). There are also famous hedge mazes in films such as *The Shining* by Stanley Kubrick and in *Harry Potter and the Goblet of Fire*.

Using distance measures as heuristics

When you can't solve real-life problems in a precise algorithmic way because their input is confused, missing, or unstable, using heuristics can help. When performing path finding using coordinates in a Cartesian plane (flat maps that rely on a set of horizontal and vertical coordinates), two simple measures can provide the distances between two points in that plane: the Euclidean distance and the Manhattan distance.

People commonly use the Euclidean distance because it derives from the Pythagorean Theorem on triangles and represents the shortest distance between two points. If you want to know the distance in line of sight between two points in a plane, say, A and B, and you know their coordinates, you can pretend they're the extremes of the hypotenuse (the longest side in a right triangle). As depicted in Figure 20-1, you calculate distance based on the length of the other two sides by creating a third point, C, whose horizontal coordinate is derived from B and whose vertical coordinate is from A.

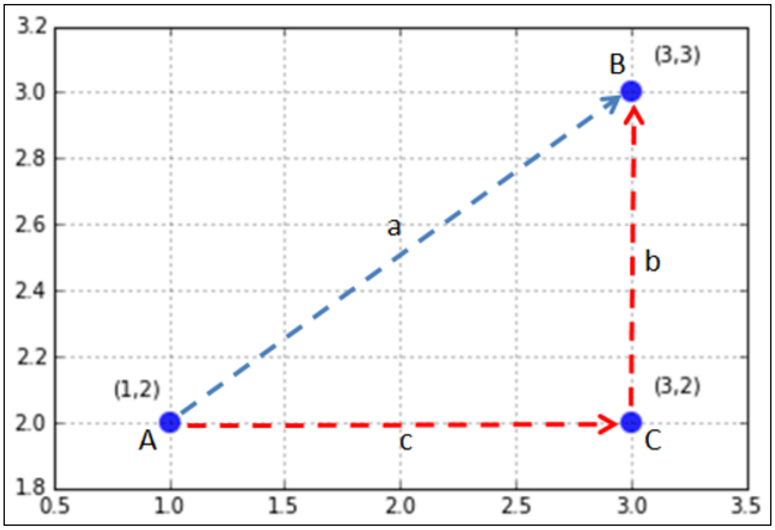


FIGURE 20-1: A and B are points on a map's coordinates.

This process translates into taking the difference between the horizontal and vertical coordinates of your two points, squaring both the differences (so that they both become positive), sum them, and finally taking the square root of the result. In this example, going from A to B uses coordinates of (1,2) and (3,3):

```
sqrt((1-3)² + (2-3)²) = sqrt(2²+1²) = sqrt(5) = 2.236
```

REMEMBER

You actually can't measure distances on the Earth's surface exactly using the Euclidean distance because its surface isn't flat but is instead near spherical. As the distances between points you measure on the Earth's surface increase, the Euclidean distance underestimation will also increase. Measures that are more appropriate when long distances are involved are the haversine distance based on latitude and longitude coordinates (see `https://www.igismap.com/haversine-formula-calculate-geographic-distance-earth/`) or the more exact Vincenty distance (see `https://metacpan.org/pod/GIS::Distance::Vincenty`).

The Manhattan distance works differently. You begin by summing the lengths of the sides b and c, which equates summing the absolute value of the differences between the horizontal and vertical coordinates of the points A and B.

```
|(1-3)| + |(2-3)| = 2 + 1 = 3
```

The Euclidean distance marks the shortest route, and the Manhattan distance provides the longest yet most plausible route if you expect obstacles when taking a direct route. In fact, the movement represents the trajectory of a taxi in Manhattan (hence the name), moving along a city block to reach its destination (taking the short route through buildings would never work). Other names for this approach are the city block distance or the taxicab distance. Consequently, if you have to move from A to B but you don't know whether you'll find obstacles between them, taking a detour through point C is a good heuristic because that's the distance you expect at worst.

Explaining Path Finding Algorithms

This last part of the chapter concentrates on explaining two algorithms, best-first search and A* (read as *A-star*), both based on heuristics. The following sections demonstrate that both of these algorithms provide a fast solution to a maze problem representing a topological or occupancy grid map that's represented as a graph. Both algorithms are widely used in robotics and video gaming.

Creating a maze

A topological or occupancy grid map resembles a hedge maze, as mentioned previously, especially if obstacles exist between the start and the end of the route.

There are specialized algorithms for both creating and processing mazes, most notably the Wall Follower (known since antiquity: You place your hand on a wall and never pull it away until you get out of the maze) or the Pledge algorithm. (Read more about the seven maze classifications at `http://www.astrolog.org/labyrnth/algrithm.htm`.) However, pathfinding is fundamentally different from maze solving because in pathfinding, you know where the target should be, whereas maze-solving algorithms try to solve the problem in complete ignorance of where the exit is.

Consequently, the procedure for simulating a maze of obstacles that a robot has to navigate takes a different and simpler approach. Instead of creating a riddle of obstacles, you create a graph of vertexes arranged in a grid (resembling a map) and randomly remove connections to simulate the presence of obstacles. The graph is undirected (you can traverse each edge in both directions) and weighted because it takes time to move from one vertex to another. In particular, it takes longer to move diagonally than t upward/downward or left/right.

