Principles of Algorithmic Problem Solving

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Preface

Algorithmic problem solving is the art of formulating efficient methods that solve problems of a mathematical nature. From the many numerical algorithms developed by the ancient Babylonians to the founding of graph theory by Euler, algorithmic problem solving has been a popular intellectual pursuit during the last few thousand years. For a long time, it was a purely mathematical endeavor with algorithms meant to be executed by hand. During the recent decades algorithmic problem solving has evolved. What was mainly a topic of research became a mind sport known as competitive programming. As a sport algorithmic problem solving rose in popularity with the largest competitions attracting tens of thousands of programmers. While its mathematical counterpart has a rich literature, there are only a few books on algorithms with a strong problem solving focus.

The purpose of this book is to contribute to the literature of algorithmic problem solving in two ways. First of all, it tries to fill in some holes in existing books. Many topics in algorithmic problem solving lack any treatment at all in the literature – at least in English books. Much of the content is instead documented only in blog posts and solutions to problems from various competitions. While this book attempts to rectify this, it is not to detract from those sources. Many of the best treatments of an algorithmic topic I have seen are as part of a well-written solution to a problem. However, there is value in completeness and coherence when treating such a large area. Secondly, I hope to provide another way of learning the basics of algorithmic problem solving by helping the reader build an intuition for problem solving. A large part of this book describes techniques using worked-through examples of problems. These examples attempt not only to describe the manner in which a problem is solved, but to give an insight into how a thought process might be guided to yield the insights necessary to arrive at a solution.

This book is different from pure programming books and most other algorithm textbooks. Programming books are mostly either in-depth studies of a specific programming language or describe various programming paradigms. A single language is used in this book – C++. The text on C++ exists for the sole purpose of enabling those readers without prior programming experience to implement the solutions to algorithm problems. Such a treatment is necessarily minimal and teach neither good coding style nor advanced programming concepts. Algorithm textbooks teach primarily algorithm analysis, basic algorithm design, and some standard algorithms and data structures. They seldom include as much problem solving as this book does. The book also falls somewhere between the practical nature of a programming book and the heavy theory of algorithm textbooks. This is in part due to the book's dual nature of being not only about algorithmic problem solving, but also competitive programming to some extent. As such there is more real code and efficient C++ implementations of algorithms included compared to most algorithm books.

Acknowledgments. First and foremost, thanks to Per Austrin who provided much valuable advice and feedback during the writing of this book. Thanks to Simon and Mårten who have competed with me for several years as Omogen Heap. Finally, thanks to several others who have read through drafts and caught numerous mistakes of my own.

Reading this Book

This book consists of two parts. The first part contains some preliminary background, such as algorithm analysis and programming in C++. With an undergraduate education in computer science most of these chapters are probably familiar to you. It is recommended that you at least skim through the first part since the remainder of the book assumes you know the contents of the preliminary chapters.

The second part makes up most of the material in the book. Some of it should be familiar if you have taken a course in algorithms and data structures. The take on those topics is a bit different compared to an algorithms course. We therefore recommend that you read through the parts even if you feel familiar with them – in particular those on the basic problem solving paradigms, i.e. brute force, greedy algorithms, dynamic programming and divide & conquer. The chapters in this part are structured so that a chapter builds upon only the preliminaries and previous chapters to the largest extent possible.

At the end of the book you can find an appendix with some mathematical background.

This book can also be used to improve your competitive programming skills. Some parts are unique to competitive programming (in particular Chapter 17 on contest strategy). This knowledge is extracted into *competitive tips*:

Competitive Tip

A competitive tip contains some information specific to competitive programming. These can be safely ignored if you are interested only in the problem solving aspect and not the competitions.

The book often refers to exercises from the Kattis online judge. These are named *Kattis Exercise*, given as problem names and IDs.

Exercise 0.1 — Kattis Exercise

Problem Name – problemid

The URL of such a problem is `http://open.kattis.com/problem/problemid`.

The C++ code in this book makes use of some preprocessor directives from a template. Even if you are familiar with C++ (or do not wish to learn it) we still recommend that you read through this template (Section 2.13) to better understand the C++ code in the book.

Part I

Preliminaries

Chapter 1

Algorithms and Problems

The greatest technical invention of the last century was probably the digital general purpose computer. It was the start of the revolution which provided us with the Internet, smartphones, tablets, and the computerization of society.

To harness the power of computers we use *programming*. Programming is the art of developing a solution to a *computational problem*, in the form of a set of instructions that a computer can execute. These instructions are what we call *code*, and the language in which they are written a *programming language*.

The abstract method that such code describes is what we call an *algorithm*. The aim of *algorithmic problem solving* is thus to, given a computational problem, devise an algorithm that solves it. One does not necessarily need to complete the full programming process (i.e. write code that implements the algorithm in a programming language) to enjoy solving algorithmic problems. However, it often provides more insight and trains you at finding simpler algorithms to problems.

1.1 Computational Problems

A ***computational problem*** generally consists of two parts. First, it needs an ***input description***, such as "a sequence of integers", "a string", or some other kind of mathematical object. Using this input, we have a goal which we wish to accomplish defined by an ***output description***. For example, a computational problem might require us to sort a given sequence of integers. This particular problem is called the *Sorting Problem*.

Sorting

Your task is to sort a sequence of integers in ascending order, i.e. from the lowest to the highest.

Input

The input is a sequence of N integers $a_0, a_1, ..., a_{N-1}$.

Output

Output a permutation a' of the sequence a, such that $a'_0 \leq a'_1 \leq ... \leq a'_{N-1}$.

A particular input to a computational problem is called an ***instance***. To the sorting problem, the sequence $3, 6, 1, -1, 2, 2$ would be an instance. The correct output for this particular problem would be $-1, 1, 2, 2, 3, 6$.

Some variations of this format appears later (such as problems without inputs) but in general this is what our problems look like.

Competitive Tip

Problem statements sometimes contain huge amounts of text. Skimming through the input and output sections before any other text in the problem can often give you a quick idea about its topic and difficulty. This helps in determining what problems to solve first.

Exercise 1.1

What is the input and output for the following computational problems?

1) Compute the greatest common divisor (Def. 16.4, page 294) of two numbers.

2) Find a root of a polynomial.

3) Multiply two numbers.

Exercise 1.2

Consider the following problem. I am thinking of an integer between 1 and 100. Your task is to find this number by asking me questions of the form "is your number higher, lower, or equal to x" for different numbers x.

This is an *interactive*, or *online*, computational problem. How would you describe the input and output to it? Why do you think it is called interactive?

1.2 Algorithms

Algorithms are the solutions to computational problems. They define a method that uses the input to a problem in order to produce the correct output. A computational problem can have many solutions. Efficient algorithms to solve the sorting problem form an entire research area! Let us look at one possible sorting algorithm as an example, called selection sort.

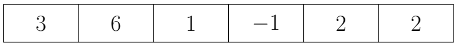
Algorithm 1.1: Selection Sort

We construct the sorted sequence iteratively one element at a time, starting with the smallest.

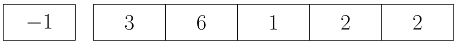
Assume that we have chosen the K smallest elements of the original sequence and have sorted them. Then, the smallest element remaining in that sequence must be the $(K+1)$'st smallest element of the original sequence. Thus, by finding the smallest element among those that remain we know what the $(K+1)$'st element of the sorted sequence is. By combining this observation with the sorted K smallest elements we can determine the sorted $K + 1$ smallest elements of the output.

If we repeat this process N times, the result is the N numbers of the original sequence, but sorted.

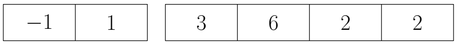
You can see this algorithm in practice, performed on our previous example instance (the sequence $3, 6, 1, -1, 2, 2$) in Figures 1.1a-1.1f.



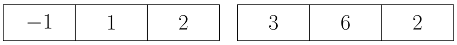
(a) Originally, we start out with the unsorted sequence `3 6 1 -1 2 2`.



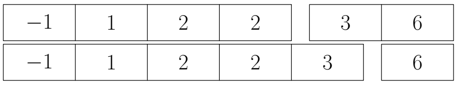
(b) The smallest element of the sequence is -1, so this is the first element of the sorted sequence.



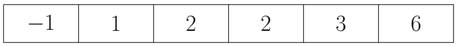
(c) We find the next element of the output by removing the -1 and finding the smallest remaining element – in this case 1.



(d) Here, there is no unique smallest element. We can choose any of the two 2's in this case.



(e) The next two elements chosen will be a 2 and a 3.



(f) Finally, we choose the last remaining element of the input sequence – the 6. This concludes the sorting of our sequence.

Figure 1.1: An example execution of Selection Sort.

So far, we have been vague about what an algorithm is exactly. Looking at our example (Algorithm 1.1) we do not have any particular structure or rigor in the description of our method. There is nothing inherently wrong with describing algorithms this way. It is easy to understand and gives the writer an opportunity to provide context as to why certain actions are performed, making the correctness of the algorithm more obvious. The main downsides of such a description are ambiguity and a lack of detail.

Until an algorithm is described in sufficient detail, it is possible to accidentally abstract away operations we may not know how to perform behind a few English words. As a somewhat contrived example, our plain text description of selection sort includes actions such as "choosing the smallest number of a sequence". While such an operation may seem very simple to us humans, algorithms are generally constructed with regards to some kind of computer. Unfortunately, computers can not map such English expressions to their code counterparts yet. Instructing a computer to execute an algorithm thus requires us to formulate our algorithm in steps small enough that even a computer knows how to perform them. In this sense, a computer is rather stupid.

The English language is also ambiguous. We are sloppy with references to "this variable" and "that set", relying on context to clarify meaning for us. We use confusing terminology and frequently misunderstand each other. Real code does not have this problem. It forces us to be specific with what we mean.

We will generally describe our algorithms in a representation called pseudo code (Section 1.4), accompanied by an online exercise to implement the code. Sometimes, we will instead give explicit code that solves a problem. This will be the case whenever an algorithm is very complex, or care must be taken to make the implementation efficient. The goal is that you should get to practice understanding pseudo code, while still ending up with correct implementations of the algorithms (thus the online exercises).

Exercise 1.3

Do you know any algorithms, for example from school? (Hint: you use many algorithms to solve certain arithmetic and algebraic problems, such as those in Exercise 1.1.)

Exercise 1.4

Construct an algorithm that solves the guessing problem in exercise 1.2. How many questions does it use? The optimal number of questions is about $\log_2 100 \approx 7$ questions. Can you achieve this?

1.2.1 Correctness

One subtle, albeit important, point that we glossed over is what it means for an algorithm to actually be ***correct***.

There are two common notions of correctness – ***partial correctness*** and ***total correctness***. The first notion requires an algorithm to, upon termination, have produced an output that fulfills all the criteria laid out in the output description. Total correctness additionally requires an algorithm to terminate within finite time. When we talk about correctness of our algorithms later on, we generally focus on the partial correctness. Termination is instead proved implicitly, as we consider a more granular measure of efficiency (called *time complexity*, Chapter 5) than just finite termination. This measure implies the termination of the algorithm, completing the proof of total correctness.

Proving that the selection sort algorithm terminates in finite time is quite easy. It performs one iteration of the selection step for each element in the original sequence (which is finite). Furthermore, each such iteration can be performed in finite time by considering each remaining element of the selection when finding the smallest one. The remaining sequence is a subsequence of the original one and is therefore also finite.

Proving that the algorithm produces the correct output is a bit more difficult to prove formally. The main idea behind a formal proof is contained within our description of the algorithm itself.

At later points in the book we will compromise on both conditions. Generally, we are satisfied with an algorithm terminating in expected finite time or answering correctly with, say, probability 0.75 for every input. Similarly, we are sometimes happy to find an *approximate* solution to a problem. What this means more concretely will become clear in due time when we study such algorithms.

Competitive Tip

Proving your algorithm correct is sometimes quite difficult. In a competition, a correct algorithm is correct even if you cannot prove it. If you have an idea you *think* is correct it may be worth testing. This is not a strategy without problems though, since it makes distinguishing between an incorrect algorithm and an incorrect implementation even harder.

Exercise 1.5

Prove the correctness of your algorithm to the guessing problem from Exercise 1.4.

Exercise 1.6

Why would an algorithm that is correct with e.g. probability 0.75 still be very useful to us?

Why is it important that such an algorithm is correct with probability 0.75 on *every* problem instance, instead of always being correct for 75% of all cases?

1.3 Programming Languages

The purpose of ***programming languages*** is to formulate methods at a level of detail where a computer can execute them. While we in textual descriptions of methods are often satisfied with describing *what* we wish to do, programming languages require considerably more constructive descriptions. Computers are quite basic creatures compared to us humans. They only understand a very limited set of instructions such as adding numbers, multiplying numbers, or moving data around within its memory. The syntax of programming languages often seems a bit arcane at first, but it grows on you with coding experience.

To complicate matters further, programming languages themselves define a spectrum of expressiveness. On the lowest level, programming deals with electrical current in your processor. Current above or below a certain threshold is used to represent the binary digits 0 and 1. Above these circuit-level electronics lie a processors own programming, often called *microcode*. Using this, a processor implements *machine code*, such as the x86 instruction set. Machine code is often written using a higher-level syntax called *Assembly*. While some code is written in this rather low-level language, we mostly abstract away details of them in high-level languages such as C++ (this book's language of choice).

This knowledge is somewhat useless from a problem solving standpoint, but intimate knowledge of how a computer works is of high importance in software engineering, and is occasionally helpful in programming competitions. Therefore, you should not be surprised about certain remarks relating to these low-level concepts.

These facts also provide some motivation for why we use something called *compilers*. When programming in C++ we can not immediately tell a computer to run our code. As you now know, C++ is at a higher level than what the processor of a computer can run. A compiler takes care of this problem by translating our C++ code into *machine code* that the processor knows how to handle. It is a program of its own and takes the code files we write as input and produces *executable* files that we can run on the computer. The process and purpose of a compiler is somewhat like what we do ourselves when translating a method from English sentences or our own thoughts into the lower level language of C++.

1.4 Pseudo Code

Somewhere in between describing algorithms in English text and in a programming language we find something called ***pseudo code***. As hinted by its name it is not quite real code. The instructions we write are not part of the programming language of any particular computer. The point of pseudo code is to be independent of what computer it is implemented on. Instead, it tries to convey the main points of an algorithm in a detailed manner so that it can easily be translated into any particular programming language. Secondly, we sometimes fall back to the liberties of the English language. At some point, we may decide that “choose the smallest number of a sequence” is clear enough for our audience.

With an explanation of this distinction in hand, let us look at a concrete example of what is meant by pseudo code. The honor of being an example again falls upon selection sort, now described in pseudo code in Algorithm 1.2.

Algorithm 1.2: Selection Sort

```
procedure SELECTIONSORT(A)
    Let $A'$ be an empty sequence
    while $A$ is not empty do
        $minIndex \leftarrow 0$
        for every element $A_i$ in $A$ do
            if $A_i < A_{minIndex}$ then
                $minIndex \leftarrow i$
        Append $A_{minIndex}$ to $A'$
        Remove $A_{minIndex}$ from $A$
    return the sequence $A'$
```

Pseudo code reads somewhat like our English language variant of the algorithm, except the actions are broken down into much smaller pieces. Most of the constructs of our pseudo code are more or less obvious. The notation *variable* $\leftarrow value$ is how we denote an *assignment* in pseudo code. For those without programming experience, this means that the variable named *variable* now takes the value $value$. Pseudo code appears when we try to explain some part of a solution in great detail but programming language specific aspects would draw attention away from the algorithm itself.

Competitive Tip

In team competitions where a team only have a single computer, a team will often have solved problems waiting to be coded. Writing pseudo code of the solution to one of these problems while waiting for computer time is an efficient way to parallelize your work. This can be practiced by writing pseudo code on paper even when you are solving problems by yourself.

Exercise 1.7

Write pseudo code for your algorithm to the guessing problem from Exercise 1.4.

1.5 The Kattis Online Judge

Most of the exercises in this book exist as problems on the ***Kattis*** web system. You can find it at `https://open.kattis.com`. Kattis is a so called ***online judge***, which has been used in the university competitive programming world finals (the International Collegiate Programming Contest World Finals) for several years. It contains a large collection of computational problems, and allows you to submit a program you have written that purports to solve a problem. Kattis will then run your program on a large number of predetermined instances of the problem called the problem's *test data*.

Problems on an online judge include some additional information compared to our example problem. Since actual computers only have a finite amount of time and memory, problems limit the amount of these resources available to our programs when solving an instance. This also means the size of inputs to a problem need to be constrained as well, or else the resource limits for a given problem would not be obtainable – an arbitrarily large input generally takes arbitrarily large time to process, even for a computer. A more complete version of the sorting problem as given in a competition could look like this:

Sorting

Time: 1s, memory: 1MB

Your task is to sort a sequence of integers in ascending order, i.e. from the lowest to the highest.

Input

The input is a sequence of N integers ($0 \leq N \leq 1000$) $a_0, a_1, ..., a_{N-1}$ ($|a_i| \leq 10^9$).

Output

Output a permutation a' of the sequence a, such that $a'_0 \leq a'_1 \leq ... \leq a'_{N-1}$.

If your program exceeds the allowed resource limits (i.e. takes too much time or memory), crashes, or gives an invalid output, Kattis will tell you so with a *rejected* judgment. There are many kinds of rejected judgments, such as *Wrong Answer*, *Time Limit Exceeded*, and *Run-time Error*. These mean your program gave an incorrect output, took too much time, and crashed, respectively. Assuming your program passes all the instances, it will be be given the *Accepted* judgment.

Note that getting a program accepted by Kattis is not the same as having a correct program – it is a necessary but not sufficient criterion for correctness. This is also a fact that can sometimes be exploited during competitions by writing a knowingly incorrect solution that one thinks will pass all test cases that the judges of the competitions designed.

We strongly recommend that you get a (free) account on Kattis so that you can follow along with the book's exercises.

Exercise 1.8

Register an account on Kattis and read the documentation at `https://open.kattis.com/help`.

Many other online judges exists, such as:

- Codeforces (`http://codeforces.com`)
- CSAcademy (`https://csacademy.com`)
- AtCoder (`https://atcoder.jp`)
- TopCoder (`https://topcoder.com`)
- HackerRank (`https://hackerrank.com`)

1.6 Additional Exercises

Exercise 1.9

1) Come up with another algorithm of sorting than Selection Sort. If you can not come up with one, you can instead read the description of *Bubble Sort* online, for example on Wikipedia[1] for exercises 2 and 3..

2) Formalize the algorithm and write it down in pseudo code.

3) Prove the correctness of the algorithm.

Exercise 1.10

Consider the following problem:

Primality

We call an integer $n > 1$ a *prime* if its only divisors are 1 and n. Determine if a particular integer is a prime.

Input

The input consists of a single integer $n > 1$.

Output

Output `yes` if the number was a prime and `no` otherwise.

1) Devise an algorithm that solves this problem.
2) Formalize the algorithm and write it down in pseudo code.
3) Prove the correctness of the algorithm.

1.7 Chapter Notes

The introductions given in this chapter are very bare, mostly stripped down to what you need to get by when solving algorithmic problems.

Many other books delve deeper into the theoretical study of algorithms than we do, in particular regarding subjects not relevant to algorithmic problem solving. *Introduction to Algorithms* [5] is a rigorous introductory text book on algorithms with both depth and width.

For a gentle introduction to the technology that underlies computers, *CODE* [19] is a well-written journey from the basics of bits and bytes all the way up to assembly code and operating systems.

Sorting algorithms are a common algorithmic example, in part because of their rich theory and the fact that the task at hand is familiar to beginners. The Wikipedia category on sorting algorithms[2] contains descriptions of many more

[1] `https://en.wikipedia.org/wiki/Bubble_sort`

[2] `https://en.wikipedia.org/wiki/Category:Sorting_algorithms`

sorting algorithms that provide a nice introduction into many algorithmic techniques.

Chapter 2

Programming in C++

In this chapter we learn some more practical matters – the basics of the C++ programming language. This language is the most common programming language within the competitive programming community for a few reasons (aside from C++ being a popular language in general). Programs coded in C++ are generally somewhat faster than most other competitive programming languages. There are also many routines in the accompanying standard code libraries that are useful when implementing algorithms.

Of course, no language is without downsides. C++ is a bit difficult to learn as your first programming language to say the least. Its error management is unforgiving, often causing erratic behavior in programs instead of crashing with an error. Programming certain things become quite verbose, compared to many other languages.

After bashing the difficulty of C++, you might ask if it really is the best language in order to get started with algorithmic problem solving. While there certainly are simpler languages we believe that the benefits of C++ weigh up for the disadvantages in the long term even though it demands more from you as a reader. Either way, it is definitely the language we have the most experience of teaching problem solving with.

When you study this chapter, you will see a lot of example code. **Type this code and run it**. We can not really stress this point enough. Learning programming from scratch – in particular a complicated language such as C++ – is not possible unless you try the concepts yourself. Additionally, we recommend that you do **every** exercise in this chapter.

Finally, know that our treatment of C++ is minimal. We do not explain all the details behind the language, nor do we teach good coding style or general software engineering principles. In fact, we frequently make use of bad coding practices. If you want to delve deeper, you can find more resources in the chapter notes.

2.1 Development Environments

Before we get to the juicy parts of C++ you need to install a compiler for C++ and (optionally) a code editor.

We recommend the editor ***Visual Studio Code***. The installation procedure varies depending on what operating system you use. We provide them for Windows, Ubuntu and macOS. If you choose to use some other editor, compiler or operating system you must find out how to perform the corresponding actions (such as compiling and running code) yourself.

Note that instructions like these tend to rot, with applications disappearing from the web, operating systems changing names, and so on. In that case, you are on your own and have to find instructions by yourself.

2.1.1 Windows

Installing a C++ compiler is somewhat complicated in Windows. We recommend installing the Mingw-w64 compiler from `http://www.mingw-w64.org/`.

After installing the compiler, you can download the installer for Visual Studio Code from `https://code.visualstudio.com/`.

2.1.2 Ubuntu

On Ubuntu, or similar Linux-based operating systems, you need to install the GCC C++ compiler, which is the most popular compiled for Linux-based systems. It is called `g++` in most package managers and can be downloaded with the command

```
sudo apt-get install g++
```

After installing the compiler, you can download the installer for Visual Studio Code from `https://code.visualstudio.com/`. Choose the `deb` installer.

2.1.3 macOS

When using macOS, you first need to install the Clang compiler by installing *Xcode* from the Mac App Store. This is also a code editor, but the compiler is bundled with it.

After installing the compiler, you can download the installer for Visual Studio Code from `https://code.visualstudio.com/`. It is available as a normal macOS package for installation.

2.1.4 Installing the C++ tools

Now that you have installed the compiler and Visual Studio Code, you need to install the C++ plugin for Visual Studio Code. You can do this by opening the program, launching Quick Open (using Ctrl+P), typing `ext install ms-vscode.cpptools`, and pressing Enter. Then, launch Quick Open again, but this time type `ext install formulahendry.code-runner` instead. Now, restart your editor.

The tools need to be configured a bit. Press Ctrl+, to open the settings dialog. In the settings dialog, go to Extensions > Run Code configuration. Here, enable Run in Terminal and Save All Files Before Run. Then, restart your editor again.

2.2 Hello World!

Now that you have a compiler and editor ready, it is time to learn the basic structure of a C++ program. The classical example of a program when learning a new language is to print the text `Hello World!`. We also solve our first Kattis problem in this section.

Start by opening Visual Studio Code and create a new file by going to File ⇒ New File. Save the file as `hello.cpp` by pressing Ctrl+S. Make sure to save it somewhere you can find it.

Now, type the code from Listing 2.1 into your editor.

Listing 2.1 Hello World!

```cpp
#include <iostream>

using namespace std;

int main() {
  // Print Hello World!
  cout << "Hello World!" << endl;
}
```

To run the program in Visual Studio Code, you press Ctrl+Alt+N. A tab below your code named `TERMINAL` containing the text `Hello World!` should appear. If no window appears, you probably mistyped the program.

Coincidentally, Kattis happens to have a problem whose output description dictates that your program should print the text `Hello World!`. How convenient. This is a great opportunity to get familiar with Kattis.

Exercise 2.1 — Kattis Exercise

Hello World! – hello

When you submit your solution, Kattis grades it and give you her judgment. If you typed everything correctly, Kattis tells you it got Accepted. Otherwise, you probably got Wrong Answer, meaning your program output the wrong text (and you mistyped the code).

Now that you have managed to solve the problem, it is time to talk a bit about the code you typed.

The first line of the code,

```
#include <iostream>
```

is used to include the `iostream` – *input and output stream* – file from the so-called *standard library* of C++. The standard library is a large collection of ready-to-use algorithms, data structures, and other routines which you can use when coding. For example, there are sorting routines in the C++ standard library, meaning you do not need to implement your own sorting algorithm when coding solutions.

Later on, we will see other useful examples of the standard library and include many more files. The `iostream` file contains routines for reading and writing data to your screen. Your program used code from this file when it printed `Hello World!` upon execution.

Competitive Tip

On some platforms, there is a special include file called `bits/stdc++.h`. This file includes the entire standard library. You can check if it is available on your platform by including it using

```
#include <bits/stdc++.h>
```

in the beginning of your code. If your program still compiles, you can use this and not include anything else. By using this you do not have to care about including any other files from the standard library which you wish to use.

The third line,

```
using namespace std;
```

tells the compiler that we wish to use code from the **st**an**d**ard library. If we did not use it, we would have to specify this every time we used code from the standard library later in our program by prefixing what we use from the library by `std::` (for example `std::cout`).

The fifth line defines our ***main function***. When we instruct the computer to run our program the computer starts looking at this point for code to execute.

The first line of the main function is thus where the program starts to run with further lines in the function executed sequentially. Later on we learn how to define and use additional functions as a way of structuring our code. Note that the code in a function – its *body* – must be enclosed by curly brackets. Without them, we would not know which lines belonged to the function.

On line 6, we wrote a ***comment***

```
// Print Hello World!
```

Comments are explanatory lines which are not executed by the computer. The purpose of a comment is to explain what the code around it does and why. They begin with two slashes // and continue until the end of the current line.

It is not until the seventh line that things start happening in the program. We use the standard library utility `cout` to print text to the screen. This is done by writing e.g.:

```
cout << "this is text you want to print. ";
cout << "you can " << "also print " << "multiple things. ";
cout << "to print a new line" << endl << "you print endl" << endl;
cout << "without any quotes" << endl;
```

Lines that do things in C++ are called ***statements***. **Note the semi colon** at the end of the line! Semi colons are used to specify the end of a statement, and are mandatory.

Exercise 2.2

Must the main function be named `main`? What happens if you changed `main` to something else and try to run your program?

Exercise 2.3

Play around with `cout` a bit, printing various things. For example, you can print a pretty haiku.

2.3 Variables and Types

The Hello World! program is boring. It only prints text – seldom the only necessary component of an algorithm (aside from the Hello World! problem on Kattis). We now move on to a new but hopefully familiar concept.

When we solve mathematical problems, it often proves useful to introduce all kinds of names for known and unknown values. Math problems often deal with classes of N students, ice cream trucks with velocity v_{car} km/h, and candy prices of p_{candy} \$/kg.

This concept naturally translates into C++ but with a twist. In most programming languages, we first need to say what ***type*** a variable has! We do not bother with this in mathematics. We say "let $x = 5$", and that is that. In C++, we need to be a bit more verbose. We must write that "I want to introduce a variable x now. It is going to be an integer – more specifically, 5". Once we have decided what kind of value x will be (in this case integer) it will always be an integer. We cannot just go ahead and say "oh, I've changed my mind. $x = 2.5$ now!" since 2.5 is of the wrong type (a decimal number rather than an integer).

Another major difference is that variables in C++ are not tied to a single value for the entirety of their lifespans. Instead, we are able to modify the value which our variables have using something called ***assignment***. Some languages does not permit this, preferring their variables to be ***immutable***.

In Listing 2.2 we demonstrate how variables are used in C++. Type this program into your editor and run it. What is the output? What did you expect the output to be?

The *first* time we use a variable in C++ we must decide what kind of values it may contain. This is called ***declaring*** the variable of a certain type. For example the statement

```
int five = 5;
```

declares an integer variable `five` and assigns the value 5 to it. The `int` part is C++ for integer and is what we call a type. After the type, we write the name of the variable – in this case `five`. Finally, we may assign a value to the variable. Note that further use of the variable never include the `int` part. We declare the type of a variable once and only once.

Listing 2.2 Variables

```
 1  #include <iostream>
 2
 3  using namespace std;
 4
 5  int main() {
 6    int five = 5;
 7    cout << five << endl;
 8    int seven = 7;
 9    cout << seven << endl;
10
11    five = seven + 2; // = 7 + 2 = 9
12    cout << five << endl;
13
14    seven = 0;
15    cout << five << endl; // five is still 9
16    cout << 5 << endl; // we print the integer 5 directly
17  }
```

Later on in Listing 2.2 we decide that 5 is a somewhat small value for a variable called `five`. We can change the value of a variable by using the *assignment operator* – the equality sign =. The assignment

```
five = seven + 2;
```

states that from now on the variable `five` should take the value given by the expression `seven + 2`. Since (at least for the moment) `seven` has the value 7 the expression evaluates to $7 + 2 = 9$. Thus `five` will actually be 9, explaining the output we get from line 12.

On line 14 we change the value of the variable `seven`. Note that line 15 still prints the value of `five` as 9. Some people find this model of assignment confusing. We first performed the assignment `five = seven + 2;`, but the value of `five` did not change with the value of `seven`. This is mostly an unfortunate consequence of the choice of = as operator for assignment. One could think that "once an equality, always an equality" – that the value of `five` should always be the same as the value of `seven + 2`. **This is not the case**. An assignment sets the value of the variable on the left hand side to the value of the expression on the right hand side at a particular moment in time, nothing more.

The snippet also demonstrates how to print the value of a variable on the screen – we `cout` it the same way as with text. This also clarifies why text needs to be enquoted. Without quotes, we can not distinguish between the text string `"hi"` and the variable `hi`.

Exercise 2.4

C++ allows declarations of immutable (constant) variables, using the keyword `const`. For example

```
const int FIVE = 5;
```

What happens if you try to perform an assignment to such a variable?

Exercise 2.5

What values will the variables `a`, `b`, and `c` have after executing the following code:

```
int a = 4;
int b = 2;
int c = 7;

b = a + c;
c = b - 2;
a = a + a;
b = b * 2;
c = c - c;
```

Here, the operator `-` denotes subtraction and `*` represents multiplication.

Once you have arrived at an answer, type this code into the main function of a new program and print the values of the variables. Did you get it right?

Exercise 2.6

What happens when an integer is divided by another integer? Try running the following code:

```
cout << (5 / 3) << endl;
cout << (15 / 5) << endl;
cout << (2 / 2) << endl;
cout << (7 / 2) << endl;
cout << (-7 / 2) << endl;
cout << (7 / -2) << endl;
```

There are many other types than `int`. We have seen one (although without its correct name), the type for text. You can see some of the most common types in Listing 2.3.

Listing 2.3 Types

```
#include <iostream>

using namespace std;

int main() {
  string text = "Johan said: \"heya!\" ";
  cout << text << endl;

  char letter = '@';
  cout << letter << endl;

  int number = 7;
  cout << number << endl;

  long long largeNumber = 888888888888LL;
  cout << largeNumber << endl;

  double decimalNumber = 513.23;
  cout << decimalNumber << endl;

  bool thisisfalse = false;
  bool thisistrue = true;
  cout << thisistrue << " and " << thisisfalse << endl;
}
```

The text data type is called `string`. Values of this type must be enclosed with double quotes. If we actually want to include a quote in a string, we type

`\"`.

There exists a data type containing one single letter, the `char`. Such a value is surrounded by single quotes. The `char` value containing the single quote is written `'\'`', similarly to how we included double quotes in strings.

Then comes the `int`, which we discussed earlier. The `long long` type contains integers just like the `int` type. They differ in how large integers they can contain. An `int` can only contain integers between -2^{31} and $2^{31} - 1$ while a `long long` extends this range to -2^{63} to $2^{63} - 1$.

Exercise 2.7

Since `\"` is used to include a double quote in a string, we can not include backslashes in a string like any other character. For example, how would you output the verbatim string `\"`? Find out how to include a literal backslash in a string (for example by searching the web or thinking about how we included the different quote characters).

Exercise 2.8

Write a program that assigns the minimum and maximum values of an `int` to a `int` variable `x`. What happens if you increment or decrement this value using `x = x + 1;` or `x = x - 1;` respectively and print its new value?

Competitive Tip

One of the most common sources for errors in code is trying to store an integer value outside the range of the type. Always make sure your values fit inside the range of an `int` if you use it. Otherwise, use `long longs`!

One of the reasons for why we do not simply use `long long` all the time is that some operations involving `long longs` can be slower using `ints` under certain conditions.

Next comes the `double` type. This type represents decimal numbers. Note that the decimal sign in C++ is a **dot**, not a comma. There is also another similar type called the `float`. The difference between these types are similar to that of the `int` and `long long`. A `double` can represent "more" decimal numbers than a `float`. This may sound weird considering that there is an infinite number of decimal numbers even between 0 and 1. However, a computer can clearly not represent every decimal number – not even those between 0 and 1. To do this, it would need infinite memory to distinguish between these numbers. Instead, they represent a limited set of numbers – those with a relatively short binary expansion, such as $(101011.01)_2$ (the number 43.25 in decimal). Doubles are able to represent numbers with higher precision than floats.

The last of our common types is the `bool` (short for ***boolean***). This type can only contain one of two values – it is either `true` or `false`. While this may look useless at a first glance, the importance of the boolean becomes apparent later.

Exercise 2.9

In the same way the integer types had a valid range of values, a `double` cannot represent arbitrarily large values. Find out what the minimum and maximum values a `double` can store is.

C++ has a construct called the ***typedef***, or type definition. It allows us to give certain types new names. Since typing `long long` for every large integer variable is very annoying, we could use a type definition to alias it with the much shorter `ll` instead. Such a typedef statement looks like this:

```
typedef long long ll;
```

On every line after this statement, we can use `ll` just as if it were a `long long`:

```
ll largeNumber = 888888888888LL;
```

Sometimes we use types with very long names but do not want to shorten them using type definitions. This could be the case when we use many different such types and typedefing them would take unnecessarily long time. We then resort to using the `auto` "type" instead. If a variable is declared as `auto` and assigned a value at the same time its type is inferred from that of the value. This means we could write

```
auto str = "a string";
```

instead of

```
string str = "a string";
```

2.4 Input and Output

In previous sections we occasionally printed things onto our screen. To spice our code up a bit we are now going to learn how to do the reverse – reading values which we type on our keyboards into a running program! When we run a program we may type things in the window that appears. Pressing the Enter key allows the program to read what we have written so far.

Reading input data is done just as you would expect, almost entirely symmetric to printing output. Instead of `cout` we use `cin`, and instead of << `variable` we use >> `variable`, i.e.

```
cin >> variable;
```

Type in the program from Listing 2.4 to see how it works.

Listing 2.4 Input

```
#include <iostream>

using namespace std;

int main() {
  string name;
  cout << "What's your first name?" << endl;
  cin >> name;

  int age;
  cout << "How old are you?" << endl;
  cin >> age;

  cout << "Hi, " << name << "!" << endl;
  cout << "You are " << age << " years old." << endl;
}
```

Exercise 2.10

What happens if you type an invalid input, such as your first name instead of your age?

When the program reads input into a string variable it only reads the text until the first whitespace. To read an entire line you should instead use the `getline` function (Listing 2.5).

Listing 2.5 getline

```cpp
#include <iostream>

using namespace std;

int main() {
  string line;
  cout << "Type some text, and press enter: " << endl;
  getline(cin, line);

  cout << "You typed: " << line << endl;
}
```

We revisit more advanced input and output concepts in Section 3.9 about the standard library.

2.5 Operators

Earlier we saw examples of what is called ***operators***, such as the assignment operator `=`, and the arithmetic operators `+ - * /`, which stand for addition, subtraction, multiplication and division. They work almost like they do in mathematics, and allow us to write code such as the one in Listing 2.6.

Listing 2.6 Operators

```
#include <iostream>

using namespace std;

int main() {
  int a = 0;
  int b = 0;

  cin >> a >> b;

  cout << "Sum: " << (a + b) << endl;
  cout << "Difference: " << (a - b) << endl;
  cout << "Product: " << (a * b) << endl;
  cout << "Quotient: " << (a / b) << endl;
  cout << "Remainder: " << (a % b) << endl;
}
```

Exercise 2.11

Type in Listing 2.6 and test it on a few different values. Most importantly, test:

- $b = 0$
- Negative values for a and/or b
- Values where the expected result is outside the valid range of an `int`

As you probably noticed, the division operator of C++ performs so-called *integer division*. This means the answer is rounded to an integer (towards 0). Hence `7 / 3 = 2`, with remainder 1, and `-7 / 3 = -2`.

Exercise 2.12

If division rounds down towards zero, how do you compute $\frac{x}{y}$ compute to an integer *away from* zero?

The snippet introduces the ***modulo*** operator, `%`. It computes the remainder of the first operand when divided by the second. As an example, `7 % 3 = 1`. Different programming languages have different behaviours regarding modulo operations on negative integers. In particular, the value of a modulo operation can be negative when including negative operands.

In case we want the answer to be a decimal number instead of performing integer division one of the operands must be a `double` (Listing 2.7).

Listing 2.7 Division Operators

```cpp
int a = 6;
int b = 4;

cout << (a / b) << endl;

double aa = 6.0;
double bb = 4.0;

cout << (aa / bb) << endl;
```

We end this section with some shorthand operators. Check out Listing 2.8 for some examples. Each arithmetic operator has a corresponding combined assignment operator. Such an operator, e.g. `a += 5;`, is equivalent to `a = a + 5`; They act as if the variable on the left hand side is also the left hand side of the corresponding arithmetic operator and assign the result of this computation to said variable. Hence, the above statement increases the variable `a` with 5.

Listing 2.8 Shorthand Operators

```cpp
int num = 0;

num += 1;
cout << num << endl;

num *= 2;
cout << num << endl;

num -= 3;
cout << num << endl;

cout << num++ << endl;
cout << num << endl;

cout << ++num << endl;
cout << num << endl;

cout << num-- << endl;
cout << num << endl;
```

It turns out that addition and subtraction with 1 is a fairly common operation. So common, in fact, that additional operators were introduced into C++ for this purpose of saving an entire character compared to the highly verbose `+=1` operator. These operators consist of two plus signs or two minus signs. For instance, `a++` increments the variable by 1.

We sometimes use the fact that these expressions also evaluate to a value. Which value this is depends on whether we put the operator before or after the variable name. By putting ++ before the variable, the value of the expression will be the incremented value. If we put it afterwards we get the original value. To get a better understanding of how this works it is best if you type the code in Listing 2.8 in yourself and analyze the results.

We end the discussion on operators by saying something about *operator precedence*, i.e. the order in which operators are evaluted in expressions. In mathematics, there is a well-defined precedence: brackets go first, then exponents, followed by division, multiplication, addition, and subtraction. Furthermore, most operations (exponents being a notable exception) have left-to-right associativity so that $5 - 3 - 1$ equals $((5 - 3) - 1) = 1$ rather than $(5 - (3 - 1)) = 3$. In C++, there are a lot of operators, and knowing precedence rules can easily save you from bugs in your future code. We recommend that you look up their precedence rules on-line.

Exercise 2.13 — Kattis Exercises

R2 – r2

Faktor – faktor

Herman – herman

Pizza Crust – pizza2

2.6 If Statements

In addition to assignment and arithmetic there are a large number of ***comparison operators***. These compare two values and evaluate to a `bool` value depending on the result of the comparison (see Listing 2.9).

Listing 2.9 Comparison Operators

```
a == b // check if a equals b
a != b // check if a and b are different
a > b // check if a is greater than b
a < b // check if a is less than b
a <= b // check if a is less than or equal to b
a >= b // check if a is greater than or equal to b
```

Exercise 2.14

Write a program that reads two integers as input, and prints the result of the different comparison operators from Listing 2.9.

A `bool` can also be ***negated*** using the `!` operator. So the expression `!false` (which we read as "not false") has the value `true` and vice versa `!true` evaluates to `false`. The operator works on any boolean expressions, so that if `b` would be a boolean variable with the value `true`, then the expression `!b` evaluates to `false`.

There are two more important boolean operators. The ***and*** operator `&&` takes two boolean values and evaluates to `true` if and only if both values were `true`. Similarly, the ***or*** operator `||` evalutes to `true` if and only if at least one of its operands were `true`.

A major use of boolean variables is in conjunction with ***if*** statements (also called ***conditional*** statements). They come from the necessity of executing certain lines of code **if** (and only if) some condition is true. Let us write a program that takes an integer as input, and tells us whether it is odd or even. We can do this by computing the remainder of the input when divided by 2 (using the modulo operator) and checking if it is 0 (even number), 1 (positive odd number) or, -1 (negative odd number). An implementation of this can be seen in Listing 2.10.

An if statement consists of two parts – a ***condition***, given inside brackets after the `if` keyword, followed by a body – some lines of code surrounded by curly brackets. The code inside the body will be executed in case the condition evaluates to `true`.

Our odd or even example contains a certain redundancy. If a number is not even we already know it is odd. Checking this explicitly using the modulo

Listing 2.10 Odd or Even

```cpp
int input;
cin >> input;
if (input % 2 == 0) {
    cout << input << " is even!" << endl;
}
if (input % 2 == 1 || input % 2 == -1) {
    cout << input << " is odd!" << endl;
}
```

operator seems to be a bit unnecessary. Indeed, there is a construct that saves us from this verbosity – the ***else*** statement. It is used after an if statement and contains code that should be run if the condition given to the condition of an if statement is `false`. We can adopt this to simplify our odd and even program to the one in Listing 2.11.

Listing 2.11 Odd or Even 2

```cpp
int input;
cin >> input;
if (input % 2 == 0) {
    cout << input << " is even!" << endl;
} else {
    cout << input << " is odd!" << endl;
}
```

There is one last if-related construct – the ***else if***. Since code is worth a thousand words, we demonstrate how it works in Listing 2.12 by implementing a helper for the children's game *FizzBuzz*. In FizzBuzz, one goes through the natural numbers in increasing order and say them out loud. When the number is divisible by 3 you instead say Fizz. If it is divisible by 5 you say Buzz, and if it is divisible by both you say FizzBuzz.

Exercise 2.15

Run the program with the values 30, 10, 6, 4. Explain the output you get.

Listing 2.12 Else If

```
int input;
cin >> input;
if (input % 15 == 0) {
    cout << "FizzBuzz" << endl;
} else if (input % 5 == 0) {
    cout << "Buzz" << endl;
} else if (input % 3 == 0) {
    cout << "Fizz" << endl;
} else {
    cout << input << endl;
}
```

Exercise 2.16 — Kattis Exercises

Aaah! – aaah
Hint: You can use `s.size()` to compute the length of a `string s`.

Quadrant Selection – quadrant

Take Two Stones – twostones

Spavanac – spavanac

2.7 For Loops

Another rudimentary building block of programs is the ***for loop***. A for loop is used to execute a block of code multiple times. The most basic loop repeats code a fixed number of times as in the example from Listing 2.13.

A for loop is built up from four parts. The first three parts are the semi-colon separated statements immediately after the `for` keyword. In the first of these parts you write some expression, such as a variable declaration. In the second part you write an expression that evaluates to a `bool`, such as a comparison between two values. In the third part you write another expression.

The first part will be executed only once – it is the first thing that happens in a loop. In this case, we declare a new variable `i` and set it to `0`.

The loop will then be repeated until the condition in the second part is false. Our example loop will repeat until `i` is no longer less than `repetitions`.

Listing 2.13 For Loops

```cpp
#include <iostream>

using namespace std;

int main() {
  int repetitions = 0;
  cin >> repetitions;

  for (int i = 0; i < repetitions; i++) {
    cout << "This is repetition " << i << endl;
  }
}
```

The third part executes after each execution of the loop. Since we use the variable `i` to count how many times the loop has executed, we want to increment this by 1 after each iteration.

Together, these three parts make sure our loop will run exactly `repetitions` times. The final part of the loop is the statements within curly brackets. Just as with the if statements, this is called the body of the loop and contains the code that will be executed in each repetition of the loop. A repetition of a loop is in algorithm language more commonly referred to as an *iteration*.

Exercise 2.17

What happens if you enter a negative value as the number of loop repetitions?

Exercise 2.18

Design a loop that instead counts backwards, from $repetitions - 1$ to 0.

Exercise 2.19 — Kattis Exercises

Stuck In A Time Loop – timeloop

FizzBuzz – fizzbuzz

Cold-puter Science – cold

Tarifa – tarifa

Trik – trik

Within a loop, two useful keywords can be used to modify the loop – `continue` and `break`. Using `continue;` inside a loop exits the current iteration and starts the next one. `break;` on the other hand, exits the loop altogether. For an example, consider Listing 2.14.

Listing 2.14 Break and Continue

```
int check = 36;

for (int divisor = 2; divisor * divisor <= check; ++divisor) {
  if (check % divisor == 0) {
    cout << check << " is not prime!" << endl;
    cout << "It equals " << divisor << " x " << (check / divisor) << endl;
    break;
  }
}

for (int divisor = 1; divisor <= check; ++divisor) {
  if (check % divisor == 0) {
    continue;
  }
  cout << divisor << " does not divide " << check << endl;
}
```

Exercise 2.20

What will the following code snippet output?

```
for (int i = 0; false; i++) {
  cout << i << endl;
}

for (int i = 0; i >= -10; --i) {
  cout << i << endl;
}

for (int i = 0; i <= 10; ++i) {
  if (i % 2 == 0) continue;
  if (i == 8) break;
  cout << i << endl;
}
```

2.8 While Loops

There is a second kind of loop, which is simpler than the for loop. It is called a ***while loop***, and works like a for loop where the initial statement and the update statement are removed, leaving only the condition and the body. It can be used when you want to loop over something until a certain condition is false (Listing 2.15).

Listing 2.15 While

```
#include <iostream>

using namespace std;

int main() {
  int num = 9;
  while (num != 1) {
    if (num % 2 == 0) {
      num /= 2;
    } else {
      num = 3 * num + 1;
    }
    cout << num << endl;
  }
}
```

The `break;` and `continue;` statements work the same way as the do in a for loop.

2.9 Functions

In mathematics a ***function*** is something that takes one or more arguments and computes some value based on them. Common functions include the squaring function $\mathrm{square}(x) = x^2$, the addition function $\mathrm{add}(x, y) = x + y$ or, the minimum function $\min(a, b)$.

Functions exists in programming as well but work a bit differently. Indeed, we have already seen a function – the `main()` function. We have implemented the example functions in Listing 2.16.

Listing 2.16 Functions

```cpp
#include <iostream>

using namespace std;

int square(int x) {
  return x * x;
}

int min(int x, int y) {
  if (x < y) {
    return x;
  } else {
    return y;
  }
}

int add(int x, int y) {
  return x + y;
}

int main() {
  int x, y;
  cin >> x >> y;
  cout << x << "^2 = " << square(x) << endl;
  cout << x << " + " << y << " = " << add(x, y) << endl;
  cout << "min(" << x << ", " << y << ") = " << min(x, y) << endl;
}
```

In the same way that a variable declaration starts by proclaiming what data type the variable contains a function declaration states what data type the function evaluates to. Afterwards, we write the name of the function followed by its arguments (which is a comma-separated list of variable declarations). Finally, we give it a body of code wrapped in curly brackets.

All of these functions contain a statement with the `return` keyword, unlike our main function. A `return` statement says "stop executing this function, and return the following value!". Thus, when we call the squaring function by `square(x)`, the function will compute the value `x * x` and make sure that `square(x)` evaluates to just that.

Why have we left a return statement out of the main function? In `main()`, the compiler inserts an implicit `return 0;` statement at the end of the function.

Exercise 2.21

What will the following function calls evaluate to?

```
square(5);
add(square(3), 10);
min(square(10), add(square(9), 23));
```

Exercise 2.22

We declared all of the new arithmetic functions above our `main` function in the example. Why did we do this? What happens if you move one below the `main` function instead? (Hint: what happens if you try to use a variable before declaring it?)

An important fact of function calling is that the arguments we send along are copied. If we try to change them by assigning values to our arguments, we will not change the original variables in the calling function (see Listing 2.17 for an example).

We can also choose to not return *anything* by using the `void` return type. This may seem useless since nothing ought to happen if we call a function but does not get anything in return. However, there are ways we can affect the program without returning.

Listing 2.17 Copying

```
void change(int val) {
  val = 0;
}

int main() {
  int variable = 100;
  cout << "Variable is " << variable << endl;
  change(variable);
  cout << "Variable is " << variable << endl;
}
```

The first one is by using ***global*** variables. It turns out that variables may be declared outside of a function. It is then available to every function in your program. Changes to a global variable by one function are also be seen by other functions (try out Listing 2.18 to see them in action).

Listing 2.18 Global Variables

```
int currentMoney = 0;

void deposit(int newMoney) {
  currentMoney += newMoney;
}
void withdraw(int withdrawal) {
  currentMoney -= withdrawal;
}

int main() {
  cout << "Currently, you have " << currentMoney << " money" << endl;
  deposit(1000);
  withdraw(2000);
  cout << "Oh-oh! Your current balance is " << currentMoney << " :(" << endl;
}
```

Secondly, we may actually change the variables given to us as arguments by declaring them as ***references***. Such an argument is written by adding a `&` before the variable name, for example `int &x`. If we perform assignments to the variable `x` within the function we change the variable used for this argument in the calling function instead. Listing 2.19 contains an example of using references.

Listing 2.19 References

```cpp
// Note &val instead of val
void change(int &val) {
  val = 0;
}

int main() {
  int variable = 100;
  cout << "Variable is " << variable << endl;
  change(variable);
  cout << "Variable is " << variable << endl;
}
```

Exercise 2.23

Why is the function call `change(4)` not valid C++? (Hint: what exactly are we changing when we assign to the reference in `func`?)

Exercise 2.24 — Kattis Exercise

Arithmetic Functions – arithmeticfunctions

Logic Functions – logicfunctions

2.10 Structures

Algorithms operate on data, usually lots of it. Programming language designers therefore came up with many ways of organizing the data our programs use. One of these constructs is the ***structure*** (also called a record, and in some languages have a close approximation called classes). Structures are a special kind of data type that can contain member variables – variables inside them – and member functions – functions which can operate on member variables.

The basic syntax used to define a structure looks like this:

```cpp
struct Point {
    double x;
    double y;
};
```

This particular structure contains two member variables, `x` and `y`, representing the coordinates of a point in 2D Euclidean space.

Once we have defined a structure we can create ***instances*** of it. Every instance has its own copy of the member variables of the structure.

To create an instance the same syntax as with other variables is used. We can access the member variables of a structure using the `instance.variable` syntax:

```
Point origin; // create an instance of the Point structure

// set the coordinates to (0, 0)
origin.x = 0;
origin.y = 0;

cout << "The origin is (" << origin.x << ", "
     << origin.y << ")." << endl;
```

As you can see structures allow us to group certain kinds of data together in a logical fashion. Later on, this will simplify the coding of certain algorithms and data structures immensely.

There is an alternate way of constructing instances called ***constructors***. A constructor looks like a function inside our structure and allows us to pass arguments when we create a new instance of a struct. The constructor receives these arguments to help set up the instance.

Let us add a constructor to our point structure, to more easily create instances:

```
struct Point {
    double x;
    double y;

    Point(double theX, double theY) {
        x = theX;
        y = theY;
    }
};
```

The newly added constructor lets us pass two arguments when constructing the instance to set the coordinates correctly. With it, we avoid the two extra statements to set the member variables.

```
Point p(4, 2.1);
cout << "The point is (" << p.x << ", " << p.y << ")." << endl;
```

Structure values can also be constructed outside of a variable declaration using the syntax

```
Point(1, 2);
```

so that we can reassign a previously declared variable with

```
p = Point(1, 2);
```

We can also define functions inside the structure. These functions work just like any other functions except they can also access the member variables of the instance that the member function is called on. For example, we might want a convenient way to mirror a certain point in the x-axis. This could be accomplished by adding a member function:

```
struct Point {
    double x;
    double y;

    Point(double theX, double theY) {
        x = theX;
        y = theY;
    }

    Point mirror() {
        return Point(x, -y);
    }
};
```

To call the member function `mirror()` on the point `p`, we write `p.mirror()`.

Exercise 2.25

Add a `translate` member function to the point structure. It should take two double values `x` and `y` as arguments, returning a new point which is the instance point translated by (x, y).