The first step is to import the necessary Python packages. The code defines the Euclidean and the Manhattan distance functions next. (You can find this code in the `A4D2E; 20; Heuristic Algorithms.ipynb` downloadable source code file; see the Introduction for details.)

```
import string
import networkx as nx
import matplotlib.pyplot as plt
import random

def euclidean_dist(a, b, coord):
    (x1, y1) = coord[a]
    (x2, y2) = coord[b]
    return ((x1 - x2)**2 + (y1 - y2)**2)**0.5

def manhattan_dist(a, b, coord):
    (x1, y1) = coord[a]
    (x2, y2) = coord[b]
    return abs(x1 - x2) + abs(y1 - y2)

def non_informative(a,b):
    return 0

def ravel(listsoflists):
    return [item for elem in listsoflists for item in elem]
```

The next step creates a function to generate random mazes. It's based on an integer number seed of your choice that allows you to recreate the same maze every time you provide the same number. Otherwise, maze generation is completely random. There is also a general function, `node_neighbors()`, to create because it provides the directions to take from a vertex in a graph, and it makes the code creating the maze more readable.

```
def node_neighbors(graph, node):
    return [exit for _,
            exit in graph.edges(node) if exit!=node]

def create_maze(seed=2, drawing=True):
    random.seed(seed)
    letters = [l for l in string.ascii_uppercase[:25]]
    checkboard = [letters[i:i+5]
                  for i in range(0, len(letters), 5)]
    Graph = nx.Graph()
    for j, node in enumerate(letters):
        Graph.add_nodes_from(node)
        x, y = j // 5, j % 5
        x_min = max(0, x-1)
        x_max = min(4, x+1)+1
        y_min = max(0, y-1)
        y_max = min(4, y+1)+1
        adjacent_nodes = ravel(
            [row[y_min:y_max]
             for row in checkboard[x_min:x_max]])
        exits = random.sample(adjacent_nodes,
                              k=random.randint(1, 4))
        for exit in exits:
            if exit not in node_neighbors(Graph, node):
                Graph.add_edge(node, exit)
    spacing = [0.0, 0.2, 0.4, 0.6, 0.8]
    coordinates = [[x, y] for x in spacing \
                   for y in spacing]
    position  = {l:c for l,c in zip(letters, coordinates)}

    for node in Graph.nodes:
        for exit in node_neighbors(Graph, node):
            length = int(round(
                    euclidean_dist(
                        node, exit, position)*10,0))
            Graph.add_edge(node,exit,weight=length)
    if drawing:
        draw_params = {'with_labels':True,
                       'node_color':'skyblue',
                       'node_size':700, 'width':2,
                       'font_size':14}
        nx.draw(Graph, position, **draw_params)
        labels = nx.get_edge_attributes(Graph,'weight')
        nx.draw_networkx_edge_labels(Graph, position,
                                     edge_labels=labels)
        plt.show()

    return Graph, position
```

The functions return a NetworkX graph (`Graph`), a favorite data structure for representing graphs, which contains 25 vertexes (or nodes, if you prefer) and a Cartesian map of points (position). The vertexes are placed on a 5-x-5 grid, as shown in Figure 20-2. The output also applies distance functions and calculates the position of vertexes.

```
graph, coordinates = create_maze(seed=7)
```

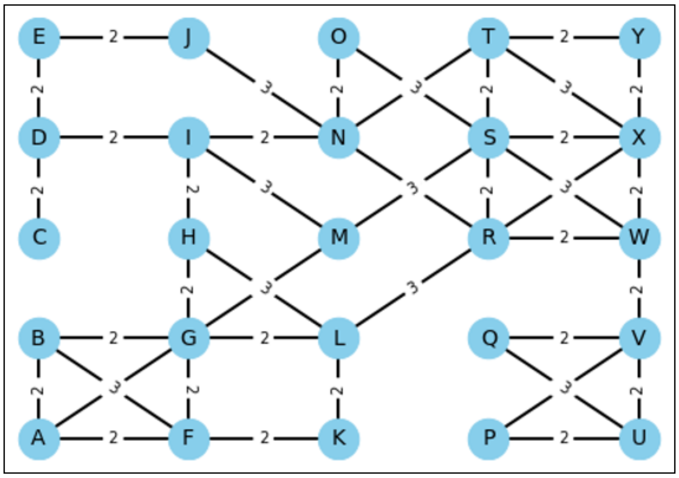


FIGURE 20-2: A maze representing a topological map with obstacles.

TIP

In the maze generated by a seed value of 7, every vertex connects with the others. Because the generation process is random, some maps may contain disconnected vertexes, which precludes going between the disconnected vertexes. To see how this works, try a seed value of 6. This actually happens in reality; for example, sometimes a robot can't reach a particular destination because it's surrounded by obstacles.

Looking for a quick best-first route

The depth-first search algorithm explores the graph by moving from vertex to vertex and adding directions to a stack data structure. When it's time to move, the algorithm moves to the first direction found on the stack. It's like moving through a maze of rooms by taking the first exit you see. Most probably, you arrive at a dead end, which isn't your destination. You then retrace your steps to the previously visited rooms to see whether you encounter another exit, but it takes a long time when you're far from your target.

Heuristics can greatly help with the repetition created by a depth-first search strategy. Using heuristics can tell you whether you're getting nearer or farther from your target. This combination is called the *best-first search* algorithm (BFS). In this case, the *best* in the name hints at the fact that, as you explore the graph, you don't take the first edge in sight. Rather you evaluate which edge to take based on the one that should take you closer to your desired outcome based on the heuristic. This behavior resembles greedy optimization (the best first), and some people also call this algorithm *greedy best-first search*. BFS will probably miss the target at first, but because of heuristics, it won't end up far from target and will retrace less than it would if using depth-first search alone.

REMEMBER

You use the BFS algorithm principally in web crawlers that look for certain information on the web. In fact, BFS allows a software agent to move in a mostly unknown graph, using heuristics to detect how closely the content of the next page resembles the initial one (to explore for better content). The algorithm is also widely used in video games, helping characters controlled by the computer move in search of enemies and bounties, thereby resembling a greedy, target-oriented behavior.