In our `mirror` function, we are not modifying any of the internal state of the function. We can make this fact clearer by declaring the function to be `const` (similarly to a `const` variable):

```
Point mirror() const {
    return Point(x, -y);
}
```

This change ensures that our function can not change any of the member variables.

Exercise 2.26

What happens if we try to change a member variable in a `const` member function?

Exercise 2.27

Fill in the remaining code to implement this structure:

```
struct Quotient {
    int nominator;
    int denominator;

    // Construct a new Quotient with the given
    // numerator and denominator
    Quotient(int n, int d) { }

    // Return a new Quotient, this instance plus
    // the "other" instance
    Quotient add(const Quotient &other) const { }

    // Return a new Quotient, this instance times
    // the "other" instance
    Quotient multiply(const Quotient &other) const { }

    // Output the value on the screen in the format n/d
    void print() const { }

};
```

Exercise 2.28 — Kattis Exercise

Bank Account – bankaccount

2.11 Arrays

In the Sorting Problem from Chapter 1 we often spoke of the data type "sequence of integers". Until now, none of the data types we have seen in C++ represents this kind of data. We present the ***array***. It is a special type of variable, which can contain a large number of variables of the same type. For example, it could be used to represent the recurring data type "sequence of integers" from the Sorting Problem in Chapter 1. When declaring an array, we specify the type of variable it should contain, its name, and its size using the syntax:

```
type name[size];
```

For example, an integer array of size 50 named `seq` would be declared with

```
int seq[50];
```

This creates 50 integer "variables" which we can refer to using the syntax `seq[index]`, starting from zero (they are zero-indexed). Thus we can use `seq[0]`, `seq[1]`, etc., all the way up to `seq[49]`. The values are called the ***elements*** of the array.

Be aware that using an index outside the valid range for a particular array (i.e. below 0 or above the size $-$ 1) can cause erratic behavior in the program without crashing it.

If you declare a global array all elements get a default value. For numeric types this is 0, for booleans this is `false`, for strings this is the empty string and so on. If, on the other hand, the array is declared in the body of a function that guarantee does not apply. Instead of being zero-initialized, the elements *can have random values*.

Later on (Section 3.1) we transition from using arrays to a structure from the standard library which serves the same purpose – the *vector*.

Exercise 2.29 — Kattis Exercise

Booking a Room – bookingaroom

I've Been Everywhere, Man – everywhere

Line Them Up – lineup

Patuljci – patuljci

2.12 The Preprocessor

C++ has a powerful tool called the ***preprocessor***. This utility is able to read and modify your code using certain rules during compilation. The commonly used `#include` is a preprocessor directive that includes a certain file in your code.

Besides file inclusion, we mostly use the `#define` directive. It allows us to replace certain tokens in our code with other ones. The most basic usage is

```
#define TOREPLACE REPLACEWITH
```

which replaces the token `TOREPLACE` in our program with `REPLACEWITH`. The true power of the define comes when using define directives with parameters. These look similar to functions and allows us to replace certain expressions with another one, additionally inserting certain values into it. We call these ***macros***. For example the macro

```
#define rep(i,a,b) for (int i = a; i < b; i++)
```

means that the expression

```
rep(i,0,5) {
    cout << i << endl;
}
```

is expanded to

```
for (int i = 0; i < 5; ++i) {
    cout << i << endl;
}
```

You can probably get by without ever using macros in your code. The reason we discuss them is because we are going to use them in code in the book so it is a good idea to at least be familiar with their meaning. They are also used in competitive programming in general,

2.13 Template

In competitive programming, one often uses a *template*, with some shorthand typedef's and preprocessor directives. Here, we given an example of the template used in some of the C++ code in this book.

```
#include <bits/stdc++.h>
using namespace std;

#define rep(i, a, b) for(int i = a; i < (b); ++i)
#define trav(a, x) for(auto& a : x)
#define all(x) x.begin(), x.end()
#define sz(x) (int)(x).size()
typedef long long ll;
typedef pair<int, int> pii;
typedef vector<int> vi;

int main() {
}
```

The `trav(a, x)` macro is used to iterate through all members of a data structure from the standard library such as the vector – the first topic of Chapter 3.

2.14 Additional Exercises

Exercise 2.30 — Kattis Exercise

Solving for Carrots – carrots

Paul Eigon – pauleigon

Dice Game – dicegame

Reverse Binary Numbers – reversebinary

Modulo – modulo

3D Printer – 3dprinter

Sibice – sibice

Kornislav – kornislav

Left Beehind – leftbeehind

2.15 Chapter Notes

C++ was invented by Danish computer scientist Bjarne Stroustrup. Bjarne has also published a book on the language, *The C++ Programming Language*[23], that contains a more in-depth treatment of the language. It is rather accessible to C++ beginners but is better read by someone who have some prior programming experience (in any programming language).

C++ is standardized by the International Organization for Standardization (ISO). These standards are the authoritative source on what C++ is. The final drafts of the standards can be downloaded at the homepage of the Standard C++ Foundation[1].

There are many online references of the language and its standard library. The two we use most are:

- `http://en.cppreference.com/w/`
- `http://www.cplusplus.com/reference/`

[1]`https://isocpp.org/`

Chapter 3

The C++ Standard Library

In this chapter we study parts of the C++ standard library. We start by examining a number of basic ***data structures***. Data structures help us organize the data we work with in the hope of making processing both easier and more efficient. Different data structures serve widely different purposes and solve different problems. Whether a data structure fit our needs depends on what operations we wish to perform on the data. We consider neither the efficiency of the various operations in this chapter nor how they are implemented. These concerns are postponed until Chapter 6.

The standard library also contains many useful algorithms such as sorting and various mathematical functions. These are discussed after the data structures.

In the end, we take a deeper look at string handling in C++ and some more input/output routines.

3.1 vector

One of the final things discussed in the C++ chapter was the fixed-size array. As you might remember the array is a special kind of data type that allows us to store multiple values of the same data type inside what appeared to us as a single variable. Arrays are a bit awkward to work with in practice. When passing them as parameters we must also pass along the size of the array. We are also unable to change the size of arrays once declared nor can we easily remove or insert elements, or copy arrays.

The *dynamic array* is a special type of array that can change size (hence the name dynamic). It also supports operations such as removing and inserting elements at any position in the list.

The C++ standard library includes a dynamic array under the name `vector`, an alternative name for dynamic arrays. To use it you must include the `vector` file by adding the line

```
#include <vector>
```

among your other includes at the top of your program.

Just like ordinary arrays vectors need to know what types they store. This is done using a somewhat peculiar syntax. To create a vector containing strings named `words` we write

```
vector<string> words;
```

This angled bracket syntax appears again later when using other C++ structures from the standard library.

Once a vector is created elements can be appended to it using the `push_back` member function. The following four statements would add the words `Simon is a fish` as separate elements to the vector:

```
words.push_back("Simon");
words.push_back("is");
words.push_back("a");
words.push_back("fish");
```

To refer to a specific element in a vector you can use the same operator `[]` as for arrays. Thus, `words[i]` refers to the i'th value in the vector (starting at 0).

```
cout << words[0] << " " << words[1] << " "; // Prints Simon is
cout << words[2] << " " << words[3] << " "; // Prints a fish
```

Just as with normal arrays accessing indices outside the valid range of the vector can cause weird behaviour in your program.

We can get the current size of an array using the `size()` member function:

```
cout << "The vector contains " << words.size() << " words" << endl;
```

There is also an `empty()` function that can be used to check if the vector contains no elements. These two functions are part of basically every standard library data structure.

Exercise 3.1 — Kattis Exercises

Vector Functions – vectorfunctions

You can also create dynamic arrays that already contain a number of elements. This is done by passing an integer argument when first declaring the vector. They are filled with the same default value as (global) arrays are when created.

```
vector<int> vec(5); // creates a vector containing 5 zeroes
```

3.1.1 Iterators

A concept central to the standard library is the *iterator*. An iterator is an object which "points to" an element in some kind of data structure (such as a vector). The type of an iterator for a data structure of type `t` is `t::iterator`. An iterator of a `vector<string>` thus has the type `vector<string>::iterator`. Most of the time we instead use the `auto` type since this is very long to type.

Not all data structures support iterators. It is most commonly used for the `vector` and the `set` (a structure we study later).

To get an iterator to the first element of a `vector`, we use `begin()`:

```
auto first = words.begin();
```

We can get the value that an iterator points at using the `*` operator:

```
cout << "The first word is " << *first << endl;
```

If we have an iterator `it` pointing at the i:th element of a vector we can get a new iterator pointing to another value by adding or subtracting an integer value to the iterator. For example, `it + 4` points to the $(i + 4)$'th element of the vector, and `it - 1` is the iterator pointing to the $(i - 1)$'st element.

Not all iterators support adding or subtracting arbitrary integer values though. Some iterators can only move one step backwards or forwards by using the ++ and - operators.

There is a special kind of iterator which points to the first position *after* the last element. We get this iterator by using the function `end()`. It allows us to iterate through a vector in the following way:

```
for (auto it = words.begin(); it != words.end(); it++) {
        string value = *it;
        cout << value << endl;
}
```

In this loop we start by creating an iterator which points to the first element of the vector. Our update condition will repeatedly move the iterator to the next element in the vector. The loop condition ensures that the loop breaks when the iterator first points to the element past the end of the vector.

In addition to the `begin()` and `end()` pair of iterators, there is also `rbegin()` and `rend()`. They work similarly, except that they are *reverse iterators* - they iterate in the other direction. Thus, `rbegin()` actually points to the last element of the vector, and `rend()` to an imaginary element before the first element of the vector. If we move a reverse iterator in a positive direction, we will actually move it in the opposite direction (i.e. adding 1 to a reverse iterator makes it point to the element *before* it in the vector).

Exercise 3.2

Use the `rbegin()/rend()` iterators to code a loop that iterates through a vector in the reverse order.

Certain operators on a vector require the use of vector iterators. For example, the `insert` and `erase` member functions, used to insert and erase elements at arbitrary positions, take iterators to describe positions. When removing the second element, we write

```
words.erase(words.begin() + 1);
```

The `insert()` function uses an iterator to know at what position an element should be inserted. If it is passed the `begin()` iterator the new element will be inserted at the start of the array. Similarly, as an alternative to `push_back()` we could have written

```
words.insert(words.end(), "food");
```

to insert an element at the end of the vector.

Exercise 3.3

After adding these two lines, what would the loop printing every element of the vector `words` output?

3.2 queue

The `queue` structure corresponds to a plain, real-life queue. It supports mainly two operations: appending an element to the back of the queue, and extracting the first element of the queue. The structure is in the `queue` file so it must be included using

```
#include <queue>
```

As with all standard library data structures declaring a queue requires us to provide the data type which we wish to store in it. To create a queue storing `int`s we would use the statement

```
queue<int> q;
```

We use mainly five functions when dealing with queues:

- `push(x)`: add the element `x` to the **back of the queue**
- `pop()`: remove the element from the **front of the queue**
- `front()`: return the element from the **front of the queue**
- `empty()`: return `true` if and only if the queue is empty
- `size()`: return the number of elements in the queue

Exercise 3.4

There is a similar data structured called a ***dequeue***. The standard library version is named after the abbreviation `deque` instead. Use one of the C++ references from the C++ chapter notes (Section 2.15) to find out what this structure does and what its member functions are called.

3.3 `stack`

A `stack` is a structure very similar to a `queue`. The difference is that when `push()`ing something to a stack, it is added first to the stack instead of last. To use it you need to include

```
#include <stack>
```

Creating a stack containing e.g. `int`s is as easy as creating a queue:

```
stack<int> q;
```

We use mainly five functions when dealing with queues:

- `push(x)`: add the element `x` to the **top of the stack**
- `pop()`: remove the element from the **top of the stack**
- `top()`: return the element from the **top of the stack**
- `empty()`: return `true` if and only if the stack is empty
- `size()`: return the number of elements in the stack

Note the change in terminology. Instead of the first and last elements being called front and back as for the queue they are instead called top and bottom in a stack.

3.4 priority_queue

The queue and stack structures are arguably unnecessary, since they can be emulated using a vector (see Sections 6.2, 6.3). This is not the case for the next structure, the `priority_queue`.

The structure is similar to a queue or a stack, but instead of insertions and extractions happening at one of the endpoints of the structure, the **greatest** element is always returned during the extraction.

The structure is located in the same file as the `queue` structure, so add

```
#include <queue>
```

to use it.

To initialize a priority queue, use the same syntax as for the other structures:

```
priority_queue<int> pq;
```

This time there is one more way to create the structure that is important to remember. It is not uncommon to prefer the sorting to be done according to some other order than descending. For this reason there is another way of creating a priority queue. One can specify a ***comparison function*** that takes two arguments of the type stored in the queue and returns true if the first one should be considered less than the second. This function can be given as an argument to the type in the following way:

```
bool cmp(int a, int b) {
    return a > b;
}

priority_queue<int, vector<int>, cmp> pq;

// or equivalently
priority_queue<int, vector<int>, greater<int>> pq;
```

Note that a priority queue by default returns the greatest element. If we want to make it return the smallest element, the comparison function needs to instead say that the smallest of the two elements actually is the greatest, somewhat counter-intuitively.

Interactions with the queue is similar to that of the other structures:

- `push(x)`: add the element `x` to the priority queue
- `pop()`: remove the **greatest** element from the priority queue
- `top()`: return the **greatest** element from the priority queue
- `empty()`: return `true` if and only if the priority queue is empty
- `size()`: return the number of elements in the priority queue

Exercise 3.5 — Kattis Exercise

I Can Guess the Data Structure! – guessthedatastructure

Akcija – akcija

Cookie Selection – cookieselection

Pivot – pivot

3.5 `set` and `map`

The final data structures to be studied in this chapter are also the most powerful: the `set` and the `map`.

The `set` structure is similar to a mathematical set (Section A.2), in that it contains a collection of unique elements. Unlike the vector, particular positions in the structure can not be accessed using the `[]` operator. This may make sets seem worse than vectors. The advantage of sets is twofold. First, we can determine membership of elements in a set much more efficently compared to when using vectors (in Chapters 5 and 6, what this means will become clear). Secondly, sets are also sorted. This means we can quickly find the smallest and greatest values of the set.

Elements are instead accessed only through iterators, obtained using the `begin()`, `end()` and `find()` member functions. These iterators can be moved using the `++` and `--` iterators, allowing us to navigate through the set in sorted (ascending) order (with `begin()` referring to the smallest element).

Elements are inserted using the `insert` function and removed using the `erase` function. A concrete example usage is found in Listing 3.1

Listing 3.1 Sets

```cpp
set<int> s;
s.insert(4);
s.insert(7);
s.insert(1);

// find returns an iterator to the element if it exists
auto it = s.find(4);
// ++ moves the iterator to the next element in order
++it;
cout << *it << endl;

// if nonexistant, find returns end()
if (s.find(7) == s.end()) {
    cout << "7 is not in the set" << endl;
}

// erase removes the specific element
s.erase(7);

if (s.find(7) == s.end()) {
    cout << "7 is not in the set" << endl;
}

cout << "The smallest element of s is " << *s.begin() << endl;
```

A structure similar to the `set` is the `map`. It is essentially the same as a set, except the elements are called *keys* and have associated *values*. When declaring a map two types need to be provided – that of the key and that of the value. To declare a map with `string` keys and `int` values you write

```cpp
map<string, int> m;
```

Accessing the value associated with a key `x` is done using the `[]` operator, for example, `m["Johan"];` would access the value associated with the `"Johan"` key.

Exercise 3.6 — Kattis Exercise

Secure Doors – securedoors

Babelfish – babelfish

Listing 3.2 Maps

```cpp
map<string, int> age;
age["Johan"] = 22;
age["Simon"] = 23;

if (age.find("Aron") == age.end()) {
    cout << "No record of Aron's age" << endl;
}

cout << "Johan is " << age["Johan"] << " years old" << endl;
cout << "Anton is " << age["Anton"] << " years old" << endl;

age.erase("Johan");
cout << "Johan is " << age["Johan"] << " years old" << endl;

auto last = --age.end();
cout << (*last).first << " is " << (*last).second << " years old" << endl;
```

3.6 Math

Many algorithmic problems require mathematical functions. In particular you there is a heavy use of square roots and trigonometric functions in geometry problems. These of these functions are be found in the

```cpp
#include <cmath>
```

library.

We list some of the most common such functions here:

- `abs(x)`: computes $|x|$ (x if $x \geq 0$, otherwise $-x$)
- `sqrt(x)`: computes $\sqrt{x}$
- `pow(x, y)`: computes x^y
- `exp(x)`: computes e^x
- `log(x)`: computes $\ln(x)$
- `cos(x) / acos(x)`: computes $\cos(x)$ and $\arccos(x)$ respectively
- `sin(x) / asin(x)`: computes $\sin(x)$ and $\arcsin(x)$ respectively
- `tan(x) / atan(x)`: computes $\tan(x)$ and $\arctan(x)$ respectively

- `ceil(x) / floor(x)`: computes $\lceil x \rceil$ and $\lfloor x \rfloor$ respectively

There are also `min(x, y)` and `max(x, y)` functions which compute the minimum and maximum of the values x and y respectively. These are not in the `cmath` library however. Instead, they are in `algorithm`.

Exercise 3.7 — Kattis Exercises

Vacuumba – vacuumba

Half a Cookie – halfacookie

Ladder – ladder

A1 Paper – a1paper

3.7 Algorithms

A majority of the algorithms we regularly use from the standard library operate on sequences. To use algorithms, you need to include

```
#include <algorithm>
```

3.7.1 Sorting

Sorting a sequences is very easy in C++. The function for doing so is named `sort`. It takes two iterators marking the beginning and end of the interval to be sorted and sorts it in-place in ascending order. For example, to sort the first 10 elements of a vector named `v` you would use

```
sort(v.begin(), v.begin() + 10);
```

Note that the right endpoint of the interval is *exclusive* – it is not included in the interval itself. This means that you can provide `v.end()` as the end of the interval if you want to sort the vector until the end.

As with `priority_queues` or `sets`, the sorting algorithm can take a custom comparator if you want to sort according to some other order than that defined by the < operator. For example,

```
sort(v.begin(), v.end(), greater<int>());
```

would sort the vector `v` in descending order. You can provide other sorting functions as well. For example, you can sort numbers by their absolute value by passing in the following comparator:

```
bool cmp(int a, int b) {
    return abs(a) < abs(b);
}
sort(v.begin(), v.end(), cmp);
```

What happens if two values have the same absolute value when sorted with the above comparator? With `sort`, this behaviour is not specified: they can be ordered in any way. Occasionally you want that values compared by your comparison function as equal are sorted in the same order as they were given in the input. This is called a ***stable sort***, and is implemented in C++ with the function `stable_sort`.

To check if a vector *is* sorted, the `is_sorted` function can be used. It takes the same arguments as the `sort` function.

Exercise 3.8 — Kattis Exercises

Shopaholic – shopaholic

Busy Schedule – busyschedule

Sort of Sorting – sortofsorting

3.7.2 Searching

The most basic search operation is the `find` function. It takes two iterators representing an interval and a value. If one of the elements in the interval equals the value, an iterator to the element is returned. In case of multiple matches the first one is returned. Otherwise, the iterator provided as the end of the interval is returned. The common usage is

```
find(v.begin(), v.end(), 5);
```

which would return an iterator to the first instance of `5` in the vector.

To find out how many times an element appears in a vector, the `count` function takes the same arguments as the `find` function and returns the total number of matches.

If the array is sorted, you can use the much faster *binary search* operations instead. The `binary_search` function takes as argument a **sorted** interval given by two iterators and a value. It returns true if the interval contains the value. The `lower_bound` and `upper_bound` functions takes the same arguments as `binary_search`, but instead returns an iterator to the first element **not less** and **greater** than the specified value, respectively. For more details on how these are implemented, read Section 10.3.

3.7.3 Permutations

In some problems, the solution involves iterating through all *permutations* (Section 15.2) of a vector. As one of few languages, C++ has a built-in functions for this purpose: `next_permutation`. The function takes two iterators as arguments and rearranges the interval they specify to be the next permutation in lexicographical order. If there is no such permutation, the interval instead becomes sorted and the function returns `false`. This suggests the following common pattern to iterate through all permutations of a vector `v`:

```
sort(v.begin(), v.end());
do {
    // do something with v
} while (next_permutation(v.begin(), v.end()));
```

This do-while-syntax is similar to the while loop, except the condition is checked *after* each iteration instead of before. It is equivalent to

```
sort(v.begin(), v.end());
while (true) {
    // do something with v
    if (!next_permutation(v.begin(), v.end())) {
        break;
    }
}
```

Exercise 3.9 — Kattis Exercises

Veci – veci

3.8 Strings

We have already used the `string` type many times before. Until now one of the essential features of a string has been omitted – a `string` is to a large extent like a `vector` of `char`s. This is especially true in that you can access the individual characters of a string using the `[]` operator. For a string

```
string thecowsays = "boo";
```

the expression `thecowsays[0]` is the character `'b'`. Furthermore, you can `push_back` new characters to the end of a string.

```
thecowsays.push_back('p');
```

would instead make the string `boop`.

Exercise 3.10 — Kattis Exercises

Detailed Differences – detaileddifferences

Autori – autori

Skener – skener

3.8.1 Conversions

In some languages, the barrier between strings and e.g. integers is more fuzzy than in C++. In Java, for example, the code `"4" + 2` would append the *character* `'2'` to the string `"4"`, yielding the string `"42"`. This is not the case in C++ (what errors do you get if you try to do this?).

Instead, there are other ways to convert between strings and other types. The easiest way is through using the `stringstream` class. A `stringstream` essentially works as a combined `cin` and `cout`. An empty stream is declared by

```
stringstream ss;
```

Values can be written to the stream using the << operator and read from it using the >> operator. This can be exploited to convert strings to and from e.g. numeric types like this:

```
stringstream numToString;
numToString << 5;
string val;
numToString >> val; // val is now the string "5"

stringstream stringToNum;
stringToNum << "5";
int val;
stringToNum >> val; // val is now the integer 5
```

Just as with `cin`, you can use a `stringstream` to determine what type the next word is. If you try to read from a `stringstream` into an `int` but the next word is not an integer, the expression will evaluate to false:

```
stringstream ss;
ss << "notaninteger";
int val;
if (ss >> val) {
    cout << "read an integer!" << endl;
} else {
    cout << "next word was not an integer" << endl;
}
```

Exercise 3.11 — Kattis Exercises

Filip – filip

Stacking Cups – cups

3.9 Input/Output

Input and output is primarily handled by the `cin` and `cout` objects, as previsouly witnessed. While they are very easy to use, adjustments are sometimes necessary.

3.9.1 Detecting End of File

The first advanced usage is reading input until we run out of input (often called reading until the *end-of-file*). Normally, input formats are constructed so that you always know beforehand how many tokens of input you need to read. For example, lists of integers are often either prefixed by the size of the list or terminated by some special sentinel value. For those few times when we need to read input until the end we use the fact that `cin >> x` is an expression that evaluates to `false` if the input reading failed. This is also the case if you try to read an `int` but the next word is not actually an integer. This kind of input loop thus looks something like the following:

```
int num;
while (cin >> num) {
    // do something with num
}
```

Exercise 3.12 — Kattis Exercises

A Different Problem – different

Statistics – statistics

3.9.2 Input Line by Line

As we stated briefly in the C++ chapter, `cin` only reads a single word when used as input to a string. This is a problem if the input format requires us to read input line by line. The solution to this is the `getline` function, which reads text until the next newline:

```
getline(cin, str);
```

Be warned that if you use `cin` to read a single word that is the last on its line, the final newline is not consumed. That means that for an input such as

```
word
blah blah
```

the code

```
string word;
```

```
cin >> word;
string line;
getline(cin, line);
```

would produce an *empty* line! After `cin >> word` the newline of the line `word` still remains, meaning that `getline` only reads the (zero) remaining characters until the newline. To avoid this problem, you need to use `cin.ignore();` to ignore the extra newline before your `getline`.

Once a line has been read we often need to process all the words on the line one by one. For this, we can use the `stringstream`:

```
stringstream line(str);
string word;
while (line >> word) {
    // do something with word
}
```

The `stringstream` takes an argument that is the string you want to process. After this, it works just like `cin` does, except reading input from the string instead of the terminal. To use `stringstream`, add the include

```
#include <sstream>
```

Exercise 3.13 — Kattis Exercises

Bacon Eggs and Spam – baconeggsandspam

Compound Words – compoundwords

3.9.3 Output Decimal Precision

Another common problem is that outputting decimal values with `cout` produces numbers with too few decimals. Many problems stipulate that an answer is considered correct if it is within some specified relative or absolute precision of the judges' answer. The default precision of `cout` is 10^{-6}. If a problem requires higher precision, it must be set manually using e.g.

```
cout << setprecision(10);
```

If the function argument is x, the precision is set to 10^{-x}. This means that the above statement would set the precision of `cout` to 10^{-10}. This precision is normally the relative precision of the output (i.e. the total number of digits to print). If you want the precision to be absolute (i.e. specify the number of digits after the decimal point) you write

```
cout << fixed;
```

Exercise 3.14 — Kattis Exercises

A Real Challenge – areal

3.10 Additional Exercises

Exercise 3.15 — Kattis Exercises

Apaxiaaaaaaaaaaaans! – apaxiaaans

Different Distances – differentdistances

Odd Man Out – oddmanout

Timebomb – timebomb

Missing Gnomes – missinggnomes

3.11 Chapter Notes

In this chapter, only the parts from the standard library we deemed most important to problem solving were extracted. The standard library is much larger than this, of course. While you will almost always get by using only what we discussed additional knowledge of the library can make you a faster, more effective coder.

For a good overview of the library, `cppreference.com`[1] contains lists of the library contents categorized by topic.

[1]`http://en.cppreference.com/w/cpp`

Chapter 4

Implementation Problems

The "simplest" kind of problem we solve is those where the statement of a problem is so detailed that the difficult part is not figuring out the solution, but implementing it in code. This type of problem is mostly given in the form of performing some calculation or simulating some process based on a list of rules stated in the problem.

The Recipe

Swedish Olympiad in Informatics 2011, School Qualifiers

You have decided to cook some food. The dish you are going to make requires N different ingredients. For every ingredient, you know the amount you have at home, how much you need for the dish, and how much it costs to buy (per unit).

If you do not have a sufficient amount of some ingredient you need to buy the remainder from the store. Your task is to compute the cost of buying the remaining ingredients.

Input

The first line of input is an integer $N \leq 10$, the number of ingredients in the dish.

The next N lines contain the information about the ingredients, one per line.

An ingredient is given by three space-separated integers $0 \le h, n, c \le 200$ – the amount you have, the amount you need, and the cost per unit for this ingredient.

Output

Output a single integer – the cost for purchasing the remaining ingredients needed to make the dish.

This problem is not particularly hard. For every ingredient we need to calculate the amount which we need to purchase. The only gotcha in the problem is the mistake of computing this as $n - h$. The correct formula is $\max(0, n - h)$, required in case of the luxury problem of having more than we need. We then multiply this number by the ingredient cost and sum the costs up for all the ingredients.

Algorithm 4.1: The Recipe

```
procedure RECIPE($N$, int[] $h$, int[] $n$, int[] $c$)
    $ans \leftarrow 0$
    for $i \leftarrow 0$ to $N - 1$ do
        $ans \leftarrow ans + \max(0, n_i - h_i) \cdot c_i$
    return $ans$
```

Generally, the implementation problems are the easiest type of problems in a contest. They do not require much algorithmic knowledge so more contestants are able to solve them. However, not every implementation problem is easy to code. Just because implementation problems are easy to spot, understand, and formulate a solution to, you should not underestimate the difficulty coding them. Contestants usually fail implementation problems either because the algorithm you are supposed to implement is very complicated with many easy-to-miss details, or because the amount of code is very large. In the latter case, you are more prone to bugs because more lines of code tend to include more bugs.

Let us study a straightforward implementation problem that turned out to be rather difficult to code.

Game Rank

Nordic Collegiate Programming Contest 2016 – Jimmy Mårdell

The gaming company Sandstorm is developing an online two player game. You have been asked to implement the ranking system. All players have a rank determining their playing strength which gets updated after every game played. There are 25 regular ranks, and an extra rank, "Legend", above that. The ranks are numbered in decreasing order, 25 being the lowest rank, 1 the second highest rank, and Legend the highest rank.

Each rank has a certain number of "stars" that one needs to gain before advancing to the next rank. If a player wins a game, she gains a star. If before the game the player was on rank 6-25, and this was the third or more consecutive win, she gains an additional bonus star for that win. When she has all the stars for her rank (see list below) and gains another star, she will instead gain one rank and have one star on the new rank.

For instance, if before a winning game the player had all the stars on her current rank, she will after the game have gained one rank and have 1 or 2 stars (depending on whether she got a bonus star) on the new rank. If on the other hand she had all stars except one on a rank, and won a game that also gave her a bonus star, she would gain one rank and have 1 star on the new rank.

If a player on rank 1-20 loses a game, she loses a star. If a player has zero stars on a rank and loses a star, she will lose a rank and have all stars minus one on the rank below. However, one can never drop below rank 20 (losing a game at rank 20 with no stars will have no effect).

If a player reaches the Legend rank, she will stay legend no matter how many losses she incurs afterwards.

The number of stars on each rank are as follows:

- Rank 25-21: 2 stars
- Rank 20-16: 3 stars
- Rank 15-11: 4 stars
- Rank 10-1: 5 stars

A player starts at rank 25 with no stars. Given the match history of a player, what is her rank at the end of the sequence of matches?

Input

The input consists of a single line describing the sequence of matches. Each character corresponds to one game; 'W' represents a win and 'L' a loss. The length of the line is between 1 and 10 000 characters (inclusive).

Output

Output a single line containing a rank after having played the given sequence of games; either an integer between 1 and 25 or "Legend".

A very long problem statement! The first hurdle is finding the energy to read it from start to finish without skipping any details. Not much creativity is needed here – indeed, the algorithm to implement is given in the statement. Despite this, it is not as easy as one would think. Although it was the second most solved problem at the contest where it was used in, it was also the one with the *worst success ratio*. On average, a team needed 3.59 attempts before getting a correct solution, compared to the runner-up problem at 2.92 attempts. None of the top 6 teams in the contest got the problem accepted on their first attempt. Failed attempts cost a lot. Not only in absolute time, but many forms of competition include additional penalties for submitting incorrect solutions.

Implementation problems get much easier when you know your programming language well and can use it to write good, structured code. Split code into functions, use structures, and give your variables good names and implementation problems become easier to code. A solution to the Game Rank problem which attempts to use this approach is given here:

```cpp
#include <bits/stdc++.h>

using namespace std;

int curRank = 25, curStars = 0, conseqWins = 0;

int starsOfRank() {
  if (curRank >= 21) return 2;
  if (curRank >= 16) return 3;
  if (curRank >= 11) return 4;
  if (curRank >= 1) return 5;
  assert(false);
}

void addStar() {
  if (curStars == starsOfRank()) {
    --curRank;
    curStars = 0;
  }
  ++curStars;
}

void addWin() {
  int curStarsWon = 1;
  ++conseqWins;
  if (conseqWins >= 3 && curRank >= 6) curStarsWon++;

  for (int i = 0; i < curStarsWon; i++) {
    addStar();
  }
}

void loseStar() {
  if (curStars == 0) {
    if (curRank == 20) return;
    ++curRank;
    curStars = starsOfRank();
  }
  --curStars;
}

void addLoss() {
  conseqWins = 0;
  if (curRank <= 20) loseStar();
}

int main() {
  string seq;
  cin >> seq;
  for (char res : seq) {
    if (res == 'W') addWin();
    else addLoss();
    if (curRank == 0) break;
    assert(1 <= curRank && curRank <= 25);
    assert(0 <= curStars && curStars <= starsOfRank());
  }
  if (curRank == 0) cout << "Legend" << endl;
  else cout << curRank << endl;
}
```

Note the use of the `assert()` function. The function takes a single boolean parameter and crashes the program with an assertion failure if the parameter evaluated to `false`. This is helpful when solving problems since it allows us to verify that assumptions we make regarding the internal state of the program indeed holds. In fact, when the above solution was written the assertions in it actually managed to catch some bugs before submitting the problem!

Exercise 4.1 — Kattis Exercise

Game Rank – gamerank

Next, we work through a complex implementation problem, starting with a long, hard-to-read solution with a few bugs. Then, we refactor it a few times until it is correct and easy to read.

Mate in One

Introduction to Algorithms at Danderyds Gymnasium

"White to move, mate in one."

When you are looking back in old editions of the New in Chess magazine, you find loads of chess puzzles. Unfortunately, you realize that it was way too long since you played chess. Even trivial puzzles such as finding a mate in one now far exceed your ability.

But, perseverance is the key to success. You realize that you can instead use your new-found algorithmic skills to solve the problem by coding a program to find the winning move.

You will be given a chess board, which satisfy:

- No player may castle.
- No player can perform an en passant[1].
- The board is a valid chess position.
- White can mate black in a single, unique move.

Write a program to output the move white should play to mate black.

Input

The board is given as a 8×8 grid of letters. The letter `.` represent an empty space, the characters `pbnrqk` represent a white pawn, bishop, knight, rook, queen and king, and the characters `PBNRQK` represents a black pawn, bishop, knight, rook, queen and king.

Output

Output a move on the form `a1b2`, where `a1` is the square to move a piece from (written as the column, `a-h`, followed by the row, `1-8`) and `b2` is the square to move the piece to.

Our first solution attempt clocks in at just under 300 lines.

```cpp
#include <bits/stdc++.h>
using namespace std;

#define rep(i,a,b) for (int i = (a); i < (b); ++i)
#define trav(it, v) for (auto& it : v)
#define all(v) (v).begin(), (v).end()
typedef pair<int, int> ii;
typedef vector<ii> vii;
template <class T> int size(T &x) { return x.size(); }

char board[8][8];

bool iz_empty(int x, int y) {
  return board[x][y] == '.';
}

bool is_white(int x, int y) {
  return board[x][y] >= 'A' && board[x][y] <= 'Z';
}

bool is_valid(int x, int y) {
  return x >= 0 && x < 8 && y >= 0 && y < 8;
}

int rook[8][2] = {
  {1, 2},
  {1, -2},
  {-1, 2},
  {-1, -2},

```

[1]If you are not aware of this special pawn rule, do not worry – knowledge of it is irrelevant with regard to the problem.

```
  {2, 1},
  {-2, 1},
  {2, -1},
  {-2, -1}
};

void display(int x, int y) {
  printf("%c%d", y + 'a', 7 - x + 1);
}

vii next(int x, int y) {
  vii res;

  if (board[x][y] == 'P' || board[x][y] == 'p') {
    // pawn

    int dx = is_white(x, y) ? -1 : 1;

    if (is_valid(x + dx, y) && iz_empty(x + dx, y)) {
      res.push_back(ii(x + dx, y));
    }

    if (is_valid(x + dx, y - 1) && is_white(x, y) != is_white(x + dx, y - 1)) {
      res.push_back(ii(x + dx, y - 1));
    }

    if (is_valid(x + dx, y + 1) && is_white(x, y) != is_white(x + dx, y + 1)) {
      res.push_back(ii(x + dx, y + 1));
    }

  } else if (board[x][y] == 'N' || board[x][y] == 'n') {
    // knight

    for (int i = 0; i < 8; i++) {
      int nx = x + rook[i][0],
      ny = y + rook[i][1];

      if (is_valid(nx, ny) && (iz_empty(nx, ny) ||
          is_white(x, y) != is_white(nx, ny))) {
        res.push_back(ii(nx, ny));
      }
    }

  } else if (board[x][y] == 'B' || board[x][y] == 'b') {
    // bishop

    for (int dx = -1; dx <= 1; dx++) {
      for (int dy = -1; dy <= 1; dy++) {
        if (dx == 0 && dy == 0)
```

```
          continue;

        if ((dx == 0) != (dy == 0))
          continue;

        for (int k = 1; ; k++) {
          int nx = x + dx * k,
            ny = y + dy * k;

          if (!is_valid(nx, ny)) {
            break;
          }

          if (iz_empty(nx, ny) || is_white(x, y) != is_white(nx, ny)) {
            res.push_back(ii(nx, ny));
          }

          if (!iz_empty(nx, ny)) {
            break;
          }
        }
      }
    }

  } else if (board[x][y] == 'R' || board[x][y] == 'r') {
    // rook

    for (int dx = -1; dx <= 1; dx++) {
      for (int dy = -1; dy <= 1; dy++) {
        if ((dx == 0) == (dy == 0))
          continue;

        for (int k = 1; ; k++) {
          int nx = x + dx * k,
            ny = y + dy * k;

          if (!is_valid(nx, ny)) {
            break;
          }

          if (iz_empty(nx, ny) || is_white(x, y) != is_white(nx, ny)) {
            res.push_back(ii(nx, ny));
          }

          if (!iz_empty(nx, ny)) {
            break;
          }
        }
      }
    }

  } else if (board[x][y] == 'Q' || board[x][y] == 'q') {
    // queen

    for (int dx = -1; dx <= 1; dx++) {
      for (int dy = -1; dy <= 1; dy++) {
        if (dx == 0 && dy == 0)
          continue;

        for (int k = 1; ; k++) {
          int nx = x + dx * k,
            ny = y + dy * k;

          if (!is_valid(nx, ny)) {
            break;
          }

          if (iz_empty(nx, ny) || is_white(x, y) != is_white(nx, ny)) {
            res.push_back(ii(nx, ny));
          }

          if (!iz_empty(nx, ny)) {
            break;
          }
        }
      }
    }


  } else if (board[x][y] == 'K' || board[x][y] == 'k') {
    // king

    for (int dx = -1; dx <= 1; dx++) {
      for (int dy = -1; dy <= 1; dy++) {
        if (dx == 0 && dy == 0)
          continue;

        int nx = x + dx,
          ny = y + dy;

        if (is_valid(nx, ny) && (iz_empty(nx, ny) ||
            is_white(x, y) != is_white(nx, ny))) {
          res.push_back(ii(nx, ny));
        }
      }
    }
  } else {
    assert(false);
  }

  return res;
}

bool is_mate() {

  bool can_escape = false;

  char new_board[8][8];

  for (int x = 0; !can_escape && x < 8; x++) {
    for (int y = 0; !can_escape && y < 8; y++) {
      if (!iz_empty(x, y) && !is_white(x, y)) {

        vii moves = next(x, y);
        for (int i = 0; i < size(moves); i++) {
          for (int j = 0; j < 8; j++)
            for (int k = 0; k < 8; k++)
              new_board[j][k] = board[j][k];

          new_board[moves[i].first][moves[i].second] = board[x][y];
          new_board[x][y] = '.';

          swap(new_board, board);


          bool is_killed = false;
          for (int j = 0; !is_killed && j < 8; j++) {
            for (int k = 0; !is_killed && k < 8; k++) {
              if (!iz_empty(j, k) && is_white(j, k)) {
                vii nxts = next(j, k);

                for (int l = 0; l < size(nxts); l++) {
                  if (board[nxts[l].first][nxts[l].second] == 'k') {
                    is_killed = true;
                    break;
                  }
                }
              }
            }
          }

          swap(new_board, board);

          if (!is_killed) {
            can_escape = true;
            break;
          }
          }

        }
      }
    }

    return !can_escape;
}

int main()
{
    for (int i = 0; i < 8; i++) {
      for (int j = 0; j < 8; j++) {
        scanf("%c", &board[i][j]);
      }

      scanf("\n");
    }

    char new_board[8][8];
    for (int x = 0; x < 8; x++) {
      for (int y = 0; y < 8; y++) {
        if (!iz_empty(x, y) && is_white(x, y)) {

          vii moves = next(x, y);

          for (int i = 0; i < size(moves); i++) {

            for (int j = 0; j < 8; j++)
              for (int k = 0; k < 8; k++)
                new_board[j][k] = board[j][k];

            new_board[moves[i].first][moves[i].second] = board[x][y];
            new_board[x][y] = '.';

            swap(new_board, board);


            if (board[moves[i].first][moves[i].second] == 'P' &&
                moves[i].first == 0) {

              board[moves[i].first][moves[i].second] = 'Q';
              if (is_mate()) {
                printf("%c%d%c%d\n", y + 'a', 7 - x + 1,
                        moves[i].second + 'a', 7 - moves[i].first + 1);
                return 0;
              }

              board[moves[i].first][moves[i].second] = 'N';
276              if (is_mate()) {
277                printf("%c%d%c%d\n", y + 'a', 7 - x + 1,
278                        moves[i].second + 'a', 7 - moves[i].first + 1);
279                return 0;
280              }
281
282            } else {
283              if (is_mate()) {
284                printf("%c%d%c%d\n", y + 'a', 7 - x + 1,
285                        moves[i].second + 'a', 7 - moves[i].first + 1);
286                return 0;
287              }
288            }
289
290            swap(new_board, board);
291          }
292        }
293      }
294    }
295
296    assert(false);
297
298    return 0;
299  }
```

That is a lot of code! Note how there are a few obvious mistakes which makes the code harder to read, such as typo of `iz_empty` instead of `is_empty`, or how the list of moves for the knight is called `rook`. Our final solution reduces this to less than half the size.

Exercise 4.2

Read through the above code carefully and consider if there are better ways to solve the problem. Furthermore, it has a bug – can you find it?

First, let us clean up the move generation a bit. Currently, it is implemented as the function `next`, together with some auxillary data (lines 25-179). It is not particularly abstract, plagued by a lot of code duplication.

The move generation does not need a lot of code. Almost all the moves of the pieces can be described in the same way, as: "pick a direction out of a list D and move at most L steps along this direction, stopping either before exiting the board or taking your own piece, or when taking another piece.". For the king and queen, D is all 8 directions one step away, with $L = 1$ for the king and L = ∞ for the queen.

Implementing this abstraction is done with little code.

```cpp
const vii DIAGONAL = {{-1, 1}, {-1, 1}, {1, -1}, {1, 1}};
const vii CROSS = {{0, -1}, {0, 1}, {-1, 0}, {1, 0}};
const vii ALL_MOVES = {{-1, 1}, {-1, 1}, {1, -1}, {1, 1},
  {0, -1}, {0, 1}, {-1, 0}, {1, 0}};
const vii KNIGHT = {{-1, -2}, {-1, 2}, {1, -2}, {1, 2},
    {-2, -1}, {-2, 1}, {2, -1}, {2, 1}};
vii directionMoves(const vii& D, int L, int x, int y) {
  vii moves;
  trav(dir, D) {
    rep(i,1,L+1) {
      int nx = x + dir.first * i, ny = y + dir.second * i;
      if (!isValid(nx, ny)) break;
      if (isEmpty(nx, ny)) moves.emplace_back(nx, ny);
      else {
        if (isWhite(x, y) != isWhite(nx, ny)) moves.emplace_back(nx, ny);
        break;
      }
    }
  }
  return moves;
}
```

A short and sweet abstraction, that will prove very useful. It handles all possible moves, except for pawns. These have a few special cases.

```cpp
vii pawnMoves(int x, int y) {
  vii moves;
  if (x == 0 || x == 7) {
    vii queenMoves = directionMoves(ALL_MOVES, 16, x, y);
    vii knightMoves = directionMoves(KNIGHT, 1, x, y);
    queenMoves.insert(queenMoves.begin(), all(knightMoves));
    return queenMoves;
  }
  int mv = (isWhite(x, y) ? - 1 : 1);
  if (isValid(x + mv, y) && isEmpty(x + mv, y))  {
    moves.emplace_back(x + mv, y);
    bool canMoveTwice = (isWhite(x, y) ? x == 6 : x == 1);
    if (canMoveTwice && isValid(x + 2 * mv, y) && isEmpty(x + 2 * mv, y)) {
      moves.emplace_back(x + 2 * mv, y);
    }
  }
  auto take = [&](int nx, int ny) {
    if (isValid(nx, ny) && !isEmpty(nx, ny)
      && isWhite(x, y) != isWhite(nx, ny))
      moves.emplace_back(nx, ny);
  };
  take(x + mv, y - 1);
  take(x + mv, y + 1);
  return moves;
}
```

This pawn implementation also takes care of promotion, rendering the logic previously implementing this obsolete.

The remainder of the move generation is now implemented as:

```
vii next(int x, int y) {
  vii moves;
  switch(toupper(board[x][y])) {
    case 'Q': return directionMoves(ALL_MOVES, 16, x, y);
    case 'R': return directionMoves(CROSS, 16, x, y);
    case 'B': return directionMoves(DIAGONAL, 16, x, y);
    case 'N': return directionMoves(KNIGHT, 1, x, y);
    case 'K': return directionMoves(ALL_MOVES, 1, x, y);
    case 'P': return pawnMoves(x, y);
  }
  return moves;
}
```

These make up a total of about 50 lines – a reduction to a third of how the move generation was implemented before. The trick was to rework all code duplication into a much cleaner abstraction.

We also have a lot of code duplication in the `main` (lines 234-296) and `is_mate` (lines 181-232) functions. Both functions loops over all possible moves, with lots of duplication. First of all, let us further abstract the move generation to not only generate the moves a certain piece can make, but all the moves a player can make. This is done in both functions, so we should be able to extract this logic into only one place:

```
vector<pair<ii, ii>> getMoves(bool white) {
  vector<pair<ii, ii>> allMoves;
  rep(x,0,8) rep(y,0,8) if (!isEmpty(x, y) && isWhite(x, y) == white) {
      vii moves = next(x, y);
      trav(it, moves) allMoves.emplace_back(ii{x, y}, it);
  }
  return allMoves;
}
```

We also have some duplication in the code *making* the moves. Before extracting this logic, we will change the structure used to represent the board. A `char[8][8]` is a tedious structure to work with. It is not easily copied or sent as parameter. Instead, we use a `vector<string>`, typedef'd as `Board`:

```
typedef vector<string> Board;
```

We then add a function to make a move, returning a new board:

```
Board doMove(pair<ii, ii> mv) {
  Board newBoard = board;
  ii from = mv.first, to = mv.second;
  newBoard[to.first][to.second] = newBoard[from.first][from.second];
  newBoard[from.first][from.second] = '.';
  return newBoard;
}
```

Hmm... there should be one more thing in common between the `main` and `is_mate` functions. Namely, to check if the current player is in check after a move. However, it seems this is not done in the `main` function – a bug. Since we do need to do this twice, it should probably be its own function:

```
bool inCheck(bool white) {
  trav(mv, getMoves(!white)) {
    ii to = mv.second;
    if (!isEmpty(to.first, to.second)
        && isWhite(to.first, to.second) == white
        && toupper(board[to.first][to.second]) == 'K') {
      return true;
    }
  }
  return false;
}
```

Now, the long `is_mate` function is much shorter and readable, thanks to our refactoring:

```
bool isMate() {
  if (!inCheck(false)) return false;
  Board oldBoard = board;
  trav(mv, getMoves(false)) {
    board = doMove(mv);
    if (!inCheck(false)) return false;
    board = oldBoard;
  }
  return true;
}
```

A similar transformation is now possible of the `main` function, that loops over all moves white make and checks if black is in mate:

```
int main() {
  rep(i,0,8) {
      string row;
      cin >> row;
      board.push_back(row);
  }
  Board oldBoard = board;
  trav(mv, getMoves(true)) {
      board = doMove(mv);
      if (!inCheck(true) && isMate()) {
          outputSquare(mv.first.first, mv.first.second);
          outputSquare(mv.second.first, mv.second.second);
          cout << endl;
          break;
      }
  }
  return 0;
}
```

Now, we have actually rewritten the entire solution. From the 300-line behemoth with gigantic functions, we have refactored the solution into few, short functions with are easy to follow. The rewritten solution is less than half the size, clocking in at less than 140 lines (the author's own solution is 120 lines). Learning to code such structured solutions comes to a large extent from experience. During a competition, we might not spend time thinking about how to structure our solutions, instead focusing on getting it done as soon as possible. However, spending 1-2 minutes thinking about how to best implement a complex solution could pay off not only in faster implementation times (such as halving the size of the program) but also in being less buggy.

Exercise 4.3 — Kattis Exercise

Mate in One – mateinone

To sum up: implementation problems should not be underestimated in terms of implementation complexity. Work on your coding best practices and spend time practicing coding complex solutions and you will see your implementation performance improve.

4.1 Additional Exercises

Exercise 4.4

Flexible Spaces – flexiblespaces

Sort of Sorting – sortofsorting

Permutation Encryption – permutationencryption

Jury Jeopardy – juryjeopardy

Fun House – funhouse

Settlers of Catan – settlers2

Cross – cross

Basic Interpreter – basicinterpreter

Cat Coat Colors – catcoat

4.2 Chapter Notes

Many good sources exist to become more proficient at writing readable and simple code. *Clean Code*[13] describes many principles that helps in writing better code. It includes good walk-throughs on refactoring, and shows in a very tangible fashion how coding cleanly also makes coding easier.

Code Complete[14] is a huge tome on improving your programming skills. While much of the content is not particularly relevant to coding algorithmic problems, chapters 5-19 give many suggestions on coding style.

Different languages have different best practices. Some resources on improving your skills in whatever language you code in are:

C++ *Effective C++*[16], *Effective Modern C++*[17], *Effective STL*[15], by Scott Meyers,

Java *Effective Java*[3] by Joshua Bloch,

Python *Effective Python*[21] by Brett Slatkin, *Python Cookbook*[2] by David Beazley and Brian K. Jones.

Chapter 5

Time Complexity

How do you know if your algorithm is fast enough before you have coded it? In this chapter we examine this question from the perspective of ***time complexity***, a common tool of algorithm analysis to determine roughly how fast an algorithm is.

We start our study of complexity by looking at a new sorting algorithm – ***insertion sort***. Just like selection sort (studied in Chapter 1), insertion sort works by iteratively sorting a sequence.

5.1 The Complexity of Insertion Sort

The insertion sort algorithm works by ensuring that all of the first i elements of the input sequence are sorted. First for $i = 1$, then for $i = 2$, etc, up to $i = n$, at which point the entire sequence is sorted.

Algorithm 5.1: Insertion Sort

Assume we wish to sort the list $a_0, a_1, ..., a_{N-1}$ of N integers. If we know that the first K elements $a_0, ..., a_{K-1}$ numbers are sorted, we can make the list $a_0, ..., a_K$ sorted by taking the element a_K and inserting it into the correct position of the already-sorted prefix $a_0, ..., a_{K-1}$.

For example, we know that a list of a single element is always sorted, so we can use that a_0 is sorted as a base case. We can then sort a_0, a_1 by checking whether a_1 should be to the left or to the right of a_0. In the first case, we swap the two numbers.

Once we have sorted a_0, a_1, we insert a_2 into the sorted list. If it is larger than a_1, it is already in the correct place. Otherwise, we swap a_1 and a_2, and keep going until we either find the correct location, or determine that the number was the smallest one in which case the correct location is in the beginning.

This procedure is then repeated for every remaining element.

In this section we determine how long time insertion sort takes to run. When analyzing an algorithm we do not attempt to compute the actual wall clock time an algorithm takes. Indeed, this would be nearly impossible a priori – modern computers are complex beasts with often unpredictable behavior. Instead, we try to approximate the *growth* of the running time, as a function of the size of the input.

Competitive Tip

While it is difficult to measure exact wall-clock time of your algorithm just by analyzing the algorithm and code, it is sometimes a good idea to benchmark your solution before you submit it to the judge. This way you trade a few minutes of time (constructing the worst-case input) for avoiding many time limit exceeded verdicts. If you are unsure of your solution and the competition format penalizes you for rejected submissions, this tradeoff can have good value.

When sorting fixed-size integers the size of the input would be the number of elements we are sorting, N. We denote the time the algorithm takes in relation to N as $T(N)$. Since an algorithm often has different behaviours depending on how an instance is constructed, this time is taken to be the *worst-case* time, over every instance of N elements.