Demonstrating BFS in Python using the previously built maze illustrates how a robot can move in a space by seeing it as a graph. The following code shows some general functions, which are also used for the next algorithm in this section. The `graph_weight()` function determines the cost of going from one vertex to another. Weight represents distance or time.

```
def graph_weight(graph, a, b):
    return graph.edges[(a, b)]['weight']
```

The path-planning algorithm simulates robot movement in a graph. When it finds a solution, the plan translates into movement. Therefore, path-planning algorithms provide an output telling you how to best move from one vertex to another; you still need a function to translate the information and determine the route to take and calculate trip length. The functions `reconstruct_path()` and `compute_path()` provide the plan in terms of steps and expected cost when given the result from the path-planning algorithm.

```
def reconstruct_path(connections, start, goal):
    if goal in connections:
        current = goal
        path = [current]
        while current != start:
            current = connections[current]
            path.append(current)
        return path[::-1]

def compute_path_dist(path, graph):
    if path:
        run = 0
        for step in range(len(path)-1):
            A = path[step]
            B = path[step+1]
            run += graph_weight(graph, A, B)
        return run
    else:
        return 0
```

Having prepared all the basic functions, the example creates a maze using a seed value of 30. This maze presents a few main routes going from vertex A to vertex Y because there are some obstacles in the middle of the map (as shown in Figure 20-3). There is also a dead end on the way (vertex I).

```
graph, coordinates = create_maze(seed=30)
start = 'A'
goal  = 'Y'
scoring = manhattan_dist
```

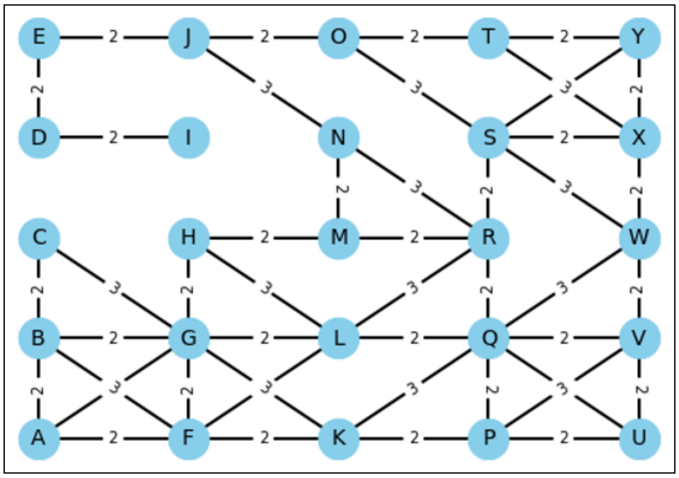


FIGURE 20-3: An intricate maze to be solved by heuristics.

The BFS implementation is a bit more complex than the depth-first search code found in Chapter 9. It uses two lists: one to hold the never-visited vertexes (called open_list), and another to hold the visited ones (closed_list). The open_list list acts as a priority queue, one in which a priority determines the first element to extract. In this case, the heuristic provides the priority, thus the priority queue provides a direction that's closer to the target. The Manhattan distance heuristic works best because of the obstacles obstructing the way to the destination:

```
# Best-first search
path = {}
open_list = set(graph.nodes())
closed_list = {start: manhattan_dist(start, goal,
                                     coordinates)}

while open_list:

    candidates = open_list&closed_list.keys()
    if len(candidates)==0:
        print ("Cannot find a way to the goal %s" % goal)
        break
    frontier = [(closed_list[node],
                 node) for node in candidates]
    score, min_node =sorted(frontier)[0]

    if min_node==goal:
        print ("Arrived at final vertex %s" % goal)
        print ('Unvisited vertices: %i' % (len(
                  open_list)-1))
        break
    else:
        print("Processing vertex %s, " % min_node, end="")

    open_list = open_list.difference(min_node)
    neighbors = node_neighbors(graph, min_node)
    to_be_visited = list(neighbors-closed_list.keys())

    if len(to_be_visited) == 0:
        print ("found no exit, retracing to %s"
               % path[min_node])
    else:
        print ("discovered %s" % str(to_be_visited))

    for node in neighbors:
        if node not in closed_list:
            closed_list[node] = scoring(node, goal,
                                        coordinates)
            path[node] = min_node

print ('\nBest path is:', reconstruct_path(
        path, start, goal))
print ('Length of path: %i' % compute_path_dist(
        reconstruct_path(path, start, goal), graph))
```

The verbose output from the example tells you how the algorithm works:

```
Processing vertex A, discovered ['F', 'B', 'G']
Processing vertex G, discovered ['H', 'C', 'L', 'K']
Processing vertex H, discovered ['M']
Processing vertex M, discovered ['R', 'N']
Processing vertex N, discovered ['J']
Processing vertex J, discovered ['E', 'O']
Processing vertex O, discovered ['S', 'T']
Processing vertex T, discovered ['Y', 'X']
Arrived at final vertex Y
Unvisited vertices: 16

Best path is: ['A', 'G', 'H', 'M', 'N', 'J', 'O', 'T', 'Y']
Length of path: 18
```

BFS keeps moving until it runs out of vertexes to explore. When it exhausts the vertexes without reaching the target, the code tells you that it can't reach the target and the robot won't budge. When the code does find the destination, it stops processing vertexes, even if `open_list` still contains vertexes, which saves time.

Finding a dead end, such as ending up in vertex `I`, means looking for a previously unused route. The best alternative immediately pops up thanks to the priority queue, and the algorithm takes it. In this example, BFS efficiently ignores 16 vertexes and takes the upward route in the map, completing its journey from A to Y in 18 steps.

TIP

You can test other mazes by setting a different seed number and comparing the BFS results with the A* algorithm described in the next section. You'll find that sometimes BFS is both fast and accurate in choosing the best way, and sometimes it's not. If you need a robot that searches quickly, BFS is the best choice.