To properly analyze an algorithm, we need to be more precise about exactly

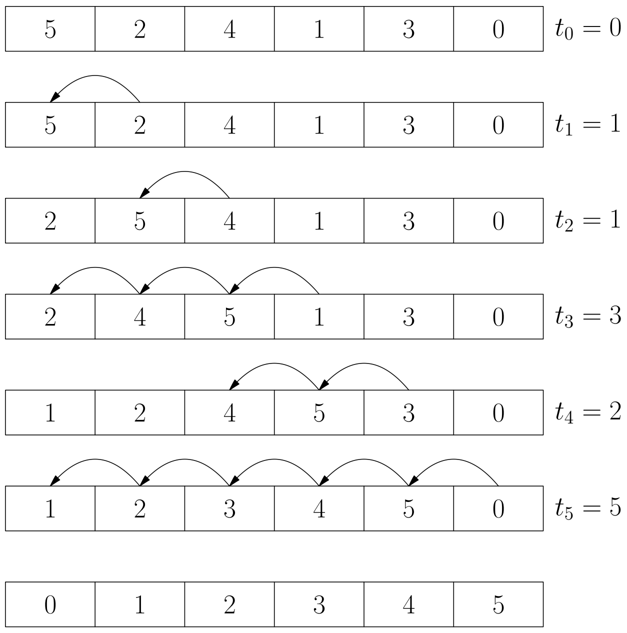


Figure 5.1: Insertion Sort sorting the sequence $2, 1, 4, 5, 3, 0$.

what it does. We give the following pseudo code for insertion sort:

Algorithm 5.2: Insertion sort

```
procedure InsertionSort($A$)    ▷ Sorts the sequence $A$ containing $N$ elements
    for $i \leftarrow 0$ to $N - 1$ do
        $j \leftarrow i$
        while $j > 0$ and $A[j] < A[j-1]$ do
            Swap $A[j]$ och $A[j-1]$
            $j \leftarrow j - 1$
```

To analyze the running time of the algorithm, we make the assumption that any “sufficiently small” operation takes the same amount of time – exactly 1 (of some undefined unit). We have to be careful in what assumptions we make regarding what a sufficiently small operation means. For example, sorting N numbers is not a small operation, while adding or multiplying two fixed-size numbers is. Multiplication of integers of arbitrary size is not a small operation (see the Karatsuba algorithm, Section 10.4).

In our program every line happens to represent a small operation. However, the two loops may cause some lines to execute more than once. The outer for loop will execute N times. The number of times the inner loop runs depends on how the input looks. We introduce the notation t_i to mean the number of iterations the inner loop runs during the i'th iteration of the outer loop. These are included in figure 5.1 for every iteration.

Now we can annotate our pseudo code with the number of times each line executes.

Algorithm 5.3: Insertion sort

```
1: procedure InsertionSort($A$)  ▷ Sorts the sequence $A$ containing N elements
2:     for $i \leftarrow 0$ to $N-1$ do                     ▷ Runs N times, cost 1
3:         $j \leftarrow i$                                 ▷ Runs N times, cost 1
4:         while $j > 0$ and $A[j] < A[j-1]$ do  ▷ Runs $\sum_{i=0}^{N-1} t_i$ times, cost 1
5:             Swap $A[j]$ och $A[j-1]$         ▷ Runs $\sum_{i=0}^{N-1} t_i$ times, cost 1
6:             $j \leftarrow j-1$                 ▷ Runs $\sum_{i=0}^{N-1} t_i$ times, cost 1
```

We can now express $T(N)$ as

$$\begin{aligned} T(N) &= N + N + \left(\sum_{i=0}^{N-1} t_i\right) + \left(\sum_{i=0}^{N-1} t_i\right) + \left(\sum_{i=0}^{N-1} t_i\right) \\ &= 3\left(\sum_{i=0}^{N-1} t_i\right) + 2N \end{aligned}$$

We still have some t_i variables left so we do not truly have a function of N. We can eliminate this by realizing that in the worst case $t_i = i$. This occurs when the list we are sorting is in descending order. Each element must then be moved to the front, requiring i swaps for the i'th element.

With this substition we can simplify the expression:

$$\begin{aligned}T(N) &= 3\left(\sum_{i=0}^{N-1} i\right) + 2N \\ &= 3\frac{(N-1)N}{2} + 2N \\ &= \frac{3}{2}(N^2 - N) + 2N \\ &= \frac{3}{2}N^2 + \frac{N}{2}\end{aligned}$$

This function grows quadratically with the number of elements of N. Since the approximate growth of the time a function takes is assigned such importance a notation was developed for it.

5.2 Asymptotic Notation

Almost always when we express the running time of an algorithm we use what is called *asymptotic notation*. The notation captures the behavior of a function as its arguments grow. For example, the function $T(N) = \frac{3}{2}N^2 + \frac{N}{2}$ which described the running time of insertion sort, is bounded by $c \cdot N^2$ for large N, for some constant c. We write

$$T(N) = O(N^2)$$

to state this fact.

Similarly, the linear function $2N+15$ is bounded by $c \cdot N$ for large N, with $c = 3$, so $2N + 15 = O(N)$. The notation only captures upper bounds though (and not the actual rate of growth). We could therefore say that $2N + 15 = O(N^2)$, even though this particular upper bound is very lax. However, N^2 is not bounded by $c \cdot N$ for any constant c when N is large, so $N^2 \neq O(N)$. This also corresponds to intuition – quadratic functions grows much faster than linear functions.

Definition 5.1 — O-notation
Let f and g be non-negative functions from $\mathbb{R}_{\geq 0}$ to $\mathbb{R}_{\geq 0}$. If there exists positive constants n_0 and c such that $f(n) \leq cg(n)$ whenever $n \geq n_0$, we say that $f(n) = O(g(n))$.

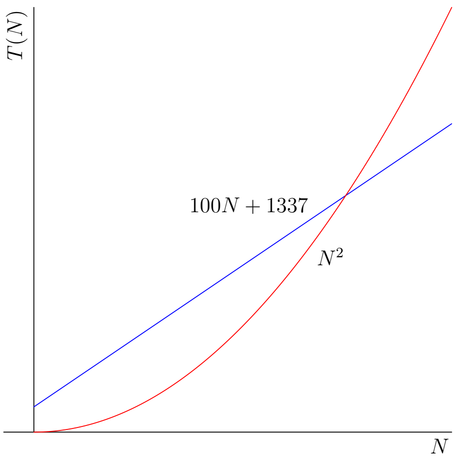


Figure 5.2: All linear functions are eventually outgrown by N^2, so $an + b = O(n^2)$.

Intuitively, the notation means that $f(n)$ grows *slower than or as fast as* $g(n)$, within a constant factor. Any quadratic function $an^2 + bn + c = O(n^2)$. Similarly, any linear function $an + b = O(n^2)$ as well. This definition implies that for two functions f and g which are always within a constant factor of each other, we have that both $f(n) = O(g(n))$ and $g(n) = O(f(n))$.

We can use this definition to prove that the running time of insertion sort is $O(N^2)$, even in the worst case.

Example 5.1 Prove that $\frac{3}{2}N^2 + \frac{N}{2} = O(N^2)$.

Proof. When $N \geq 1$ we have $N^2 \geq N$ (by multiplying both sides with N).

This means that

$$\frac{3}{2}N^2 + \frac{N}{2} \leq \frac{3}{2}N^2 + \frac{N^2}{2} = \frac{4}{2}N^2 = 2N^2$$

for $N \geq 1$. Using the constants $c = 2$ and $n_0 = 1$ we fulfill the condition from the definition. $\square$

For constants k we say that $k = O(1)$. This is a slight abuse of notation, since neither k nor 1 are functions, but it is a well-established abuse. If you prefer, you can instead assume we are talking about functions $k(N) = k$ and $1(N) = 1$.

Competitive Tip

The following table describes approximately what complexity you need to solve a problem of size n if your algorithm has a certain complexity when the time limit is about 1 second.

Complexity	n
$O(\log n)$	$2^{(10^7)}$
$O(\sqrt{n})$	10^{14}
$O(n)$	10^7
$O(n \log n)$	10^6
$O(n\sqrt{n})$	10^5
$O(n^2)$	$5 \cdot 10^3$
$O(n^2 \log n)$	$2 \cdot 10^3$
$O(n^3)$	300
$O(2^n)$	24
$O(n2^n)$	20
$O(n^2 2^n)$	17
$O(n!)$	11

Table 5.1: Approximations of needed time complexities

Note that this is in no way a general rule – while complexity does not bother about constant factors, wall clock time does!

Complexity analysis can also be used to determine *lower bounds* of the time an algorithm takes. To reason about lower bounds we use Ω-notation. It is similar to O-notation except it describes the reverse relation.

Definition 5.2 — Ω-notation
Let f and g be non-negative functions from $\mathbb{R}_{\geq 0}$ to $\mathbb{R}_{\geq 0}$. If there exists positive constants n_0 and c such that $cg(n) \leq f(n)$ for every $n \geq n_0$, we say that $f(n) = \Omega(g(n))$.

We know that the complexity of insertion sort has an upper bound of $O(N^2)$ in the worst-case, but does it have a lower bound? It actually has the same lower bound as upper bound, i.e. $T(N) = \Omega(N^2)$.

Example 5.2 Prove that $\frac{3}{2}N^2 + \frac{N}{2} = \Omega(N^2)$.

Proof. When $N \geq 1$, we have $\frac{3}{2}N^2 + \frac{N}{2} \geq N^2$. Using the constants $c = 1$ and $n_0 = 1$ we fulfill the condition from the definition. □

In this case, both the lower and the upper bound of the worst-case running time of insertion sort coincided (asymptotically). We have another notation for when this is the case:

Definition 5.3 — Θ-notation
If $f(n) = O(g(n))$ and $f(n) = \Omega(g(n))$, we say that $f(n) = \Theta(g(n))$.

Thus, the worst-case running time for insertion sort is $\Theta(n^2)$.

There are many ways of computing the time complexity of an algorithm. The most common case is when a program has K nested loops, each of with performs $O(M)$ iterations. The complexity of these loops are then $O(M^K \cdot f(N))$ if the inner-most operation takes $O(f(N))$ time. In Chapter 10, you also see some ways of computing the time complexity of a particular type of recursive solution, called Divide and Conquer algorithms.

Exercise 5.1

Find a lower and an upper bound that coincide for the best-case running time for insertion sort.

Exercise 5.2

Give an $O(n)$ algorithm and an $O(1)$ algorithm to compute the sum of the n first integers.

Exercise 5.3

Prove, using the definition, that $10n^2 + 7n - 5 + \log^2 n = O(n^2)$. What constants c, n_0 did you get?

Exercise 5.4

Prove that $f(n) + g(n) = \Theta(\max\{f(n), g(n)\})$ for non-negative functions f and g.

Exercise 5.5

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

Exercise 5.6

Prove that $(n + a)^b = O(n^b)$ for positive constants a, b.

5.2.1 Amortized Complexity

Consider the following algorithm:

Algorithm 5.4: Counting occurances

```
1: procedure CountOccurances($A, v$)    ▷ Count the number of occurances of the value $v$ in the sequence $A$
2:     $N \leftarrow$ length of $A$
3:     $i \leftarrow 0$
4:     $ans \leftarrow 0$
```

```
 5:     while $i \neq N$ do
 6:         while $i < N$ and $A[i] \neq v$ do
 7:             $i \leftarrow i + 1$
 8:         if $i \neq N$ then
 9:             $ans \leftarrow ans + 1$
10:             $i \leftarrow i + 1$
```

It computes the number of occurances of a certain value in a sequence (in a somewhat cumbersome way). We repeatedly scan through the sequence A to find the next occurance of v. Whenever we find one, we increase the answer by 1 and resume our scanning. This procedure is continued until we have scanned through the entire sequence.

What is the time complexity of this procedure? How do we handle the fact that neither the outer nor the inner loop of the algorithm repeats a predictable number of iterations each time? For example, the other loop would iterate N times if every element equals v, but only once if it does not contain the value at all. Similarly, the the number of iterations of the inner loop depends on the *position* of the elements in A which equals v.

We find help in a technique called ***amortized complexity***. The concept of amortization is best known from loans. It represents the concept of periodically paying of some kind of debt until it has been paid off in full.

When analyzing algorithms, the "debt" is the running time the algorithm has. We try to prove that the algorithm has a given running time by looking at many, possibly uneven parts that together over the long run sums up to the total running time, similarly to how a loan can be paid of by amortization.

A quick analysis of the counting algorithm gives us a good guess that the algorithm runs in time $\Theta(N)$. It should be clear that it is the inner loop at lines 6-7 that dominates the running time of the algorithm. The question is how we compute the number of times it executes even though we do not know how many times it executes nor how many iterations each execution takes? We try the amortization trick by looking at how many iterations it performs over all those executions, no matter how many they are. Assume that the loop is run k times (**including the final time when the condition first is false**) and each run iterates b_i times ($1 \leq i \leq k$). We claim that

$$b_1 + b_2 + \cdots + b_k = \Theta(N)$$

Our reasoning is as follows. There are two ways the variable i can increase. It can either be increased inside the loop at line 7, or at line 10. If the loop executes N times in total, it will certainly complete and never be executed again since the loop at line 5 completes too. This gives us $\sum_{i=1}^{k} b_i = O(N)$.

On the other hand, we get one iteration for every time i is incresed. If i is increased on line 7, it was done within a loop iteration. If i is increased on line 9, we instead count the final check if the loop just before it once. Each addition of i seems happen together with an iteration of the loop, so $\sum_{i=1}^{k} b_i = \Omega(N)$. Together, these two results prove our claim.

This particular application of amortized complexity is called the *aggregate method*.

Exercise 5.7

Consider the following method of implementing adding 1 to an integer represented by its binary digit.

Algorithm 5.5: Binary Addition

```
1: procedure BinaryIncrement(D)
2:     $i \leftarrow 0$
3:     while $D[i] = 1$ do                ▷ Add 1 to the $i$'th digit
4:         $D[i] = 0$    ▷ We add 1 to a 1 digit, resulting in a 0 digit plus a carry
5:         $i \leftarrow i + 1$
6:     $D[i] = 1$                ▷ We add 1 to a digit not resulting in a carry
```

The algorithm is the binary version of the normal addition algorithm where the two addends are written above each other and each resulting digit is computed one at a time, possibly with a carry digit.

What is the amortized complexity of this procedure over 2^n calls, if D starts out as 0?

5.3 NP-complete problems

Of particular importance in computer science are the problems that can be solved by algorithms running in polynomial time (often considered to be the "tractable" problems). For some problems we do not yet know if there is an algorithm whose time complexity is bounded by a polynomial. One particular class of these are the ***NP-complete problems***. They have the property that they are all reducible to one another, in the sense that a polynomial-time algorithm to any one of them yields a polynomial-time algorithm to all the others. Many of these NP-complete problems (or problems reducible to such a problem, a property called ***NP-hardness***) appear in algorithmic problem solving. It is good to know that they exist and that it is unlikely that you can find a polynomial-time solution. During the course of this book, you will occasionally see such problems with their NP-completeness mentioned.

5.4 Other Types of Complexities

There are several other types of complexities aside from the time complexity. For example, the ***memory complexity*** of an algorithm measures the amount of memory it uses. We use the same asymptotic notation when analyzing memory complexity. In most modern programming competitions, the allowed memory usage is high enough for the memory complexity not be a problem – if you get memory limit problems you also tend to have time limit problems. However, it is still of interest in computer science (and thus algorithmic problem solving) and computer engineering in general.

Another common type of complexity is the ***query complexity***. In some problems (like the Guessing Problem from chapter 1), we are given access to some kind of external procedure (called an *oracle*) that computes some value given parameters that we provide. A procedure call of this kind is called a *query*. The number of queries that an algorithm makes to the oracle is called its query complexity. Problems where the algorithm is allowed access to an oracle often bound the number of queries the algorithm may make. In these problems the query complexity of the algorithm is of interest.

5.5 The Importance of Constant Factors

In this chapter, we have essentially told you not to worry about the constant factors that the Θ notation hides from you. While this is true when you are solving problems in theory, only attempting to get a good asymptotic time complexity, constant factors can unfortunately be of large importance when implementing the problems subject to time limits.

Speeding up a program that has the correct time complexity but still gets *time limit exceeded* when submitted to an online judge is half art and half engineering. The first trick is usually to generate the worst-case test instance. It is often enough to create a test case where the input matches the input limits of the problem, but sometimes your program behaves differently depending on how the input looks. In these cases, more complex reasoning may be required.

Once the worst-case instance has been generated, what remains is to improve your code until you have gained a satisfactory decrease in how much time our program uses. When doing this, focus should be placed on those segments of your code that takes the longest wall-clock time. Decreasing time usage by 10% in a segment that takes 1 second is clearly a larger win than decreasing time usage by 100% in a segment that takes 0.01 seconds.

There are many tricks to improving your constant factors, such as:

- using symmetry to perform less calculations
- precomputing oft-repeated expressions, especially involving trigonometric functions
- passing very large data structures by reference instead of by copying
- avoiding to repeatedly allocate large amounts of memory
- using SIMD (single instruction, multiple data) instructions

5.6 Additional Exercises

Exercise 5.8

Prove that if $a(x) = O(b(x))$ and $b(x) = O(c(x))$, then $a(x) = O(c(x))$ This means functions can be ordered by their asymptotic growth.

Exercise 5.9

Order the following functions by their asymptotic growth *with proof*!

- x
- $\sqrt{x}$
- x^2
- 2^x
- e^x
- $x!$
- $\log x$
- $\frac{1}{x}$
- $x \log x$
- x^3

Exercise 5.10

Prove that if $a(x) = O(b(x))$ and $c(x) = O(d(x))$, then $a(x) + c(x) = O(b(x) + d(x))$.

5.7 Chapter Notes

Advanced algorithm analysis sometimes use complicated discrete mathematics, including number theoretical (as in Chapter 16) or combinatorial (as in Chapter 15) facts. *Concrete Mathematics* [7] by Donald Knuth, et al, does a thorough job on both accounts.

An Introduction to the Analysis of Algorithms [8] by Sedgewick and Flajolet has a more explicit focus on the analysis of algorithms, mainly discussing combinatorial analysis.

The study of various kinds of complexities constitute a research area called *computational complexity theory*. *Computational Complexity* [18] by Papadimitriou is a classical introduction to computational complexity, although *Computational Complexity: A Modern Approach* [1] by Arora and Barak is a more modern textbook, with recent results that the book by Papadimitriou lack.

While complexity theory is mainly concerned about the limits of specific computational models on problems that *can* be solved within those models, what can not be done by computers is also interesting. This is somewhat out of scope for an algorithmic problem solving book (since we are interested in those problems which can be solved), but is still of general interest. A book on e.g. automata theory (such as *Introduction to Automata Theory, Languages, and Computation* [24] by Ullman et al) can be a good compromise, mixing both some foundations of the theory of computation with topics more applicable to algorithms (such as automatons and languages).

Chapter 6

Foundational Data Structures

In this chapter we discuss some of the basic data structures in algorithms. We have chosen an approach that is perhaps more theoretic than many other problem solving texts. In particular, we have chosen to explicitly discuss not only the data structures themselves and their complexities, but also their implementations. We do this mainly because we believe that their implementations show useful algorithmic techniques. While you may feel that you can simply skip this chapter if you are familiar with all the data structures, we advise that you still read through the sections for the structures for which you lack confidence in their implementations.

6.1 Dynamic Arrays

The most basic data structure is the ***fixed-size array***. It consists of a fixed size block of memory and can be viewed as a sequence of N variables of the same type T. It supports the operations:

- $\mathrm{T}\ \mathtt{arr}[] = \text{new}\ \mathrm{T}[\textit{size}]$: creating a new array, with a given size.

Complexity: $\Theta(1)$[1]

- delete arr: deleting an existing array.
  Complexity: $\Theta(1)$

- $arr[index]$: accessing the value in a certain access a value.
  Complexity: $\Theta(1)$

In Chapter 2 we saw how to create fixed-size arrays where we knew the size beforehand. In C++ we can create fixed-size arrays using an expression as size instead. This is done using the syntax above, for example:

```
int size = 5;
int arr[] = new int[size];
arr[2] = 5;
cout << arr[2] << endl;
delete arr;
```

Exercise 6.1

What happens if you try to create an array with a negative size?

The fixed-size array can be used to implement a more useful data structure, the ***dynamic array***. This is an array that can change size when needed. For example, we may want to repeatedly insert values in the array without knowing the total number of values beforehand. This is a very common requirement in programming problems. In particular, we want to support two additional operations in addition to the operations supported by the fixed-size array.

- insert(pos, val): inserting a value in the array at a given position.
  Amortized complexity: $\Theta(size - pos)$
  Worst case complexity: $\Theta(size)$

- remove(pos): erase a position in an array.
  Complexity: $\Theta(size - pos)$

The complexities we list above are a result of the usual implementation of the dynamic array. A key consequence of these complexities is that addition and

[1]This complexity is debatable, and highly dependent on what computational model one uses. In practice, this is roughly "constant time" in most memory management libraries used in C++. In all Java and Python implementations we tried, it is instead linear in the size.

removal of elements to the end of the dynamic array takes $\Theta(1)$ amortized time.

A dynamic array can be implemented in numerous ways, and underlies the implementation of essentially every other data structure that we use. A naive implementation of a dynamic array is using a fixed-size array to store the data and creating a new one with the correct size whenever we add or remove an element, copying the elements from the old array to the new array. The complexity for this approach is linear in the size of the array for every operation that changes the size since we need to copy $\Theta(size)$ elements during every update. We need to do better than this.

To achieve the targeted complexity, we can instead modify this naive approach slightly by not creating a new array *every* time we have to change the size of the dynamic array. Whenever we need to increase the size of the dynamic array, we create a fixed-size array that is *larger* than we actually need it to be. For example, if we create a fixed-size array with n more elements than our dynamic array needs to store, we will not have to increase the size of the backing fixed-size array until we have added n more elements to the dynamic array. This means that a dynamic array does not only have a size, the number of elements we currently store in it, but also a capacity, the number of elements we *could* store in it. See Figure 6.1 for a concrete example of what happens when we add elements to a dynamic array that is both within its capacity and when we exceed it.

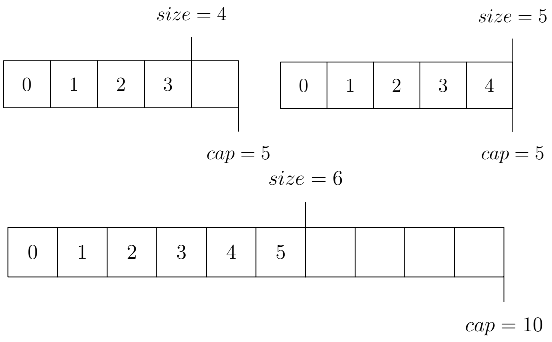


Figure 6.1: The resizing of an array when it overflows it capacity.

To implement a dynamic array in C++, we could use a structure storing as members the capacity, size and backing fixed-size array of the dynamic array. An example of how such a structure could look can be found in Listing 6.1.

Listing 6.1 The dynamic array structure

```
struct DynamicArray {

  int capacity;
  int size;
  int backing[];

  DynamicArray() {
    capacity = 10;
    size = 0;
    backing = new int[10];
  }

};
```

We are almost ready to add and remove elements to our array now. First, we need to handle the case where insertion of a new element would result in the size of the dynamic array would exceed its capacity, that is when $size = capacity$. Our previous suggestion was to allocate a new, bigger one, but just how big? If we always add, say, 10 new elements to the capacity, we have to perform the copying of the old elements with every 10'th addition. This still results in additions to the end of the array taking linear time on average. There is a neat trick that avoids this problem; creating the new backing array with **double** the current capacity.

This ensures that the complexity of all copying needed for an array up to some certain capacity have an amortized complexity of $\Theta(cap)$. Assume that we have just increased the capacity of our array to cap, which required us to copy $\frac{cap}{2}$ elements. Then, the previous increase will have happened at around capacity $\frac{cap}{2}$ and took time $\frac{cap}{4}$. The one before that occurred at capacity $\frac{cap}{4}$ and so on.

We can sum of all of this copying:

$$\frac{cap}{2} + \frac{cap}{4} + \cdots \leq cap$$

Since each copy is assumed to take $\Theta(1)$ time, the total time to create this array was $\Theta(cap)$. As $\frac{cap}{2} \leq size \leq cap$, this is also $\Theta(size)$, meaning that adding $size$ elements to the end of the dynamic array takes amortized $\Theta(size)$ time.

When implementing this in code, we use a function that takes as argument the capacity we require the dynamic array to have and ensures that the backing array have this size, possibly by creating a new one double in size until it is sufficiently large. Example code for this can be found in Listing 6.2.

Listing 6.2 Ensuring that a dynamic array have sufficient capacity

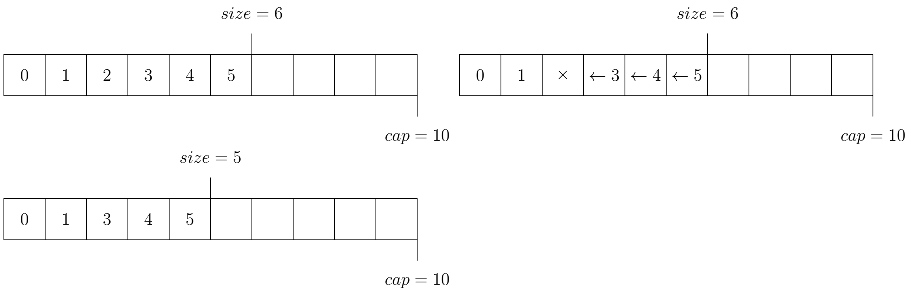
```
void ensureCapacity(int need) {
  while (capacity < need) {
    int newBacking[] = new int[2 * capacity];
    for (int i = 0; i < size; i++)
      newBacking[i] = backing[i];
    delete backing;
    backing = newBacking;
  }
}
```

With this method in hand, insertion and removal of elements is actually pretty simple. Whenever we remove an element, we simply need to move the elements coming after it in the dynamic array forward one step. When adding an element, we reverse this process by moving the elements coming after the position we wish to insert a new element at one step towards the back. Figure 6.2 shows the effects of these operations in a concrete way.

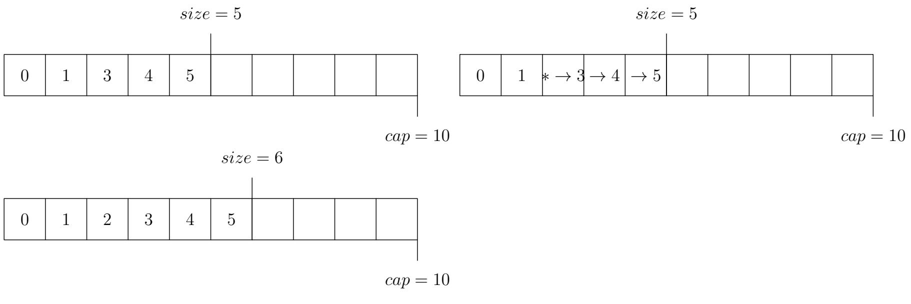
Exercise 6.2

Implement insertion and removal of elements in a dynamic array.

Dynamic arrays are called `vectors` in C++ (Section 3.1). They have the same complexities as the one described at the beginning of this section.



(a) The removal of the element 2 at index 2.