Going heuristically around by A*

The A* algorithm speedily produces best shortest paths in a graph by combining the Dijikstra greedy search discussed in Chapter 9 with an early stop (the algorithm stops when it reaches its destination vertex) and a heuristic estimate (usually based on the Manhattan distance) that hints at the graph area to explore first. A* was developed at the Artificial Intelligence Center of Stanford Research Institute (now called SRI International) in 1968 as part of the Shakey the robot project. Shakey was the first mobile robot to autonomously decide how to go somewhere, although it was limited to wandering around a few rooms in the labs. (If you watch the video at `https://www.youtube.com/watch?v=qXdn6ynwpiI`, you see that it's the person filming who's shaky, not the robot. But, as always, it's easier to blame the robot.) Shakey was a milestone robotic implementation that demonstrated how it was technologically possible to build a mobile robot operating without human supervision at the end of the 1960s.

To render Shakey fully autonomous, its developers came up with the A* algorithm, the Hough transform (an image-processing transformation to detect the edges of an object), and the visibility graph method (a way to represent a path as a graph). The article at `http://www.ai.sri.com/shakey/` describes Shakey in more detail and even shows it in action. The A* algorithm is currently the best available algorithm when you're looking for the shortest route in a graph and you must deal with partial information and expectations (as captured by the heuristic function guiding the search). A* is able to

- **Find the shortest path solution every time:** The algorithm can do this if such a path exists and if A* is properly informed by the heuristic estimate. A* is powered by the Dijkstra algorithm, which guarantees always finding the best solution.
- **Find the solution faster than any other algorithm:** A* can do this if given access to a fair heuristic — one that provides the right directions to reach the target proximity in a similar, though even smarter, way as BFS.
- **Computes weights when traversing edges:** Weights account for the cost of moving in a certain direction. For example, turning may take longer than going straight, as in the case of Shakey the robot.

REMEMBER

A proper, fair, *admissible* heuristic provides useful information to A* about the distance to the target by never overestimating the cost of reaching it. Moreover, A* makes greater use of its heuristic than BFS, therefore the heuristic must perform calculations quickly or the overall processing time will be too long.

The Python implementation in this example uses the same code and data structures used for BFS, but there are differences between them. The main differences are that as the algorithm proceeds, it updates the cost of reaching from the start vertex to each of the explored vertexes. In addition, when it decides on a route, A* considers the shortest path from the start to the target, passing by the current vertex, because it sums the estimate from the heuristic with the cost of the path computed to the current vertex. This process allows the algorithm to perform more computations than BFS when the heuristic is a proper estimate and to determine the best path possible.

TIP

Finding the shortest path possible in cost terms is the core Dijkstra algorithm function. A* is simply a Dijkstra algorithm in which the cost of reaching a vertex is enhanced by the heuristic of the expected distance to the target. Chapter 9 describes the Dijkstra algorithm in detail. Revisiting the Chapter 9 discussion will help you better understand how A* operates in leveraging heuristics.

```
# A*
open_list = set(graph.nodes())
closed_list = {start: manhattan_dist(
        start, goal, coordinates)}
visited = {start: 0}
path = {}

while open_list:

    candidates = open_list&closed_list.keys()
    if len(candidates)==0:
        print ("Cannot find a way to the goal %s" % goal)
        break
    frontier = [(closed_list[node],
                 node) for node in candidates]
    score, min_node =sorted(frontier)[0]

    if min_node==goal:
        print ("Arrived at final vertex %s" % goal)
        print ('Unvisited vertices: %i' % (len(
                open_list)-1))
        break
    else:
        print("Processing vertex %s, " % min_node, end="")

    open_list = open_list.difference(min_node)
    current_weight = visited[min_node]
    neighbors = node_neighbors(graph, min_node)
    to_be_visited = list(neighbors-visited.keys())
    for node in neighbors:
        new_weight = current_weight + graph_weight(
                     graph, min_node, node)
        if node not in visited or \
        new_weight < visited[node]:
            visited[node] = new_weight
            closed_list[node] = manhattan_dist(node, goal,
                        coordinates) + new_weight
            path[node] = min_node

    if to_be_visited:
        print ("discovered %s" % to_be_visited)
    else:
        print ("getting back to open list")

print ('\nBest path is:', reconstruct_path(
        path, start, goal))
print ('Length of path: %i' % compute_path_dist(
        reconstruct_path(path, start, goal), graph))
```

When the A* has completed analyzing the maze, it outputs a best path that's shorter than the BFS solution:

```
Processing vertex A, discovered ['F', 'B', 'G']
Processing vertex B, discovered ['C']
Processing vertex F, discovered ['L', 'K']
Processing vertex G, discovered ['H']
Processing vertex C, getting back to open list
Processing vertex K, discovered ['Q', 'P']
Processing vertex H, discovered ['M']
Processing vertex L, discovered ['R']
Processing vertex P, discovered ['U', 'V']
Processing vertex M, discovered ['N']
Processing vertex Q, discovered ['W']
Processing vertex R, discovered ['S']
Processing vertex U, getting back to open list
Processing vertex N, discovered ['J']
Processing vertex V, getting back to open list
Processing vertex S, discovered ['Y', 'X', 'O']
Processing vertex W, getting back to open list
Processing vertex X, discovered ['T']
Processing vertex J, discovered ['E']
Arrived at final vertex Y
Unvisited vertices: 5

Best path is: ['A', 'F', 'L', 'R', 'S', 'Y']
Length of path: 13
```

This solution comes at a cost: A* explores almost all the present vertexes, leaving just five vertexes unconsidered. As with Dijkstra, its worst running time is `O(v²)`, where `v` is the number of vertexes in the graph; or `O(e + v*log(v))`, where `e` is the number of edges, when using min-priority queues, an efficient data structure when you need to obtain the minimum value for a long list. The A* algorithm is not different in its worst running time than Dijkstra's, though on average, it performs better on large graphs because it first finds the target vertex when correctly guided by the heuristic measurement (in the case of a routing robot, the Manhattan distance).

6

The Part of Tens

IN THIS PART . . .

Developing advanced data processing approaches

Relying more heavily on automation and automatic responses

Performing data manipulation tasks faster

Ensuring algorithms behave as needed and desired

IN THIS CHAPTER

» Considering sort and search routines

» Using random numbers

» Making data smaller

» Ensuring that data remains secret, and more . . .

Chapter 21
Ten Algorithms That Are Changing the World

It's hard to imagine an algorithm doing much of anything physical, much less changing the world. However, algorithms today appear everywhere, and you might not even realize just how much effect they have on your life.

Most people realize that online stores and other sales venues rely on algorithms to determine which add-on products to suggest based on previous purchases. However, most people are unaware of the uses of algorithms in medicine, many of which help a doctor decide what diagnosis to provide.

Algorithms appear in the oddest places. The timing of traffic lights often depends on the calculations of algorithms. Algorithms help your smartphone talk to you, and algorithms make your television do more than any television has done in the past. Consequently, it's not all that impossible to believe that algorithms are poised to change the world. This chapter highlights ten of them.

REMEMBER

For algorithm purists, you can say that the algorithm has changed the world throughout the centuries, so nothing has really changed for thousands of years. The Babylonians used algorithms to perform factorization and find square roots as early as 1800 to 1600 BCE (`https://www.historyofinformation.com/detail.php?entryid=4379`). Al-Khawarizmi described algorithms to solve both linear and quadratic equations around 820 AD (`https://www.newscientist.com/people/muhammad-ibn-musa-al-khwarizmi/`). This chapter focuses on computer-based algorithms, but algorithms have been around for a long time.

Using Sort Routines

Without ordered data, most of the world would come to a stop. To use data, you must be able to find it. You can find hundreds of sort algorithms explained on sites such as `https://betterexplained.com/articles/sorting-algorithms/` and as part of this book (see Chapter 7).

However, the three most common sort routines are merge sort, quick sort, and heapsort because of the superior speed they provide (see the time comparisons at `https://www.cprogramming.com/tutorial/computersciencetheory/sortcomp.html`). The sort routine that works best for your application depends on the following:

- What you expect the application to do
- The kind of data you work with
- The computing resources you have available

The point is that the capability to sort data into whatever form an application needs to accomplish a task makes the world run, and this capability is changing how the world works.

Some businesses today thrive as a result of using sorting algorithms. For example, consider the fact that Google exists because it helps people find things, and this ability resides substantially in the capability to sort data to make it readily accessible. Consider just how hard it would be to find an item on Amazon without the sort routine. Even that recipe application on your computer at home relies heavily on sort routines to keep the data it contains in order. In fact, it probably wouldn't be too much of a stretch to say that any substantial application relies heavily on sort routines.

Looking for Things with Search Routines

As with sort routines, search routines appear in nearly every application of any size today. The applications appear everywhere, even in places that you might not think too much about, such as your car. Finding information quickly is an essential part of daily life. For example, imagine being late for an appointment and suddenly discovering that your GPS can't find the address you need. As with sort routines, search routines come in all shapes and sizes, and you can find them described on sites such as `https://tekmarathon.com/2012/10/05/best-searching-algorithm-2/` and `https://www.geeksforgeeks.org/searching-algorithms/`. In fact, if anything, there are more search routines than sort routines because search requirements are often more strenuous and complex. You find a lot of search routines discussed in this book as well (see Chapter 7).

Shaking Things Up with Random Numbers

All sorts of things would be a lot less fun without randomness. For example, imagine starting Solitaire and seeing precisely the same game every time you start it. No one would play such a game. Consequently, random number generation is an essential part of the gaming experience. In fact, as expressed in a number of chapters in this book, some algorithms actually require some level of randomness to work properly (see the "Considering why randomization is needed" section of Chapter 17 as an example). You also find that testing works better when using random values in some cases (see the "Choosing a particular kind of compression" section of Chapter 14 as an example).

REMEMBER

The numbers that you obtain from an algorithm are usually from Pseudo-Random Number Generators (PRNGs), which means that you can potentially predict the next number in a series by knowing the algorithm and the seed value used to generate the number. That's why this information is so closely guarded. It's possible to install hardware on a computer to create a True Random Number Generator (TRNG), as described in the article "Generating Random Numbers Is a Lot Harder Than You Think" at `https://betterprogramming.pub/generating-random-numbers-is-a-lot-harder-than-you-think-b121c3e75d08`. Unfortunately, TRNGs come with some problems, like creating insecure cryptography in some cases. So, the article also describes the Cryptographically-Secure Pseudo-random Number Generator (CSPRNG). In other words, you may encounter all sorts of methods of creating random numbers, each with their own target use.

TECHNICAL STUFF

Computer hardware-based methods of creating random numbers can rely on atmospheric noise or temperature changes (see `https://engineering.mit.edu/engage/ask-an-engineer/can-a-computer-generate-a-truly-random-number/` for details). In fact, you can get a hardware-based random number solution, such as TrueRNG (`https://www.amazon.com/exec/obidos/ASIN/B01KR2JHTA/datacservip0f-20/`) and ChaosKey (`https://altusmetrum.org/ChaosKey/`) (schematic only) and plug it into your USB slot to generate what likely are true random numbers. The interesting thing about the ChaosKey site is that it provides you with a schematic to show how it collects random noise and changes it into a random number.

Performing Data Compression

Chapter 14 discusses data compression techniques and uses the kind of compression that you normally find used for files. However, data compression affects every aspect of computing today. For example, most graphics, video, and audio files rely on data compression. Without data compression, you couldn't possibly obtain the required level of throughput to make tasks such as streamed movies work.