(b) The insertion of the element 2 into index 2.

Figure 6.2: Adding and removing elements of a dynamic vector.

Exercise 6.3

Assume that you want to implement shrinking of an array where many elements were deleted so that the capacity is unnecessarily large. We will call this shrinking function whenever we perform a removal, to see if we potentially want to shrink the array. What is the problem with the following implementation?

```
1: procedure ShrinkVector(V)
2:     while $2 \cdot V.capacity > V.size$ do
3:         $arr \leftarrow$ new T[$V.capacity/2$]
4:         copy the elements of $V.backing$ to $arr$
5:         $V.backing \leftarrow arr$
6:         $V.capacity \leftarrow V.capacity/2$
```

Exercise 6.4

How can we do *any* removal in $\Theta(1)$ if we do not care about the ordering of values in the array?

6.2 Stacks

The ***stack*** is a data structure that contains an ordered lists of values and supports the following operations:

- push(val): inserting a value at the top of the stack.
  Amortized complexity: $\Theta(1)$

- pop(): remove the value at the top of the stack.
  Complexity: $\Theta(1)$

- top(): get the value at the top of the stack.
  Complexity: $\Theta(1)$

In C++, the stack is called a `stack` (Section 3.3).

The structure is easily implemented with the above time complexities using a dynamic vector. After all, the vector supports exactly the same operations that a stack requires.

Exercise 6.5

Implement a stack using a dynamic vector.

6.3 Queues

The ***queue*** is like the vector and the stack an ordered list of values, but instead of removing and getting values from the end like the stack, it gets the value from the *front*.

- push(val): inserting a value at the end of the queue.
  Amortized complexity: $\Theta(1)$

- pop(): remove the value at the front of the queue.
  Amortized complexity: $\Theta(1)$

- front(): get the value at the front of the queue.
  Complexity: $\Theta(1)$

As previously seen, C++ has an implementation of the queue called `queue` (Section 3.2).

Implementing a queue can also be done using a vector. After all, the operations and complexities are nearly the same; only removing the value of the front is wrong. To fix this, one can simply hold a *pointer* to what the front of the queue is in the vector. Removing the front element is then equivalent to moving the pointer forward one step. To see this how this would work in practice, see an example push and pop operation in Figure 6.3.

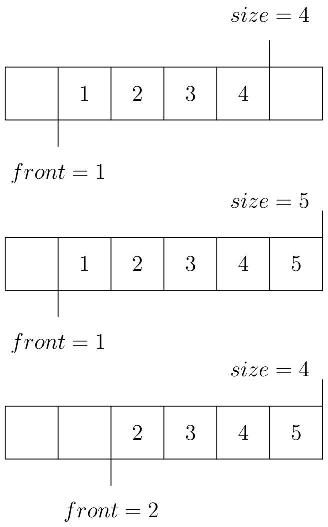


Figure 6.3: Pushing and poping elements in a queue

Exercise 6.6

Implement a queue using a vector.

Exercise 6.7

A queue can also be implemented using two stacks. How?

In a similar manner, a stack can also be implemented using two queues. How?

6.4 Graphs

Finally, we discuss a data structure called a *graph*. Graphs are very important objects in algorithmic problem solving. If you are not familiar with them, you should first read appendix Section A.4 that introduces you to the mathematical terminology of graphs. This chapter instead deals with the *representation* of graphs in an algorithm.

There are three common ways of reprensenting graphs in algorithms: *adjacency matrices*, *adjacency lists* and *adjacency maps*. Occasionally we also represent graphs *implicitly* – for example by a function that gives us the neighbours of a single vertex. This latter representation is common when dealing with searches in the graph corresponding to the positions in a game such as chess.

In the following sections, we present the representation of the directed, unweighted graph in Figure 6.4.

6.4.1 Adjacency Matrices

An adjacency matrix represents a graph $G = (V, E)$ with $|V|$ as a 2D $|V| \times |V|$ matrix in the following way:

Definition 6.1 If $G = (V, E, w)$ is a directed, weighted graph and $V = \{v_1, ..., v_n\}$, the graph's ***adjacency matrix*** the $|V| \times |V|$-matrix $A = (a_{i,j})$ where $a_{i,j} = w(v_i v_j)$.

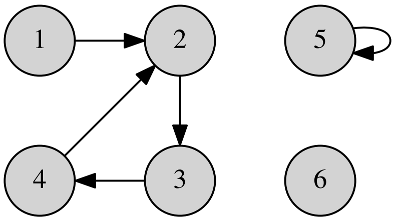


Figure 6.4: An example graph with 6 verices and 5 edges.

For undirected graphs, we set $a_{i,j} = a_{j,i} = w(\{v_i, v_j\})$.

For unweighted graphs, we set $a_{i,j} = 1$.

This representation uses $\Theta(|V|^2)$ memory, and takes $O(1)$ time for adding, modifying and removing edges. To iterate through the neighbours of a vertex, you need $\Theta(|V|)$ time, independent of the number of neighbours of the vertex itself.

Adjacency matrices are best to use when $|V|^2 \approx |E|$, i.e. when the graph is *dense*.

The adjacency matrix for the directed, unweighted graph in Figure 6.4 is:

$$\begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

6.4.2 Adjacency Lists

Another way to represent graphs is by using lists of neighbours for every vertex. This approach is called ***adjacency lists***. This only requres $\Theta(|E| + |V|)$ memory, which is better when your graph have few edges, i.e. it is *sparse*. If you use a vector to represent each list of neighbours, you also get $\Theta(1)$ addition and removal (if you know the index of the edge and ignore their order) of edges, but it takes $O(|V|)$ time to determine if an edge exists. On the upside, iterating through the neighbours of a vertex takes time proportional to the number of neighbours instead of the number of vertices in the graph. This means that iterating through all the neighbours of all vertices takes time $\Theta(|E| + |V|)$ instead of $\Theta(|V|^2)$ as for the adjacency matrix. For large, sparse graphs this is clearly better!

When representing weighted graphs, the list usually contains pairs of $(\textit{neighbour}, \textit{weight})$ for the edges instead. For undirected graphs, both endpoints of an edge contains the other in their adjaceny lists.

6.4.3 Adjacency Maps

An *adjacency map* combines the adjacency matrix with the adjacency list to get the benefits of both the matrix ($\Theta(1)$ time to check if an edge exists) and the lists (low memory usage and fast neighbourhood iteration). Instead of using lists of neighbours for each vertex, we can use a hash table for each vertex.

This has the same time and memory complexities as the adjacency lists, but it also allows for checking if an edge is present in $\Theta(1)$ time. The downsides are that hash tables have a higher constant factor than the adjacency list, and that you lose the ordering you have of your neighbours (if this is important). The adjacency map also inherits another sometimes important property from the matrix: you can *remove* arbitrary edges in $\Theta(1)$ time!.

Exercise 6.8

Given a graph, which representation or representations are suitable if

a) $|V| = 1000$ and $|E| = 499500$

b) $|V| = 10000$ and $|E| = 20000$

c) $|V| = 1000$ and $|E| = 10000$

6.5 Priority Queues

Now, let us look at our first more complicated data structure. The ***priority queue*** is an unordered bag of elements, from which we can get and remove the largest one quickly. It supports the operations

- push(val): inserting a value into the heap.
  Complexity: $O(\log n)$

- pop(): remove the largest value in the heap.
  Complexity: $\Theta(\log n)$

- getMax(): get the largest value in the heap.
  Complexity: $\Theta(1)$

This is implemented as `priority_queue` in C++ (Section 3.4, although one often instead use a `set` which not only supports the same operations with the same compplexities, but also supports erasing elements.

In this chapter, we look closely at one particular implementation of a priority queue called a *heap*. The heap will be implemented using another data structure called a *binary tree*, which we need to describe first.

6.5.1 Binary Trees

A ***binary tree*** is a rooted tree where every vertex have either 0, 1 or 2 children. In Figure 6.5, you can see an example of a binary tree.

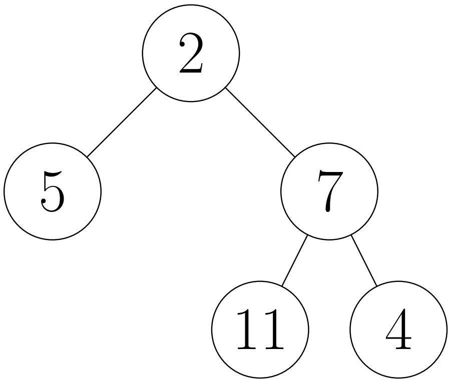


Figure 6.5: A binary tree

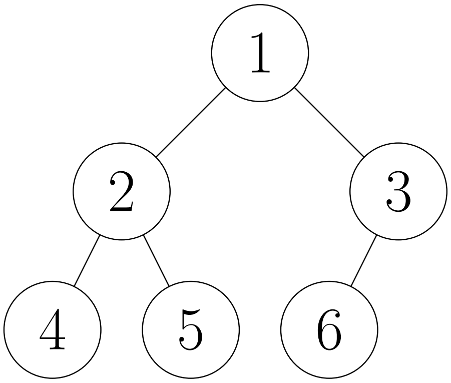


Figure 6.6: A complete binary tree

We call a binary tree *complete* if every level of the tree is completely filled, except possibly the bottom one. If the bottom level is not filled, all the vertices need to be as far as possible to the left. In a complete binary tree, we can order every vertex as we do in Figure 6.6, i.e. from the top down, left to right at each layer.

The beauty of this numbering is that we can use it to store a binary tree in a vector. Since each vertex is given a number, we can map the number of each vertex into a position in a vector. The n vertices of a complete binary tree then occupy all the indices $[1, n]$. An important property of this numbering is that it is easy to compute the number of the parent, left child and right child of a vertex. If a vertex has number i, the parent simply have number $\lfloor \frac{i}{2} \rfloor$, the left child has number $2i$ and the right child has number $2i + 1$.

Exercise 6.9

Prove that the above properties of the numbering of a complete binary tree hold.

A heap is implemented as a complete binary tree, which we in turn implement by a backing vector in the manner described. In the implementation, we use the following convenience functions:

```
1: function PARENT($i$) return $i/2$
2: function LEFT($i$) return $2i$
3: function RIGHT($i$) return $2i + 1$
```

Note: if you use a vector to represent a complete binary tree in this manner it needs to have the size $n + 1$ where n is the number of vertices, since the tree numbering is 1-indexed and the vector is 0-indexed!

6.5.2 Heaps

A ***heap*** is a special kind of complete binary tree. More specifically, it should always satisfy the following property: *a vertex always have a higher value than its immediate children*. Note that this condition acts transitively, which means that a vertex also has a higher value than its grand-children, and their children and so on. In particular, a consequence of this property is that the root will always be the largest value in the heap. As it happens, this is precisely the property we want. You can see an example of a heap in Figure 6.7

We start our description of a heap somewhat backwards, with the function needed to get the largest element:

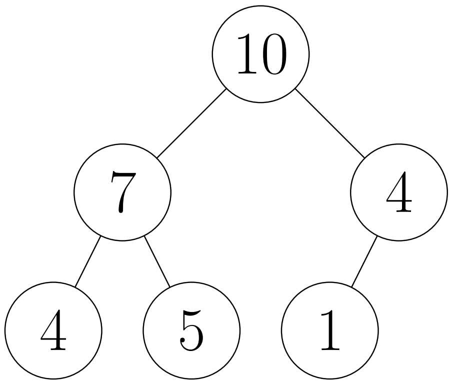


Figure 6.7: A heap

```
1: procedure GET-MAX(tree) return tree[1]
```

Of course, the complicated operations on the heap is to add and remove elements in a manner that satisfy this property. We start with the simplest one, adding a new element. Since we represent the heap using a vector, adding a new element to a heap can be done by appending the element to the vector. In this manner, we ensure that the underlying binary tree is still complete. However, it may be that the value we added is now larger than its parent. If this is the case, we can fix the violation of our heap property by swapping the value with its parent. This does not guarantee that the value still is not larger than its parent. In fact, if the newly added element is largest in the heap, it would have to be repeatedly swapped up to the top! This procedure, of moving the newly added element up in the tree until it is no longer larger than its parent (or it becomes the root) *bubbling up*.

```
1: procedure PUSH(x, tree)
2:     tree.push_back(x)
3:     Bubble − Up(tree.size() − 1, tree)
```

Pushing a value reduces to appending it to the tree and bubbling it up. You can see this procedure in action in Figure 6.8.

Removing a value is slightly harder. First of, the tree will no longer be a binary tree – it is missing its root! To rectify this, we can take the last element of

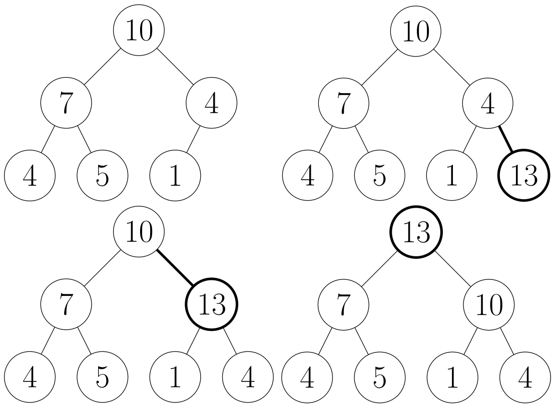


Figure 6.8: Adding a new value and bubbling it up.

```
1: procedure BUBBLE-UP(idx, tree)
2:     while idx > 1 do
3:         if tree[idx] > tree[Parent(idx)] then
4:             Swap tree[idx] and tree[Parent(idx)]
5:             idx ← Parent(idx)
6:         else
7:             break
```

the tree and put it as root instead. This keeps the binary tree complete, but may cause it to violate the heap property since our new root may be smaller than either or both of its children. The solution to this problem is similar as to that of adding an element. Instead of bubbling up, we bubble it down by repeatedly swapping it with one of its children until it no longer is greater than any of its children. The only question mark is which of its children we should bubble down to, in case the element is smaller than both of its children. The answer is clearly the largest of the two children. If we take the smaller of the two children, we will again violate the heap property.

```
1: procedure REMOVE-MAX(x, tree)
2:     tree[1] ← tree[tree.size() − 1]
3:     tree.pop_back()
4:     Bubble − Down(1, tree)
```

Just as with pushing, poping a value is done by a combination of removing the value and fixing the heap to satisfy the heap property again.

```
procedure BUBBLE-DOWN(idx, tree)
    while true do
        largest ← idx
        if Left(idx) < tree.size() and tree[Left(idx)] > tree[largest] then
            largest ← Left(idx)
        if Right(idx) < tree.size() and tree[Right(idx)] > tree[largest] then
            largest ← Right(idx)
        if largest = idx then

            break
        else
            Swap tree[idx] and tree[largest]
            idx ← largest
```
[1]

A final piece of our analysis is missing. It is not yet proven that the time complexity of adding and removing elements are indeed $O(\log n)$. To do this, we first need to state a basic fact of complete binary trees: their height is at most $\log_2 n$. This is easily proven by contradiction. Assume that the height of the tree is at least $\log_2 n + 1$. We claim that any such tree must have strictly more than n vertices. Since all but the last layers of the tree must be complete, it must have at least $1 + 2 + \cdots + 2^{\log_2 n} = 2^{\log_2 n+1} - 1$ vertices. But $2^{\log_2 n+1} - 1 = 2n + 1 > n$ for positive n – the tree has more than n vertices. This means that a tree with n vertices cannot have more than height $\log_2 n$.

The next piece of the puzzle is analyzing just how many iterations the loops in the bubble up and bubble down procedures can perform. In the bubble up procedure, we keep an index to a vertex that, for every iteration, moves up in the tree. This can only happen as many times as there are levels in the tree. Similarly, the bubble down procedure tracks a vertex that moves down in the tree for every iteration. Again, this is bounded by the number of levels in the tree. We are forced to conclude that since the complexity of each iteration is $\Theta(1)$ as they only perform simple operations, the complexities of the procedures as a whole are $O(\log n)$.

Exercise 6.10 — Kattis Exercise

Binary Heap – heap

Exercise 6.11

Prove that adding an element using Push never violates the heap property.

Exercise 6.12

To construct a heap with n elements by repeatedly adding one at a time takes $O(n \log n)$ time, since the add function takes $O(\log n)$ time in the worst case.

One can also construct it in $\Theta(n)$ time in the following way: arbitrarily construct a complete binary tree with all the n elements. Now, call Bubble-Down on each of the elements in reverse order $n, n-1, \ldots, 2, 1$.

Prove that this correctly constructs a heap, and that is takes $\Theta(n)$ time.

6.6 Chapter Notes

For a more rigorous treatment of the basic data structures, we again refer to *Introduction to Algorithms* [5]. If you want to dive deeper into proper implementations of the algorithms in C++, *Data Structures and Algorithm Analysis in C++*[25] covers what we brought up in this chapter and a bit more.

Part II

Basics

Chapter 7

Brute Force

Many problems are solved by testing a large number of possibilities. For example, chess engines work by testing countless variations of moves and choosing the ones resulting in the "best" positions. This approach is called ***brute force***. Brute force algorithms exploit that computers are fast, resulting in you having to be less smart. Just as with chess engines, brute force solutions might still require some ingenuity. The same brute force problem might have a simple algorithm which requires a computer to evaluate 2^{40} options, while some deeper analysis might be able to reduce this to 2^{20}. This would be a huge reduction in running time. Different approaches to brute force may be the key factor in reaching the latter case instead of the former. In this chapter, we will study a few such techniques.

7.1 Optimization Problems

In an ***optimization problem***, we have some ***solution set*** S and a ***value function*** f. The goal is to find an $x \in S$ which maximize $f(x)$, i.e., optimizing the function.

Optimization problems constitute a large class of the problems that we solve in algorithmic problem solving, such as the Max Clique problem and the Buying Books problems we will study in this chapter. One of the most famous optimization problems is the NP-complete *Travelling Salesman Problem*. The problem seeks the shortest cycle that visits all vertices of a weighted graph. The practical applications of this problem are many. A logistics company that must perform a number of deliveries probably want to minimize the distance traveled when visiting all the points of delivery. When planning your backpacking vacation, you may prefer to minimize the cost of travelling between all your destinations. In this problem, the solution set S would consist of all cycles in the graph that visit all the vertices, with $f(x)$ being the sum of all edges in the cycle x.

The brute force technique essentially consists of evaluating $f(x)$ for a large number (sometimes even all) of $x \in S$. For large S, this is slow.

The focus of this chapter and the chapters on Greedy Algorithms (Chapter 8) and Dynamic Programming (Chapter 9) will be to develop techniques that exploit particular structures of optimization problems to avoid evaluating the entire set S.

7.2 Generate and Test

Our first brute force method is the ***generate and test*** method. This particular brute force strategy consists of *generating* solutions – naively constructing candidate solutions to a problem – and then *testing* them – removing invalid solutions. It is applicable whenever the number of candidate solutions is quite small.

Max Clique

In a graph, a subset of the vertices form a ***clique*** if each pair of vertices is connected by an edge. Given a graph, determine the size of the largest clique.

Input

The first line of input contains an integer N and M – the number of vertices and the number of edges of the graph. The vertices are numbered $0, 1, \ldots, N-1$. The next M lines contain the edges of the graph. An edge is given as two space-separated integers A and B – the endpoints of the graph.

Output

Output a single number – the size of the largest clique in the graph.

This problem is one of the so-called NP-complete problems we mentioned in Chapter 5. Thus, a polynomial-time solution is out of reach. We will solve the problem for $N \leq 15$.

Let us analyze whether a generate and test approach is suitable. First of all, we must define what our candidate solutions are. In this problem, only one object comes naturally; subsets of vertices. For every such candidate, we must first test whether it is a clique, and then compute its size, picking the largest clique to arrive at our answer.

In the Max Clique problem, there are only 2^N subsets of vertices (and thus candidate solutions), which is a quite small number. Given such a set, we can verify whether it is a clique in $O(N^2)$ time, by checking if every pair of vertices in the candiate set has an edge between them. To perform this check in $\Theta(1)$ time, we keep a 2D vector adj such that $adj[i][j]$ is true if and only if vertices i and j are adjacent to each other. This gives us a total complexity of $O(2^N \cdot N^2)$. According to our table of complexities (Table 5.1), this should be fast enough for $N = 15$. A C++ implementation for this can be seen in Algorithm 7.1. Note the nifty use of integers interpreted as bitsets to easily iterate over every possible subset of an N-element set, a common technique of generate and test solutions based on subsets.

Algorithm 7.1: Max Clique

```
int main() {
  int N, M;
  cin >> N >> M;
  vector<vector<bool>> adj(N, vector<bool>(N));
  rep(i,0,M) {
    int A, B;
    cin >> A >> B;
    adj[A][B] = adj[B][A] = true;
  }
  rep(i,0,N) adj[i][i] = true;
  rep(i,0,1<<N) {
    rep(j,0,N) {
      if (!(i & (1 << j))) continue;
      rep(k,0,N) {
        if (!(i & (1 << k))) continue;
        if (!adj[j][k]) goto skip;
      }
    }
    ans = max(ans, __builtin_popcount(i));
skip:;
  }
  cout << ans << endl;
}
```

This kind of brute force problem is often rather easy to spot. There will be a very small input limit on the parameter you are to brute force over. The solution will often be subsets of some larger base set (such as the vertices of a graph).

Exercise 7.1 — Kattis Exercises

4 thought – 4thought

Lifting Walls – walls

Let us look at another example of this technique, where the answer is not just a subset.

The Clock

Swedish Olympiad in Informatics 2004, School Qualifiers

When someone asks you what time it is, most people respond "a quarter past five", "15:29" or something similar. If you want to make things a bit harder, you can answer with the angle between the minute and the hour hands, since this uniquely determines the time. However, many people are unused to this way of specifying the time, so it would be nice to have a program which translates this to a more common format.

We assume that our clock have no seconds hand, and only display the time at whole minutes (i.e., both hands only move forward once a minute).

The angle is determined by starting at the hour hand and measuring the number of degrees clockwise to the minute hand. To avoid decimals, this angle will be specified in tenths of a degree.

Input

The first and only line of input contains a single integer $0 \leq A < 3600$, the angle specified in tenths of a degree.

Output

Output the time in the format `hh:mm` between 00:00 and 11:59.

It is difficult to come up with a formula that gives the correct times as a function of the angles between the hands on a clock. Instead, we can turn the problem around. If we know what the time is, can we compute the angle between the two hands of the clock?

Assume that the time is currently h hours and m minutes. The minutes hand will then be at angle $\frac{360}{60}m = 6m$ degrees. Similarly, the hour hand moves $\frac{360}{12}h = 30h$ degrees due to the hours, and $\frac{360}{12}\frac{1}{60}m = 0.5m$ degrees due to the minute. While computing the current time directly from the angle is difficult, computing the angle directly from the current time is easy.

Our solution will be to test the $60 \cdot 12 = 720$ different times, and pick the one which matched the given angle (Algorithm 7.2).

Algorithm 7.2: The Clock

```
procedure CLOCK($A$)
    for $h \leftarrow 0$ to $11$ do
        for $m \leftarrow 0$ to $59$ do
            $hourAng \leftarrow 300h + 5m$
            $minuteAng \leftarrow 60m$
            $angBetween \leftarrow (hourAng - minuteAng + 3600) \bmod 3600$
            if $angBetween = A$ then
                return $h{:}m$
```

Competitive Tip

Sometimes, competitions pose problems which are solvable quite fast, but a brute force algorithm will suffice as well. As a general rule, code the simplest correct solution that is fast enough, even if you see a faster one.

Exercise 7.2 — Kattis Exercises

All about that base – allaboutthatbase

Natjecanje – natjecanje

Perket – perket

7.3 Backtracking

Backtracking is a variation of the generate and test method. Most of the time it is faster, but it can sometimes be more difficult to code (in particular when the solutions are subsets).

Let us return to the Max Clique problem. In the problem, we generated all the candidate solutions (i.e., subsets of vertex) by using bitsets. In problems where the candidate solutions are other objects than subsets, or the number of subsets is too large to iterate through, we need to construct the solutions in another way. Generally, we do this recursively. For example, when generating subsets, we would go through every element one at a time, and decide whether to include it. Backtracking extends generate and test to not only testing all the candidate solutions, but also these partial candidates. Thus, a backtracking approach can be faster than an iterative approach, by testing fewer candidate solutions.

For example, assume that two vertices a and b are not connected by an edge in the graph. If we decide to include a in our solution, we already know that a candidate solution can not include b. Thus, we have managed to reduce four choices – including or excluding a and b – to three choices, by eliminating the inclusion of both vertices. Algorithm 7.3 contains a C++ implementation of this.

Algorithm 7.3: Max Clique, Recursive Variant

```
// excluded is a bit set containing the vertices with a chosen neighbour
int best(int at, int excluded, int clique, const vector<int>& adjacent) {
  if (at == sz(adjacent)) return clique;
    // Case 1: Not including the current vertex
  int answer = best(at + 1, excluded, clique, adjacent);
    // Case 2: We can include the current vertex
  if (!((1 << at)&excluded)) {
    answer = max(answer,
      best(at + 1, excluded | ~adjacent[at], clique + 1, adjacent));
  }
  return answer;
}

int main() {
  int N, M;
  cin >> N >> M;
  vector<int> adjacent(N);
  rep(i,0,M) {
    int A, B;
    cin >> A >> B;
    adjacent[A] |= 1 << B;
    adjacent[B] |= 1 << A;
  }
  cout << best(0, 0, 0, adjacent) << endl;
}
```

As written, this version has the same complexity as the generate-and-test version. Our improvement only generated fewer branches whenever the graph contained edges. In the case where the graph consists of N vertices and no edges, this is not the case. The recursion then degenerates to branching twice N times, resulting in a $\Theta(2^n)$ complexity.

Backtracking works whenever we can construct our solutions iteratively (as in constructing it part by part), and quickly determine whether such a partial solution can possibly be completed to an admissible solution.

Exercise 7.3 — Kattis Exercises

Class Picture – classpicure

Boggle – boggle

Geppetto – geppetto

Map Colouring – mapcolouring

Sudokunique – sudokunique

All Friends – friends

As a general principle, backtracking seems simple enough. Some backtracking solutions require a bit more ingenuity, as in the next problem.