However, data compression finds even more uses than you might expect. Just about every Database Management System (DBMS) relies on data compression to make data fit in a reasonable amount of space on disk. Cloud computing wouldn't work without data compression because downloading items from the cloud to local machines would take too long. Even web pages often rely on data compression to get information from one place to another.

Keeping Data Secret

The concept of keeping data secret isn't new. In fact, it's one of the oldest reasons to use an algorithm of some sort. The word cryptography actually comes from two Greek words: *kryptós* (hidden or secret) and *graphein* (writing). In fact, the Greeks were probably the first users of cryptography (see `https://www.britannica.com/topic/cipher`), and ancient texts report that Julius Caesar used encrypted missives to communicate with his generals. The point is, keeping data secret is one of the longest running battles in history. The moment one party finds a way to keep a secret, someone else finds a way to make the secret public by breaking the cryptography. General uses for computer-driven cryptography today include:

- **Confidentiality:** Ensuring that no one can see information exchanged between two parties
- **Data integrity:** Reducing the likelihood that someone or something can change the content of data passed between two parties
- **Authentication:** Determining the identity of one or more parties
- **Nonrepudiation:** Reducing the ability of a party to say they didn't commit a particular act

TIP

Besides keeping a secret when using computers, the history of computer-based cryptographic algorithms is long and interesting. The "Hiding Your Secrets with Cryptography" section of Chapter 14 offers a good overview of cryptographic techniques. You can also find a list of commonly used algorithms (both present and historical) at https://www.axel.org/2021/05/28/history-of-encryption/ and https://komodoplatform.com/en/academy/history-of-cryptology/. The guide at https://www.owasp.org/index.php/Guide_to_Cryptography provides additional details on how cryptography works.

Changing the Data Domain

The Fourier Transform and Fast Fourier Transform (FFT) make a huge difference in how applications perceive data. These two algorithms transform data from the frequency domain (how fast a signal oscillates) to the time domain (the time differential between signal changes). In fact, it's impossible to get any sort of computer hardware degree without having spent time working with these two algorithms extensively. Timing is everything.

REMEMBER

By knowing how often something changes, you can figure out the time interval between changes and therefore know how long you have to perform a task before a change in state requires that you do something else. These algorithms commonly see use in filters of all sorts. Without the filtering effects of these algorithms, reproducing video and audio faithfully through a streamed connection would be impossible. All these applications sound rather advanced, and they are, but some amazing tutorials give you a better sense of how these algorithms work (see the tutorial at https://w.astro.berkeley.edu/~jrg/ngst/fft/fft.html as an example). The tutorial at https://betterexplained.com/articles/an-interactive-guide-to-the-fourier-transform/ is possibly the most interesting and especially entertaining if you like smoothies.

Analyzing Links

The capability to analyze relationships is something that has made modern computing unique. The capability to first create a representation of these relationships and then analyze them is the subject of Part 3 of this book. The whole idea of the web, in fact, is to create connections, and connectivity was a consideration at the start of what has become a worldwide phenomenon. Without the capability to analyze and utilize links, applications such as databases and email wouldn't work. You couldn't communicate well with friends on Facebook.

As the web has matured and people have become more in tune with devices that make connectivity both simpler and ubiquitous, applications such as Facebook and sales sites such as Amazon have made greater use of link analysis to do things like sell you more products. Of course, some of this connectivity has a negative outcome (see `https://www.pcmag.com/opinions/facebook-a-tool-for-evil` and `https://www.minotdailynews.com/opinion/national-columnists/2021/10/facebook-the-new-evil-empire/` as examples), but for the most part, link analysis does make it possible for people to remain better informed and in better contact with the world around them.

Of course, link analysis does more than inform in a connected sort of way. Consider the use of link analysis to provide driving directions or to find casual links between human activity and disease. Link analysis enables you to see the connection between things that you might not ordinarily consider but that do have an impact on your daily life. Because of link analysis, you might live longer because a doctor can advise you on which habits to change to correct issues that could become problems later. The point is that connections exist everywhere, and link analysis offers a method to determine where these connections exist and whether they're actually important.

Spotting Data Patterns

Data doesn't exist in a vacuum. All sorts of factors affect data, including biases that color how humans perceive data. Chapter 10 discusses how data tends to cluster in certain environments and how analysis of these clusters can tell you all sorts of things about the data.

TIP

Pattern analysis is at the forefront of some of the more amazing uses of computers today. For example, the Viola–Jones object detection framework (see `https://towardsdatascience.com/understanding-face-detection-with-the-viola-jones-object-detection-framework-c55cc2a9da14` for details) makes real-time facial recognition possible. This algorithm could enable people to create better security in places like airports where nefarious individuals currently ply their trade. Similar algorithms could help your doctor detect cancers of various sorts long before the cancer is actually visible to the human eye. Earlier detection makes a full recovery a higher probability. The same holds true for all sorts of other medical problems (such as finding bone fractures that are currently too small to see but cause pain nonetheless).

You also find pattern recognition used for more mundane purposes. For example, pattern analysis lets people detect potential traffic problems before they occur. It's also possible to use pattern analysis to help farmers grow more food at a lower cost by applying water and fertilizer only when necessary. The use of pattern recognition can also help move drones around fields so that the farmer becomes more time efficient and can work more land at a lower cost. Without algorithms, these sorts of patterns, which have such a high impact on daily life, can't be recognized.

Dealing with Automation and Automatic Responses

The proportional integral derivative algorithm is quite a mouthful. Just try saying it three times fast! However, it's one of the most important secret algorithms you've never heard about, yet rely on every day. You can find some details about this algorithm at `https://www.ni.com/en-us/innovations/white-papers/06/pid-theory-explained.html`, including a block diagram showing one potential implementation.

REMEMBER

The proportional integral derivative algorithm relies on a control loop feedback mechanism to minimize the error between the desired output signal and the real output signal. You see it used all over the place to control automation and automatic responses. For example, when your car goes into a skid because you brake too hard, this algorithm helps ensure that the Automatic Braking System (ABS) actually works as intended. Otherwise, the ABS could overcompensate and make matters worse.

Just about every form of machinery today uses the proportional integral derivative algorithm. In fact, robotics wouldn't be possible without it. Imagine what would happen to a factory if all the robots constantly overcompensated for every activity they engaged in. The resulting chaos would quickly convince owners to stop using machines for any purpose whatsoever.

Creating Unique Identifiers

It seems as if everyone is just a number. Actually, not just one number — lots and lots of numbers. People's credit cards all have a number, as do people's driver's license and government identifier. Likewise for all sorts of other businesses and organizations. People actually have to keep lists of all the numbers because they simply have too many to track. Yet, each of these numbers must identify the person uniquely to some party. Behind all this uniqueness are various kinds of algorithms.

Chapter 7 discusses hashes, which are one way to ensure uniqueness. Underlying both hashes and cryptography is integer factorization, a kind of algorithm that breaks really large numbers into prime numbers. In fact, integer factorization is one of the hardest kinds of problems to solve with algorithms, but people are working on the problem all the time. So much of society today depends on your ability to identify yourself uniquely that the hidden secrets of creating these identifiers is an essential part of a modern world.

IN THIS CHAPTER

» Performing tasks faster and better

» Solving new problem types

» Considering the feasibility of hypercomputers

» Employing one-way functions, and more . . .

Chapter 22 Ten Algorithmic Problems Yet to Solve

Algorithms have indeed been around for centuries, so you'd think that scientists would have discovered and perfected every algorithm by now. Unfortunately, the opposite is true. Solving a problem using a particular algorithm often presents a few more questions that the algorithm doesn't solve and that didn't seem apparent until someone did come up with the solution. In addition, changes in technologies and lifestyle often present new challenges that call for yet more algorithms. For example, the connected nature of society and the use of robots have both increased the need for new algorithms.

As presented in Chapter 1, algorithms consist of a series of steps used to solve a problem, and you shouldn't confuse them with other entities, such as equations. An algorithm is never a solution in search of a problem. No one would create a series of steps to solve a problem that doesn't yet exist (or may never exist). In addition, many problems are interesting but have no pressing need for a solution. Consequently, even though everyone knows about the problem and understands that someone might want a solution for it, no one is in a hurry to create the solution.

This chapter is about algorithmic problems that would serve a purpose should someone find a solution for them. In short, the reason you need to care about this chapter is that you might find a problem that you'd really like to solve, and you might even decide to become part of the team that solves it.

Solving Problems Quickly

As machine learning takes off and people increasingly count on computers to solve problems, the issue of how quickly a computer can solve a problem becomes critical. The P-versus-NP problem simply asks whether a computer can solve a problem quickly when it can verify the solution to the problem quickly (see the "Considering NP complete problems" section of Chapter 15 for details). In other words, if the computer can reasonably ascertain that a human response to a problem is correct in polynomial time or less, can it also solve the problem itself in polynomial time or less?

John Nash originally discussed this question in the 1950s in letters to the National Security Agency (NSA), and the discussion arose again in letters between Kurt Gödel and John von Neumann. In addition to machine learning (and AI in general), this particular problem is a concern to many other fields, including mathematics, cryptography, algorithm research, game theory, multimedia processing, philosophy, and economics.

Solving 3SUM Problems More Efficiently

The 3SUM problem asks whether, given a set of real numbers, any three of these numbers will sum to zero. The problem can even be generalized to k numbers for special purposes, thus becoming a k-SUM problem. At first, 3SUM doesn't seem like a problem worth solving. It's generally used in computational geometry to solve problems like these:

- Determining when a point set contains three *collinear* points (points lying on the same straight line)
- Calculating the area of the union of a set of triangles
- Deciding whether one convex polygon can be placed within another convex polygon

However, many situations occur in real life that involve three actors, and the sum of their interactions should be zero (as in a zero-sum game). One easy example is in a mediated financial transaction. You can find an even more pertinent example in the exchange of carbon credits for carbon neutrality, which involves exchanging emissions for credits between companies or countries to maintain a stable emission of carbon dioxide.

Although you can easily solve the 3SUM problem in $O(n^2)$ time, various computer scientists have worked to lower the time complexity of solving the 3SUM algorithm. After various improvements, the current best algorithm can solve the 3SUM problem in $O(n^2(\log \log n)^{O(1)}/\log^2 n)$, but scientists believe that on theoretical grounds, the boundary can be even pushed lower.

Making Matrix Multiplication Faster

Matrix multiplication is used almost everywhere now to solve a wide range of problems. The problem is that matrix multiplication is slow — really slow — because it takes so many steps. The current goal is to reach multiplication steps of n^2, according to the article at `https://www.quantamagazine.org/mathematicians-inch-closer-to-matrix-multiplication-goal-20210323/`. (The current math textbook approach requires n^3 steps.) Achieving the goal would mean taking four steps to multiply a 2-x=2 matrix instead of the eight multiplication steps (and some additions) that it takes now. According to `https://iq.opengenus.org/unsolved-problems-in-algorithms/`, matrix multiplication is one of the top unsolved problems in algorithms.

So where do you see matrix multiplication used? Many uses are the sort of things that mathematicians and graphic artists love, such as skewing the Mona Lisa so that she looks weird (see `https://betterexplained.com/articles/matrix-multiplication/`). The discussion at `https://www.quora.com/What-are-some-of-the-real-time-applications-of-Matrix-multiplication` gives you some useful real-world ideas, like where to locate a new firehouse.