Basin City Surveillance

Nordic Collegiate Programming Contest 2014 – Pål G. Drange and Markus S. Dregi

BASIN CITY is known for her incredibly high crime rates. The police see no option but to tighten security. They want to install traffic drones at different intersections to observe who's running on a red light. If a car runs a red light, the drone will chase and stop the car to give the driver an appropriate ticket. The drones are quite stupid, however, and a drone will stop before it comes to the next intersection as it might otherwise lose its way home, its home being the traffic light to which it is assigned. The drones are not able to detect the presence of other drones, so the police's R&D department found out that if a drone was placed at some intersection, then it was best not to put any drones at any of the neighbouring intersections. As is usual in many cities, there are no intersections in Basin City with more than four other neighbouring intersections.

The drones are government funded, so the police force would like to buy as many drones as they are allowed to. Being the programmer-go-to for the Basin City Police Department, they ask you to decide, for a given number of drones, whether it is feasible to position exactly this number of drones.

Input

The first line contains an integer k ($0 \leq k \leq 15$), giving the number of drones to position. Then follows one line with $1 \leq n \leq 100\,000$, the total number of intersections in Basin City. Finally follow n lines describing consecutive intersections. The i'th line describes the i'th intersection in the following format: The line starts with one integer d ($0 \leq d \leq 4$) describing the number of intersections neighbouring the i'th one. Then follow d integers denoting the indices of these neighbouring intersections. They will be all distinct and different from i. The intersections are numbered from 1 to n.

Output

If it is possible to position k drones such that no two neighbouring intersections have been assigned a drone, output a single line containing `possible`. Otherwise, output a single line containing `impossible`.

At a first glance, it is not even obvious whether the problem is a brute force problem, or if some smarter principle should be applied. After all, $100\,000$ vertices is a huge number of intersections! We can make the problem a bit more reasonable with our first insight. If we have a large number of intersections, and every intersection is adjacent to very few other intersection, it is probably very easy to place the drones at appropriate intersections. To formalize this insight, consider what happens when we place a drone at an intersection.

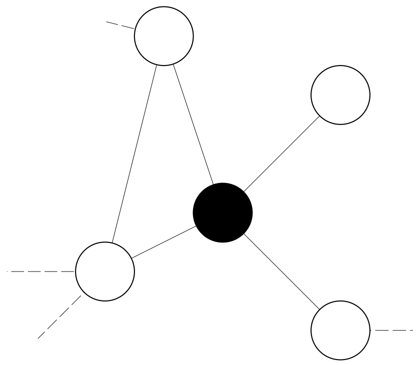


Figure 7.1: The intersections affected by placing a drone at an intersection.

By placing a drone at the intersection marked in black in Figure 7.1, at most five intersections are affected – the intersection we placed the drone at, along with its neighbouring intersections. If we would remove these five intersections, we would be left with a new city where we need to place $k-1$ drones. This simple fact – which is the basis of a recursive solution to the problem – tells us that if we have $N \geq 5k-4$ intersections, we immediately know the answer is *possible*. The -4 terms comes from the fact that when placing the final drone, we no longer care about removing its neighbourhood, since no further placements will take place.

Therefore, we can assume that the number of vertices is less than $5 \cdot 15 - 4 = 71$, i.e., $n \leq 70$. This certainly makes the problem seem much more tractable. Now, let us start developing solutions to the problem.

First of all, we can attempt to use the same algorithm as we used for the Max Clique problem. We could recursively construct the set of our k drones by, for each intersection, try to either place a drone there or not. If placing a drone at an intersection, we would forbid placing drones at any neighbouring intersection.

Unfortunately, this basically means that we are testing every intersection when placing a certain drone somewhere. This would give us a complexity of $O(n^k)$. More specifically, the execution time $T(n,k)$ would satisfy $T(n,k) \approx T(n-1,k) + T(n-1,k-1)$, which implies $T(n,k) \approx \binom{n}{k} = \Omega(n^k)$ (see Section 15.4 for more details). For $n = 70, k = 15$, this will almost certainly be way too high. The values of n and k do suggest that an exponential complexity is in order, just not of this kind. Instead, something similar to $O(c^k)$ where c is a small constant would be a better fit. One way of achiving such a complexity would be to limit the number of intersections we must test to place a drone at before trying one that definitely works. If we could manage to test only c such intersections, we would get a complexity of $O(c^k)$.

The trick, yet again, comes from Figure 7.1. Assume that we choose to include this intersection in our solution, but still can not construct a solution. The only reason this case can happen is (aside from bad previous choices) that no optimal solution includes this intersection. What could possibly stop this intersection from being included in an optimal solution? Basically, one of its neighbours would have to be included in every optimal solution. Fortunately for us, this gives us just what we need to improve our algorithm – either a given intersection, or one of its neighbours, must be included in any optimal solution.

We have accomplished our goal of reducing the number of intersections to test for each drone to a mere 5, which will give us a complexity of about $O(5^k)$ (possibly with an additional polynomial factor in n depending on implementation). This is still too much, unless, as the jury, noted, some "clever heuristics" are applied. Fortunately for us, applying a common principle will speed things up dramatically (even giving us a better time complexity).

First of all, we can partition the intersections into sets that are connected by sequences by roads. These sets are all independent of each other, so we can solve them separately by computing the maximal number of drones we can place in every such set, until we have processed enough sets to place k drones.

With this in hand, we can use the following insight: if we at every step branch on the intersection with the fewest neighbours, we will instead achieve a complexity of $O(4^k)$. After branching on the first drone, there will always be one intersection with at most 3 neighbours – leaving us with only 4 choices we must test when placing a drone. We can prove this easily by contradiction. Assume that after placing a number of drones, every intersection has exactly 4 neighbours. Then, none of these intersections can be the neighbour of an intersection we have removed so far. However, this means the set of intersections removed so far and the remaining intersections are disconnected, a contradiction.

While such an algorithm would be significantly faster than the $O(5^k)$, further improvements are possible. Again, let us consider under what circumstances a certain intersection is excluded from any optimal solution. We have already concluded that if this is the case, then one of its neighbours must be included in any optimal solution. Can it ever be the case that only *one* of its neighbours are included in an optimal solution, as in Figure 7.2?

Clearly, this is never the case. We can simply move the drone to the intersection from its neighbour, since there is no other neighbour causing problems. Now, we are basically done. For any intersection, there will either be an optimal solution including it, or two of its neighbours. Since an intersection has at most 4 neighbours, it has at most 6 pairs of neighbours. This means our recursion will take time $T(k) = T(k-1) + 6T(k-2)$ in the worst case. This recurrence has the solution 3^k, since $3^{k-1} + 6 \cdot 3^{k-2} = 3^{k-1} + 2 \cdot 3^{k-1} = 3 \cdot 3^{k-1} = 3^k$. A final improvement would be to combine this insight with the independence of the connected subsets of intersections. The second term of the time recurrence would then be a 3 instead of a 6 (as 3 neighbours make 3 pairs). Solving this

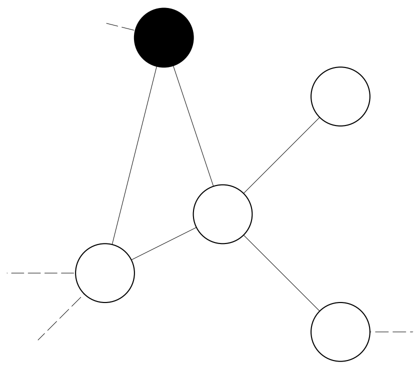


Figure 7.2: Placing a drone at a single neighbour of an intersection.

recurrence would give us the complexity $O(2.31^k)$ instead.

The general version of this problem (without the bounded degree) is called *Independent Set*

So, what is the take-away regarding backtracking? First of all, find a way to construct candidate solutions iteratively. Then, try to integrate the process of testing the validity of a complete solution with the iterative construction, in the hope of significantly reducing the number of candidate solutions which need evaluating. Finally, we might need to use some additional insights, such as what to branch on (which can be something complicated like the neighborhood of a vertex), deciding whether to backtrack or not (i.e., improving the testing part) or reducing the number of branches necessary (speeding up the generation part).

Exercise 7.4 — Kattis Exercises

Domino – domino

Fruit Baskets – fruitbaskets

Infiltration – infiltration

Vase Collection – vase

7.4 Fixing Parameters

The parameter fixing technique is also similar to the generate and test method, but is not used to test the solution set itself. Instead, you perform brute force to *fix* some parameter in the problem by trying possible values they can assume. Hopefully, fixing the correct parameters allows you to solve the remaining problem easily. The intuition is that while any particular choice of parameter may be wrong, testing every choice allows us to assume that we at some point used the correct parameter.

Buying Books

Swedish Olympiad in Informatics 2010, Finals

You are going to buy N books, and are currently checking the different internet M book shops for prices. Each book is sold by at least one book store, and can vary in prices between the different stores. Furthermore, if you order anything from a certain book store, you must pay for postage. Postage may vary between book stores as well, but is the same no matter how many books you decide to order. You may order books from any number of book stores. Compute the smallest amount of money you need to pay for all the books.

Input

The first line contains two integers $1 \leq N \leq 100$ – the number of books, and $1 \leq M \leq 15$ – the number of book stores.

Then, M descriptions of the book stores follow. The description of the i'th store starts with a line containing two integers $0 \leq P_i \leq 1\,000$ (the postage for this book store), and $1 \leq L_i \leq N$ (the number of books this store sells). The next L lines contains the books sold by the store. The j'th book is described by two integers $0 \leq B_{i,j} < N$ – the (zero-indexed) number of a book being sold here, and $1 \leq C_{i,j} \leq 1000$ – the price of this book at the current book store.

Output

Output a single integer – the smallest amount of money you need to pay for the books.

If we performed naive generate and test on this problem, we would probably get something like 15^{100} solutions (testing every book shop for every book). This is infeasible. So, why can we do better than this? There must be some hidden structure in the problem which makes testing all those possibilities unnecessary. To find this structure, we will analyze a particular candidate solution as given by the naive generate and test method. Can we find a simple criteria for when a solution obvious cannot be optimal?

It turns out that yes, we can. Assume that we, in a particular solution, bought a book from some book store A, but it was available for a lower price at book store B. If this is an optimal solution we must not have bought any books from B.

When this happens, i.e., you notice very simple constraints which immediately disqualify many of the solution candidates from being optimal, it is a good sign you may be able to restructure your brute force in order to avoid evaluating many of them. In our case, this observation hints that making a choice for every book is not particularly good.

We *could* decide to use this fact to turn our generate and test into a backtracking algorithm, by pruning away any solution where we have bought a book which is available at a cheaper price from another book store we also used. Unfortunately, this is easily defeated by giving most of the books equal prices at most of the book stores.

Instead, let us use the observation differently. The entirety of the observation quite plainly told us that we do not really have any choice in where we buy the books! Indeed, once we know what book stores we have bought from, we are forced to buy the book from the cheapest store that is used. At this point, we are basically done. We have reduced the amount of information we need to fix to solve the problem to "which book stores will we purchase from?". This parameter has only 2^{15} possibilities. After fixing it, we can compute the rest of the answer using the "cheapest store for each book" rule. Since we test every possible such parameter, we must also include the optimal one. The pseudo code for this solution is in Algorithm 7.4.

Algorithm 7.4: Buying Books

```
procedure BuyingBooks(books N, stores M, costs C, postages P)
    answer ← ∞
    for every $S \subseteq [M]$ do
        $cost \leftarrow 0$
        for every $s \in S$ do
            $cost \leftarrow cost + P_s$
        for every $b \in [N]$ do
            $cost \leftarrow cost + \min_{i \in S} C_{i,b}$
        $answer \leftarrow \min(answer, cost)$
    return $answer$
```

Alternatively, we could have come to the same insight by simply asking ourselves "can we bruteforce over the number of book shops?". Whenever you have a parameter about this size in such a problem, this is a question worth asking. However, the parameter to brute force over is not always this explicit, as in the following problem, which asks us to find all integer solutions to an equation in a certain interval.

Integer Equation

Codeforces Round #262, Problem B

Find all integers $0 < x < 10^9$ which satsify the equation

$$x = a \cdot s(x)^b + c$$

where a, b and c are given integers, and $s(x)$ is the digit sum of x.

Input

The input contains the three integers a, b, and c such that

$$|a| \leq 10\,000$$

$$1 \leq b \leq 5$$

$$|c| \leq 10\,000$$

Output

Output a single integer – number of integer solutions x to the equation.

In this problem, the only explicit object we have is x. Unfortunately, 10^9 is a tad too many possibilities. If we study the equation a bit closer, we see that $s(x)$ also varies as a function of x. This is helpful, since $s(x)$ has far fewer options than x. In fact, a number bounded by 10^9 has at most 9 digits, meaning it has a maximum digit sum of $9 \cdot 9 = 81$. Thus, we can solve the problem by looping over all the possibles values of $s(x)$. This uniquely fixes our right hand side, which equals x. Given x, we verify that $s(x)$ has the correct value. Whenever we have such a function, i.e., one with a large domain (like x in the problem) but a small image (like $s(x)$ in the problem), this technique can be used by brute forcing over the image instead.

Exercise 7.5 — Kattis Exercises

Shopping Plan – shoppingplan

7.5 Meet in the Middle

The *meet in the middle* technique is essentially a special case of the parameter fixing technique. The general theme will be to fix half of the parameter space and build some fast structure such that when testing the other half of the parameter space, we can avoid explicitly re-testing the first half. It is a space-time tradeoff, in the sense that we improve the time usage (testing half of the parameter space much faste much faster), by paying with increased memory usage (to save the pre-computed structures).

Subset Sum

Given a set of integers S, is there some subset $A \subseteq S$ with a sum equal to T?

Input

The first line contains an integer N, the size of S, and T. The next line contains N integers $s_1, s_2, ..., s_N$, separated by spaces – the elements of S. It is guaranteed that $s_i \neq s_j$ for $i \neq j$.

Output

Output `possible` if such a subset exists, and `impossible` otherwise.

In this problem, we have N parameters in our search space. For each element of S, we either choose to include it in A or not – a total of two choices for each parameter. This naive attempt at solving the problem (which amounts to computing the sum of every subset) gives us a complexity of $O(2^N)$. While sufficient for e.g. $N = 20$, we can make an improvement that makes the problem tractable even for $N = 40$.

As it happens, our parameters are to a large extent independent. If we fix e.g. the $\frac{N}{2}$ first parameters, the only constraint they place on the remaining $\frac{N}{2}$ parameters is the sum of the integers in subset they decide. This latter constraint takes $O(2^{\frac{N}{2}})$ time to check for each choice of the first half of parameters if we use brute force. However, the computation performed is essentially the same, only differing in what sum we try to find. We will instead trade away some memory in order to only compute this information once, by first computing all possible sums that the latter half of the elements can form. This information can be inserted into a hash set, which allows us to determine if a sum can be formed by the elements in $\Theta(1)$ instead. Then, the complexity is instead $\Theta(N2^{\frac{N}{2}})$ in total.

Algorithm 7.5: Subset Sum

```
procedure SubsetSum(set S, target T)
    $N \leftarrow |S|$
    $left \leftarrow \frac{N}{2}$
    $right \leftarrow N - left$
    $Lset \leftarrow$ the $left$ first elements of $S$
    $Rset \leftarrow S \setminus Lset$
    $Lsums \leftarrow$ new $\mathtt{set}$
    for each $L \subseteq Lset$ do
        $Lsums.\mathtt{insert}(\sum_{l \in L} l)$
    for each $R \subseteq Rset$ do
        $sum \leftarrow \sum_{r \in R} r$
        if $Lsums.\mathtt{contains}(T - sum)$ then
            output $\mathtt{true}$
            return
    output $\mathtt{false}$
```

Exercise 7.6 — Kattis Exercises

Closest Sums – closestsums

Maximum Loot – maxloot

Celebrity Split – celebritysplit

Circuit Counting – countcircuits

Indoorienteering – indoorienteering

Key to Knowledge – keytoknowledge

Knights in Fen – knightsfen

Rubrik's Revenge in ... 2D!? 3D? – rubriksrevenge

7.6 Chapter Notes

r notes

Chapter 8

Greedy Algorithms

In this chapter, we are going to look at another standard technique to solve some categories of search and optimization problems faster than naive brute-force, by exploiting properties of *local optimality*.

8.1 Optimal Substructure

Most optimization problems we study consist of making a series of sequential choices. They are often be of the following form: Given a weighted, directed acyclic graph (DAG) on N vertices, what is the "best" path from a vertex S to another vertex T? This graph is almost never be given explicitly. Instead, it hides behind the problem as a set of states (the vertices). At each state, we are to make some choice that takes us to another state (traversing an edge). If the path consists of edges $e_1, e_2, \ldots, e_k$, the function we are to maximize will be of the form

$$G(e_1, e_2, \ldots, e_k) = g(e_1, g(e_2, g(\ldots, g(e_k, 0))))$$

where g is a function from $E \times R$ to R. We will denote $B(v)$ as the maximum value of $G(e_1, e_2, \ldots, e_k)$ over all paths from v to T. Often, g will be the negative sum of the edge weights, meaning we look for the shortest path from S to T. If $g(e, x)$ is increasing in x, we say that problems exhibiting this property has *optimal substructure*.

One way to solve the problem would be to evaluate G for every path in the graph. Unfortunately, the number of paths in a general graph can be huge (growing exponentially with the number of vertices). However, the optimal substructure property allows us to make a simplification. Assume that S has neighbors $v_1, v_2, ..., v_m$. Then by the definition of B and g, $B(s) = \max(g(\{s, v_i\}, B(v_i))$. Thus, we can solve the problem by first solving **the same problem** on all vertices v_i instead.

Change-making Problem, Denominations $1, 2, 5$

Given an infinite number of coins of denominations $1, 2, 5$, determine the smallest number of coins needed to sum up to T.

Input

The input contains a single integer $1 \leq T \leq 10^6$.

Output

Output a single integer, the minimum number of coins needed.

We can phrase this problem using the kind of graph we previously discussed. Let the graph have vertices labeled $0, 1, 2, ..., T$, representing the amount of money we wish to sum up to. For a vertex labeled x, we add edges to vertices labeled $x - 1$, $x - 2$, $x - 5$ (if those vertices exist), weighted 1. Traversing such an edge represents adding a coin of denomination 1, 2 or 5. Then, the Change-making Problem can be phrased as computing the shortest path from the vertex T to 0. The corresponding graph for $T = 5$ can be seen in Figure 8.1.

So, how does this graph formulation help us? Solving the problem on the graph as before using simple recursion would be very slow (with an exponential complexity, even). In Chapter 9 on Dynamic Programming, we will see how to solve such problems in polynomial time. For now, we will settle with solving problems exhibiting yet another property besides having optimal substructure – that of local optimality.

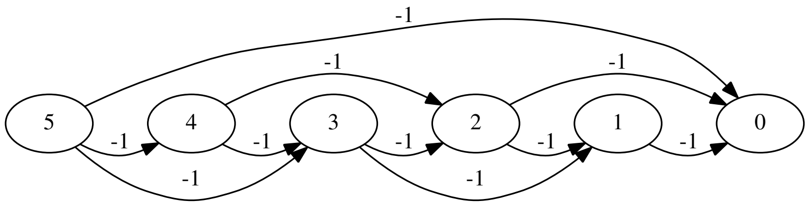


Figure 8.1: The Change-making Problem, formulated as finding the shortest path in a DAG, for $K = 5$.

Exercise 8.1

Compute the shortest path from each vertex in Figure 8.1 to T using the optimal substructure property.

8.2 Locally Optimal Choices

Greedy algorithms solve this kind of problem by making what is called a *locally optimal choice*. We generally construct our shortest path iteratively, one edge at a time. We start out at the first vertex, S, and need to choose an edge to traverse. A greedy algorithm chooses the edge which locally looks like a good choice, without any particular thought about future edges.

For example, consider how you would solve the Change-making Problem yourself. You would probably attempt to add the 5 coin as many times as possible, until you need to add less than 5. This makes sense locally, since 5 is the largest amount we may charge at a time. When we need to add less than 5, we would probably instead add coins worth 2, until we need to add either 0 or 1. In the latter case, we would add a final 1 coin.

Intuitively, this makes sense. Adding the highest amount every time *ought* to be the best possible. For this problem, this is actually true. However, if the denominations were different, this could fail (Exercise 8.2).

Exercise 8.2

Prove that the greedy choice may fail if the coins have denominations $1, 6$ and 7.

Assume that the optimal solution uses the 1, 2 and 5 coins a, b and c times respectively. We then have that either:

$a = 1, b \leq 1$ If $b \geq 2$, we could exchange one 1 coin and two 2 coins for one 5 coin.

$a = 0, b \leq 2$ If $b \geq 3$, we could exchange three 2 coins one 1 coin and one 5 coin.

If $a \geq 2$, we could instead add a single 2 coin instead of two 1 coins.

This means that the possibilities for a and b are few:

- $a = 0, b = 0$: value 0
- $a = 1, b = 0$: value 1
- $a = 0, b = 1$: value 2
- $a = 1, b = 1$: value 3
- $a = 0, b = 2$: value 4

Now, assume that we use exactly c coins of value 5, so that $T = 5c + r$. We know that $0 \leq r < 5$. Otherwise, we would be summing up to an amount larger than 4 without using any 5 coins, but this is impossible based on the above list. This means c must be as large as possible, i.e. it is optimal to add as many 5 coins as possible – which the greedy choice will. Then, only the cases 0, 1, 2, 3 and 4 remain. Looking at the list of those cases, we see that their optimal solutions correspond to how the greedy algorithm works. Thus, the greedy algorithm will always give the optimal answer.

Competitive Tip

If you have the choice between a greedy algorithm and another algorithm (such as one based on brute force or dynamic programming), use the other algorithm unless you are certain the greedy choice works.

Proving the correctness of a locally optimal choice is sometimes very cumbersome. In the remainder of the chapter, we are going to look at a few standard problems that are solvable using a greedy algorithm. Take note of the kind of arguments we are going to use – there are a few common types of proofs which are often used in proofs of greedy algorithms.

8.3 Scheduling

Scheduling problems are a class of problems which deals with constructing large subsets of non-overlapping intervals, from some given set of intervals.

The classical Scheduling Problem is the following.

Scheduling Problem

Given is a set of half-open (being open on the right) intervals S. Determine the largest subset $A \subseteq S$ of non-overlapping intervals.

Input

The input contains the set of intervals S, where $|S|$.

Output

The output should contain the subset A.

We will construct the solution iteratively, adding one interval at a time. When looking for greedy choices to perform, extremal cases are often the first ones you should consider. Hopefully, one of these extremal cases can be proved to be included in an optimal solution. For intervals, some extremal cases would be:

- a shortest interval,
- a longest interval,
- an interval overlapping as few other intervals as possible,
- an interval with the leftmost left endpoint (and symmetrically, the rightmost right endpoint),
- an interval with the leftmost right endpoint (and symmetrically, the rightmost left endpoint).

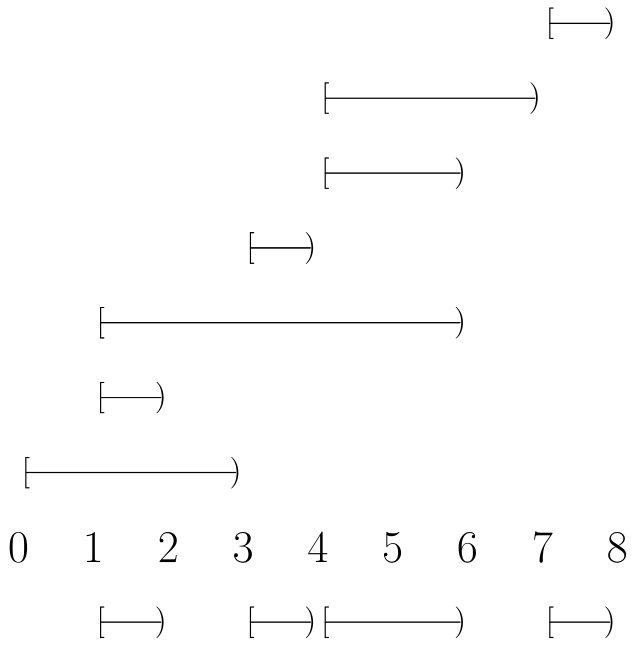


Figure 8.2: An instance of the scheduling problem, with the optimal solution at the bottom.

As it turns out, we can always select an interval satisfying the fifth case. In the example instance in Figure 8.2, this results in four intervals. First, the interval with the leftmost right endpoint is the interval $[1, 2)$. If we include this in the subset A, intervals $[0, 3)$ and $[1, 6)$ must be removed since they overlap $[1, 2)$. Then, the interval $[3, 4)$ would be the one with the leftmost right endpoint of the remaining intervals. This interval overlaps no other interval, so it should obviously be included. Next, we would choose $[4, 6)$ (overlapping with $[4, 7)$), and finally $[7, 8)$. Thus, the answer would be $A = \{[1, 2), [3, 4), [4, 6), [7, 8)\}$.

Algorithm 8.1: Scheduling

```
procedure SCHEDULING(set S)
    ans ← new set
    Sort $S$ by right endpoint
    *highest* $\leftarrow \infty$
    **for** each interval $[l, r) \in S$ **do**
        **if** $l \geq$ *highest* **then**
            *ans*.insert($[l, r)$)
            *highest* $\leftarrow r$
        *Lsums*.insert($\sum_{l \in L} l$)
    **return** *ans*
```

We can prove that this strategy is optimal using a ***swapping argument***, one of the main greedy proof techniques. In a swapping argument, we attempt to prove that given any solution, we can always modify it in such a way that our greedy choice is no worse. This is what we did in the Change-making Problem, where we argued that an optimal solution had to conform to a small set of possibilities, or else we could swap some set of coins for another (such as two coins worth 1 for a single coin worth 2).

Assume that the optimal solution does not contain the interval $[l, r)$, an interval with the leftmost right endpoint. The interval $[l', r')$ that has the leftmost right endpoint *of the intervals in the solution*, must have $r' > r$. In particular, this means any other interval $[a, b)$ in the solution must have $a \geq r'$ (or else the intervals would overlap). However, this means that the interval $[l, r)$ does not overlap any other interval either, since $a \geq r' > r$ so that $a \geq r$. Then, swapping the interval $[l, r)$ for $[l', r')$ still constitute a valid solution, of the same size. This proves that we could have included the interval $[l, r)$ in the optimal solution. Note that the argument in no way say that the interval $[l, r)$ *must* be in an optimal solution. It is possible for a scheduling problem to have many distinct solutions. For example, in the example in Figure 8.2, we might just as well switch $[4, 6)$ for $[4, 7)$ and still get an optimal solution.