Determining Whether an Application Will End

One of the problems that Alan Turing proposed in 1936 is the issue of whether an algorithm, given a description of a program and an input, could determine whether the program would eventually halt (the *halting problem*). When working with a simple application, it's easy to determine in many cases whether the program will halt or continue running in an endless loop. However, as program complexity increases, determining the result of running the program with any given input becomes harder. A Turing machine can't make this determination; the result is buggy code with infinite loops. No amount of testing that uses current technology can solve this issue.

REMEMBER

A *hypercomputer* is a computing model that goes beyond the Turing machine to solve problems such as the halting problem. However, such machines aren't possible using current technology. If they were possible, you would be able to ask them all kinds of imponderables that computers can't currently answer. The article at `https://www.newscientist.com/article/mg22329781-500-what-will-hypercomputers-let-us-do-good-question/` gives you a good idea of what would happen if someone were able to solve this problem. You can read about a potential future implementation at `https://www.foprc.org/quantum-hypercomputing-by-means-of-evanescent-photons.php`.

Creating and Using One-Way Functions

A one-way function is a function that's easy to use to obtain an answer in one direction, but nearly impossible to use with the inverse of that answer. In other words, you use a one-way function to create something like a hash that would appear as part of a solution for cryptography, personal identification, authentication, or other data security needs.

REMEMBER

The existence of a one-way function is less mystery and more a matter of proof. Many telecommunications, e-commerce, and e-banking systems currently rely on functions that are purportedly one way, but no one truly knows whether they really are one way. The existence of a one-way function is currently a hypothesis, not a theory (see an explanation of the difference between the two at `https://www.diffen.com/difference/Hypothesis_vs_Theory`). If someone were able to prove that a one-way function exists, data security issues would be easier to solve from a programming perspective.

Multiplying Really Large Numbers

Really large numbers exist in many places. For example, consider performing the calculations involving distances to Mars, or perhaps Pluto. Methods currently do exist for performing multiplication on really large numbers, but they tend to be slow because they require multiple operations to complete. The problem occurs when the numbers are too large to fit in the processor's registers. At that point, the multiplication must occur in more than one step, which slows things considerably. The current solutions include:

- Gauss's complex multiplication algorithm
- Karatsuba multiplication

- Toom-Cook
- Fourier transform methods

Even though many of the methods currently available produce acceptable results, they all take time, and when you have a lot of calculations to perform, the time problem can become critical. Consequently, large-number multiplication is one of those problems that requires a better solution than those available today.

Dividing a Resource Equally

Dividing resources equally may not seem hard, but humans, being the envious sort, might see the resource as being unequally divided unless you can find a way to assure everyone that the division is indeed fair. This is the envy-free cake-cutting problem. When you cut a cake, no matter how fairly you attempt to do it, there is always the perception that the division is unfair. Creating a fair division of resources is important in daily life to minimize strife between stakeholders in any organization, making everyone more efficient.

TIP

Two solutions already exist for the envy-free cake-cutting problem with a specific number of people, but no general solution exists. When there are two people involved, the first cuts the cake and the second chooses the first piece. In this way, both parties are assured of an equal division. The problem becomes harder with three people, but you can find the Selfridge-Conway solution for the problem at `https://archive.ochronus.com/cutting-the-pie/`. (The site discusses pie but the process is the same.) However, after you get to four people, no solution exists.

Reducing Edit Distance Calculation Time

The *edit distance* between two strings is the number of operations required to transform one string into the other string. The distance calculation revolves around the Levenshtein distance operations, which are the removal, insertion, or substitution of a character in the string. This particular technique sees use in natural language interfaces, DNA sequence quantification, and all sorts of other places where you can have two similar strings that require some sort of comparison or modification.

A number of solutions for this problem currently exist, all of them quite slow. In fact, most of them take $O(n^2)$ time, so the time required to perform a transformation quickly adds up to the point where humans can see pauses in the processing of input. The pause isn't quite so bad when using a word processor that performs automatic word checks and changes a misspelled word into the correct one. However, when using voice interfaces, the pause can become quite noticeable and cause the human operator to make mistakes. The current goal is to allow edit distance calculation in subquadratic time: $O(n^{2-\epsilon})$.

Playing the Parity Game

At first, solving a game might not seem all that useful in real life. Yes, games are fun and interesting, but they don't really provide a background for doing anything useful — at least, that's the general theory. However, game theory does come into play in a large number of real-life scenarios, many of which involve complex processes that someone can understand more easily as games than as actual processes. In this case, the game helps people understand automated verification and controller synthesis, among other things. You can read more about the parity game at `http://www.sciencedirect.com/science/article/pii/S0890540115000723`. In fact, you can play it if you'd like, at `https://www.abefehr.com/parity/`.

Understanding Spatial Issues

To put this particular problem into context, think about moving boxes around in a warehouse, or some other situations that cause you to consider the space in which things move. Obviously, if you have many boxes in a big warehouse and they all require a forklift to pick up, you don't want to try to figure out how to store them optimally by physically rearranging them. This is where you need to work through the problem by visualizing a solution.

However, the question is whether all spatial problems have a solution. In this case, think about one of those kids' puzzles that has you putting a picture together by sliding the little tiles around. It seems as if a solution should exist in all cases, but in some situations, a bad starting point can result in a situation that has no solution. You can find a discussion of such a problem at `https://math.stackexchange.com/questions/754827/does-a-15-puzzle-always-have-a-solution`.

TIP

Mathematicians such as Sam Loyd (see `https://www.mathsisfun.com/puzzles/sam-loyd-puzzles-index.html`) often use puzzles to demonstrate complex math problems, some of which have no solution today. Visiting these sites is fun because you not only get some free entertainment but also food for thought. The issues these puzzles raise do have practical applications, but they're presented in a fun way.

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John's Dedication

This book is dedicated to all of the people who have supported me through the various transitions in my life.

Luca's Dedication

I dedicate this book to my wife, Yukiko, whom I always find curious and ready to marvel at the wonders of this amazing and baffling technological world. With love.

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