This solution can be implemented in $\Theta(|S| \log |S|)$ time. In Algorithm 8.1, this is accomplished by sort performing a sort (in $\Theta(|S| \log |S|)$), followed by a loop for each interval, where each iteration takes $\Theta(1)$ time.

Exercise 8.3

For each of the first four strategies, find a set of intervals where they fail to find an optimal solution.

We can extend the problem to choosing exactly K disjoint subsets of non-overlapping intervals instead, maximizing the sum of their sizes. The solution is similar to the original problem, in that we always wish to include the interval with the leftmost right endpoint in one of the subsets if possible. The question is then, what subset? Intuitively, we wish to choose a subset there the addition of our new interval causes as little damage as possible. This subset is the one with the rightmost right endpoint that we can place the interval in. Proving this is similar to the argument we used when deciding what interval to choose, and is a good exercise to practice the swapping argument.

Exercise 8.4

Prove that choosing to place the interval in the subset with the rightmost right endpoint is optimal.

Exercise 8.5 — Kattis Exercises

Entertainment Box – entertainmentbox

Disastrous Downtime – downtime

8.4 Chapter Notes

Determining whether coins of denominations D can even be used to construct an amount T is an NP-complete problem in the general case[12]. It possible to determine what cases can be solved using the greedy algorithm described in polynomial time though[4]. Such a set of denominations is called a *canonical coin system*.

Introduction to Algorithms[5] also treats the scheduling problem in its chapter in greedy algorithms. It also brings up the connection between greedy problems and a concept known as *matroids*, which is well worth studying.

Chapter 9

Dynamic Programming

This chapter will study a technique called *dynamic programming* (often abbreviated DP). In one sense, it is simply a technique to solve the general case of the best path in a directed acyclic graph problem (Section 8.1) in cases where the graph does not admit locally optimal choices, in time approximately equal to the number of edges in the graph. For graphs which are essentially trees with a unique path to each vertex, dynamic programming is no better than brute force. In more interconnected graphs, where many paths lead to the same vertex, the power of dynamic programming shines through. It can also be seen as a way to speed up recursive functions (called *memoization*), which will be our first application.

First, we will see a familiar example – the Change-making problem, with a different set of denominations. Then, we will discuss a little bit of theory, and finally round of with a few concrete examples and standard problems.

9.1 Best Path in a DAG

We promised a generalization that can find the best path in a DAG that exhibit optimal substructure even when locally optimal choices does not lead to an optimal solution. In fact, we already have such a problem – the Change-making Problem from Section 8.1, but with certain other sets of denominations. Exercise 8.2 even asked you to prove that the case with coins worth 1, 6 and 7 could not be solved in the same greedy fashion.

So, how can we adapt our solution to this case? The secret lies in the graph formulation of the problem which we constructed (Figure 8.1). For the greedy solution, we essentially performed a recursive search on this graph, except we always knew which edge to pick. When we do not know, the solution ought to be obvious – let us test *all* the edges.

Algorithm 9.1: Change-making Problem

```
procedure CHANGEMAKING(denominations D, target T)
    if T = 0 then
        return 0
    $ans \leftarrow \infty$
    for denomination $d \in \{1, 6, 7\}$ do
        if $T \geq d$ then
            $ans = \min(ans, 1 + ChangeMaking(D, T - d)$
    return ans
```

This solution as written is actually exponential in T (it is $\Omega(3^{\frac{T}{7}})$). The recursion tree for the case $T = 10$ can be seen in Figure 9.1.

The key behind the optimal substructure property is that the answer for any particular call in this graph with the same parameter c is the same, independently of the previous calls in the recursion. Right now, we perform calls with the same parameters multiple times. Instead, we can save the result of a call the first time we perform it (Algorithm 9.2).

Algorithm 9.2: Change-making Problem, memoizatoin

```
$memo = $ new $\mathtt{int}[T + 1]$
```

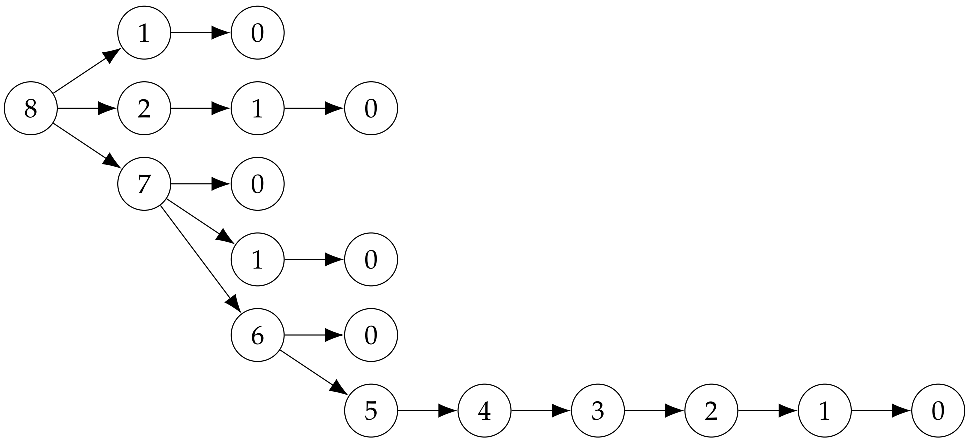


Figure 9.1: The recursion tree for the Change-making problem with $T = 10$.

```
set $memo[i] = -1$ for all $i$
procedure ChangeMaking(denominations $D$, target $T$)
    if $T = 0$ then
        return $0$
    if $memo[T] \neq -1$ then
        return $memo[T]$
    $ans \leftarrow \infty$
    for denomination $d \in D$ do
        if $T \geq d$ then
            $ans = \min(ans, 1 + ChangeMaking(D, T - d))$
    $memo[T] \leftarrow ans$
    return $ans$
```

Theis new algorithm is actually linear in T instead of exponential. The call graph now looks very different (Figure 9.2), since all calls with the same parameter will be merged (as such calls are only evaluated once).

Note the similarity between this graph and our previous DAG formulation of the Change-making problem (Figure 8.1).

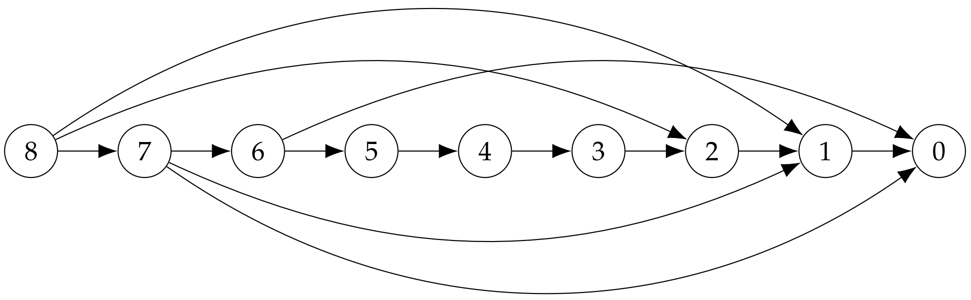


Figure 9.2: The recursion tree for the Change-making problem with $T = 10$, with duplicate calls merged.

9.2 Dynamic Programming

With these examples in hand, we are ready to give a more concrete characterization of dynamic programming. In principle, it can be seen as solving the kind of "sequence of choices" problems that we used bruteforce to solve, but where different choices can result in the same situation. For example, in the Change-making Problem, after adding two coins worth 1 and 6, we might just as well have added a 7 coin instead. After we have performed a sequence of choices, *how* we got to the resulting state is no longer relevant – only where we can go from there. Basically, we throw away the information (what exact coins we used) that is no longer needed. This view of dynamic programming problems as having a "forgetful" property, that the exact choices we have made do not affect the future, is useful in most dynamic programming problems.

Another, more naive view, is that dynamic programming solutions are simple recursions, where we happen to solve the same recursive subproblem a large number of times. In this view, a DP solution is basically nothing more than a recursive solution – find the correct base cases, a fast enough recursion, and memoize the results.

More pragmatically, DP consists of two important parts – the states of the DP, and the computation of a state. Both of these parts are equally important. Fewer states generally mean less computations to make, and a better complexity per state gives a better complexity overall.

9.2.1 Bottom-Up Computation

When applied to a dynamic programming problem, memoization is sometimes called *top-down dynamic programming* instead. The name is inspired from the way we compute the solution to our problem by starting at the largest piece at the top of the recursion tree, and recursively breaking it down to smaller and smaller pieces.

There is an alternative way of implementing a dynamic programming solution, which (not particularly surprisingly) is called *bottom-up dynamic programming*. This method instead constructs the solutions to our sub-problems in the other order, starting with the base case and iteratively computing solutions to larger sub-problems.

For example, we might just as well compute the solution to the Change-making problem the following way:

Algorithm 9.3: Change-making Problem, Bottom-Up

```
procedure ChangeMaking(denominations D, target T)
    $ans = \text{new int}[T + 1]$
    set $ans[i] = \infty$ for all $i$
    set $ans[0] = 0$
    for $i = 1$ to $T$ do
        for denomination $d \in D$ do
            if $i \geq d$ then
                $ans[i] = \min(ans[i], 1 + ans[i - d])$
    return $ans[T]$
```

How do you choose between bottom-up and top-down? Mostly, it comes down to personal choice. A dynamic programming solution will almost always be fast enough no matter if you code it recursively or iteratively. There are some performance concerns, both ways. A recursive solution is affected by the overhead of recursive function calls. This problem is not as bad in C++ as in many other languages, but it is still noticeable. When you notice that the number of states in your DP solution is running a bit high, you might want to consider coding it iteratively. Top-down DP, on the other hand, has the upside that only the states reachable from the starting state will be visited. In some DP solutions, the number of unreachable states which are still in some sense "valid" enough to be computed bottom-up is significant enough that excluding them weighs up for the function call overhead. In extreme cases, it might turn out that an entire parameter is uniquely given by other parameters (such as the Ferry Loading problem in Section 9.3). While we probably would notice when this is the case, the top-down DP saves us when we do not.

9.2.2 Order of Computation and Memory Usage

For top-down DP, the memory usage is often quite clear and unavoidable. If a DP solution has N states, it will have an $\Omega(N)$ memory usage. For a bottom-up solution, the situation is quite different.

Firstly, let us consider one of the downsides of bottom-up DP. When coding a top-down DP, you do not need to bother with the structure of the graph you are solving your problem on. For a bottom-up DP, you need to ensure that whenever you solve a subproblem, you have already solved its subproblems too. This requires you to define an *order of computation*, such that if the subproblem a is used in solving subproblem b, a is computed before b.

In most cases, such an order is quite easy to find. Most parameters can simply be increasing or decreasing, using a nested loop for each parameter. When a DP is done over intervals, the order of computation is often over increasing or decreasing length of the interval. DP over trees usually require a post-order traversal of the tree. In terms of the recurring graph representation we often use for DP problems, the order of computation must be a topological ordering of the graph.

While this order of computation business may seem to be nothing but a nuisance that bottom-up users have to deal with, it is related to one of the perks of bottom-up computation. If the order of computation is chosen in a clever way, we need not save every state during our computation. Consider e.g. the Change-making Problem again, which had the following recursion:

$$\mathrm{change}(n) = \begin{cases} 0 & \text{if } n = 0 \\ \min(\mathrm{change}(n-1), \mathrm{change}(n-6), \mathrm{change}(n-7)) & \text{if } n > 0 \end{cases}$$

It should be clear that using the order of computation $0, 1, 2, 3, \ldots$, once we have computed e.g. $\mathit{change}(k)$, the subproblems $\mathit{change}(k-7), \mathit{change}(k-8), \ldots$ etc. are never used again.

Thus, we only need to save the value of 7 subproblems at a time. This $\Theta(1)$ memory usage is pretty neat compared to the $\Theta(K)$ usage needed to compute $\mathit{change}(K)$ otherwise.

Competitive Tip

Generally, memory limits are very generous nowadays, somewhat diminishing the art of optimizing memory in DP solutions. It can still be a good exercise to think about improving the memory complexity of the solutions we will look at, for the few cases where these limits are still relevant.

9.3 Multidimensional DP

Now, we are going to look at a DP problem where our state consists of more than one variable. The example will demonstrate the importance of carefully choosing your DP parameters.

Ferry Loading

Swedish Olympiad in Informatics 2013, Online Qualifiers

A ferry is to be loaded with cars of different lengths, with a long line of cars currently queued up for a place. The ferry consists of four lanes, each of the same length. When the next car in the line enters the ferry, it picks one of the lanes and parks behind the last car in that line. There must be safety margin of 1 meter between any two parked cars.

Given the length of the ferry and the length of the cars in the queue, compute the maximal amount of cars that can park if they choose the lanes optimally.

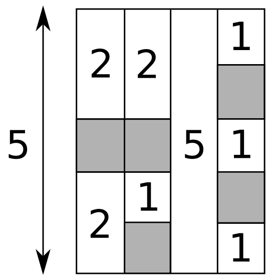


Figure 9.3: An optimal placement on a ferry of length 5 meters, of the cars with lengths 2, 1, 2, 5, 1, 1, 2, 1, 1, 2 meters. Only the first 8 cars could fit on the ferry.

Input

The first line contains the number of cars $0 \leq N \leq 200$ and the length of the ferry $1 \leq L \leq 60$. The second line contains N integers, the length of the cars $1 \leq a_i \leq L$.

Output

Output a single integer – the maximal number of cars that can be loaded on the ferry.

The ferry problem looks like a classical DP problem. It consists of a large number of similar choices. Each car has 4 choices – one of the lanes. If a car of length m chooses a lane, the remaining length of the chosen lane is reduced by $m + 1$ (due to the safety margin). After the first c cars have parked on the ferry, the only thing that has changed are the lengths of the ferry. As a simplification, we increase the initial length of the ferry by 1, to accommodate an imaginary safety margin for the last car in a lane in case it is completely filled.

This suggests a DP solution with nL^4 states, each state representing the number of cars so far placed and the lengths of the four lanes:

Algorithm 9.4: Ferry Loading

```
int dp[201][62][62][62][62] = {-1};

int ferry(int c, vi used, const vi& A) {
  if (c == sz(A)) return 0;
  int& ans = dp[c][left[0]][left[1]][left[2]][left[3]];
  if (ans != -1) return ans;
  rep(i,0,4) {
    if (used[i] + A[i] + 1 > L + 1) continue;
    used[i] += A[i] + 1;
    ans = max(ans, ferry(c + 1, left, A) + 1);
    used[i] -= A[i] + 1;
  }
  return ans;
}
```

Unfortunately, memoizing this procedure would not be sufficient. The size of our memoization array is $200 \cdot 60^4 \approx 2.6 \cdot 10^9$, which needs many gigabytes of memory.

The trick in improving this is basically the same as the fundamental principle of DP. In DP, we reduce a set of choices to a smaller set of information, which represent the effects of those choices. This removes information which turned out to be redundant. In our case, we do not care about what lanes cars chose, only their remaining lengths. Our suggested solution still has some lingering redundancy though.

In Figure 9.3 from the problem statement, we have an example assignment of the cars $2, 1, 2, 5, 1, 1, 2, 1$. These must use a total of $3+2+3+6+2+2+3+2 = 23$ meters of space on the ferry. We define $U(c)$ to be the total usage (i.e., lengths plus the safety margin) of the first c cars. Note that $U(c)$ is a strictly increasing function in c, meaning it is in bijection to $[n]$. Let $u_1(c), u_2(c), u_3(c), u_4(c)$ be the usage of the four lanes individually in some given assignment. Then, we have that $U(c) = u_1(c) + u_2(c) + u_3(c) + u_4(c)$. The four terms on the right are four parameters in our memoization. The left term is not, but it has a bijection with c, which is a parameter in the memoization. Thus, we actually have a redundancy in our parameters. We can eliminate the parameter c, since it is uniquely defined given the values $u_1(c), u_2(c), u_3(c), u_4(c)$. This simplification leaves us with $60^4 \approx 13\,000\,000$ states, which is well within reason.

9.4 Subset DP

Another common theme of DP is subsets, where the state represents a subset of something. The subset DP is used in many different ways. Sometimes (as in Subsection 9.6.3), the problem itself is about sets and subsets. Another common usage is to reduce a solution which requires us to test permutations of something into instead constructing permutations iteratively, using DP to remember only what elements so far used in the permutation, and not the exact assignment.

Amusement Park

Swedish Olympiad in Informatics 2012, Online Qualifiers

Lisa has just arrived at an amusement park, and wants to visit each of the N attractions exactly once. For each attraction, there are two identical facilities at different locations in the park. Given the locations of all the facilities, determine which facility Lisa should choose for each attraction, in order to minimize the total distance she must walk. Originally, Lisa is at the entrance at coordinates $(0, 0)$. Lisa must return to the entrance once she has visited every attraction.

Input

The first line contains the integer $1 \leq N \leq 15$, the number of attractions Lisa wants to visit. Then, N lines follow. The i'th of these lines contains four integers $-10^6 \leq x_1, y_1, x_2, y_2 \leq 10^6$. These are the coordinates (x_1, y_1) and (x_2, y_2) for the two facilities of the i'th attraction.

Output

First, output the smallest distance Lisa must walk. Then, output N lines, one for each attraction. The i'th line should contain two numbers a and f – the i'th attraction Lisa visited (a number between 1 and N), and the facility she visited (1 or 2).

Consider a partial walk, where we have visited a set S of attractions and currently stand at coordinates (x, y). Then, any choice up to this point is irrelevant for the remainder of the problem, which suggests that these parameter S, x, y is a good DP state. Note that (x, y) only have at most 31 possibilities – two for each attraction, plus the entrance at $(0, 0)$. Since we have at most 15 attractions, the set S of visited attractions has 2^{15} possibilities. This gives us $31 \cdot 2^{15} \approx 10^6$ states. Each state can be computed in $\Theta(N)$ time, by choosing what attraction to visit next. All in all, we get a complexity of $\Theta(N^2 2^N)$. When coding DP over subsets, we generally use bitsets to represent the subset, since these map very cleanly to integers (and therefore indices into a vector):

Algorithm 9.5: Amusement Park

```
double best(int at, int visited) {
  // 2N is the number given to the entrance point
  if (visited == (1<<N) - 1) return dist(at, 2*N);
  double ans = inf;
  rep(i,0,N) {
    if (visited&(1<<N)) continue;
    rep(j,0,2) {
      // 2i + j is the number given to the j'th facility
            // of the i'th attraction
      int nat = 2 * i + j;
      ans = min(ans, dist(at + nat) + best(nat, visited | (1<<i)));
    }
  }
  return ans;
}
```

9.5 Digit DP

Digit DP are a class of problems where we count numbers with certain properties that contain a large number of digits, up to a certain limit. These properties are characterized by having the classical properties of DP problems, i.e. being easily computable if we would construct the numbers digit-by-digit by remembering very little information about what those numbers actually were.

Palindrome-Free Numbers

Baltic Olympiad in Informatics 2013 – Antti Laaksonen

A string is a palindrome if it remains the same when it is read backwards. A number is palindrome-free if it does not contain a palindrome with a length greater than 1 as a substring. For example, the number 16276 is palindrome-free whereas the number 17276 is not because it contains the palindrome 727. The number 10102 is not valid either, since it has 010 as a substring (even though 010 is not a number itself).

Your task is to calculate the total number of palindrome-free numbers in a given range.

Input
The input contains two numbers $0 \leq a \leq b \leq 10^{18}$.

Output
Your output should contain one integer: the total number of palindrome-free numbers in the range $a, a+1, ..., b-1, b$ (including a and b).

First, a common simplification when solving counting problems on intervals. Instead of computing the answer for the range $a, a+1, ..., b-1, b$, we will solve the problem for the intervals $[0, a)$ and $[0, b+1)$. The answer is then the answer for the second interval with the answer for the first interval removed. Our lower limit will then be 0 rather than a, which simplifies the solution.

Next up, we need an essential observation to turn the problem into a standard application of digit DP. Palindromes as general objects are very unwieldly in our situation. Any kind of iterative construction of numbers would have to bother with digits far back in the number since any of them could be the edge of a palindrome. Fortunately, it turns out that any palindrome must contain a rather short palindromic subsequence, namely one of length 2 (for even-length palindromes), or length 3 (for odd-length palindromes). This means that when constructing the answer recursively, we only need to care about the last two digits. When adding a digit to a partially constructed number, it may not be equal to either of the last two digits.

Before arriving at the general solution, we will solve the problem when the upper limit was 999...999 – the sequence consisting of n nines. In this case, a simple recursive function will do the trick:

Algorithm 9.6: Palindrome-Free Numbers

```
ll sol(int at, int len, int b1, int b2) {
    if (at == len) return 1; // we have successfully constructed a number
    ll ans = 0;
    rep(d,0,10) {
        // this digit would create a palindrome
        if (d == b2 || d == b1) continue;
        // let -1 represent a leading 0, to avoid the palindrome check
        bool leadingZero = b2 == -1 && d == 0;
        ans += sol(at + 1, len, b2, leadingZero ? -1 : d);
    }
    return ans;
}

// we start with an empty number with leading zeroes
sol(0, n, true, -1, -1);
```

We fix the length of all numbers to have length n, by giving shorter numbers leading zeroes. Since leading zeroes in a number are not subject to the palindrome restriction, they must be treated differently. In our case, they are given the special digit -1 instead, resulting in 11 possible "digits". Once this function is memoized, it will have $n \cdot 2 \cdot 11 \cdot 11$ different states, with each state using a loop iterating only 10 times. Thus, it uses on the order of $1000n$ operations. In our problem, the upper limit has at most 19 digits. Thus, the solution only requires about 20 000 operations.

Once a solution has been formulated for this simple upper limit, extending it to a general upper limit is quite natural. First, we will save the upper limit as a sequence of digits L. Then, we need to differentiate between two cases in our recursive function. The partially constructed number is either equal to the corresponding partial upper limit, or it is less than the limit. In the first case, we are still constrained by the upper limit – the next digit of our number can not exceed the next digit of the upper limit. In the other case, the the upper limit is no longer relevant. If a prefix of our number is strictly lower than the prefix of the upper limit, our number can never exceed the upper limit.

This gives us our final solution:

Algorithm 9.7: Palindrome-Free Numbers, General Case

```
vector<int> L;

ll sol(int at, int len, bool limEq, int b1, int b2) {
    if (at == len) return 1;
    ll ans = 0;
    // we may not exceed the limit for this digit
    // if equal to the prefix of the limit
    rep(d,0,(limEq ? L[at] + 1 : 10)) {
        if (d == b2 || d == b1) continue;
        // the next step will be equal to the prefix if it was now,
        // and our added digit was exactly the limit
        bool limEqNew = limEq && d == L[at];
        bool leadingZero = b2 == -1 && d == 0;
        ans += sol(at + 1, len, limEqNew, b2, leadingZero ? -1 : d);
    }
    return ans;
}

// initially, the number is equal to the
// prefix limit (both being the empty number)
sol(0, n, true, true, -1, -1);
```

9.6 Standard Problems

Many problems are variations of known DP problems, or have them as parts of their solutions. This section will walk you through a few of them.

9.6.1 Knapsack

The knapsack problem is one of the most common standard DP problem. The problem itself has countless variations. We will look at the "original" knapsack problem, with constraints making it suitable for a dynamic programming approach.

Knapsack

Given is a knapsack with an integer capacity C, and n different objects, each with an integer weight and value. Your task is to select a subset of the items with maximal value, such that the sum of their weights does not exceed the capacity of the knapsack.

Input

The integer C giving the capacity of the knapsack, and an integer n, giving the number of objects. This is followed by the n objects, given by their value v_i and weight w_i.

Output

Output the indicies of the chosen items.

We are now going to attempt to formulate an $O(nC)$ solution. As is often the case when the solution is a subset of something in DP solutions, we solve the problem by looking at the subset as a sequence of choices – to either include an item in the answer or not. In this particular problem, our DP state is rather minimalistic. Indeed, after including a few items, we are left only with the remaining items and a smaller knapsack to solve the problem for.

Letting $K(c, i)$ be the maximum value using at most weight c and the i first items, we get the recursion

$$K(c, i) = \max \begin{cases} K(c, i-1) \\ K(c - w_i, i-1) + v_i & \text{if } w_i \leq c \end{cases}$$

Translating this recursion into a bottom-up solution gives a rather compact algorithm (Algorithm 9.8).

Algorithm 9.8: Knapsack

```
procedure KNAPSACK(capacity C, items n, values V, weights W)
    best ← new int[n + 1][C + 1]
    fill best with $-\infty$
    best[0][C] = 0
    for i from 0 to n − 1 do
        for j from 0 to C do
            if $j \geq W[i]$ then
                best[i + 1][j] ← max(best[i][j], best[i][j − W[i]] + V[i])
    return best
```

However, this only helps us compute the answer. The problem asks us to explicitly construct the subset. This step, i.e., tracing what choices we made to arrive at an optimal solution is called *backtracking*.

For this particular problem, the backtracking is relatively simple. One usually proceeds by starting at the optimal state, and then consider all transitions that lead to this state. Among these, the "best" one is picked. In our case, the transitions correspond to either choosing the current item, or not choosing it. Both lead to two other states which are simple to compute. In the first case, the state we arrived from must have the same value and capacity, while in the second case the value should differ by $V[i]$ and the weight by $W[i]$:

Algorithm 9.9: Knapsack Construction

```
procedure KnapsackConstruct(capacity $C$, items $n$, values $V$, weights $W$)
    $best \leftarrow \texttt{Knapsack}(C, n, V, W)$
    $bestCap \leftarrow C$
    for $i$ from $C$ to $0$ do
        if $best[N][i] > best[N][bestCap]$ then
            $bestCap \leftarrow i$
    for $i$ from $N$ to $1$ do
        if $W[i] \leq bestCap$ then
            $newVal \leftarrow best[i-1][bestCap - W[i]]$
            if $newVal = best[i][bestCap] + V[i]$ then
                $ans.\texttt{add}(i)$
                $bestCap \leftarrow bestCap - W[i]$
    output $ans$
```

Exercise 9.1 — Kattis Exercise

Knapsack – knapsack

Walrus Weights – walrusweights

9.6.2 Longest Common Subsequence

Longest Common Subsequence

A sequence $a_1, a_2, ..., a_n$ has $c_1, c_2, ..., c_k$ as a *subsequence* if there exists indices $p_1 < p_2 < ..., < p_k$ such that $a_{p_i} = c_i$. For example, the sequence

$\langle 1, 1, 5, 3, 3, 7, 5 \rangle$, has $\langle 1, 3, 3, 5 \rangle$ as one of its sub-sequences.

Given two sequences $A = \langle a_1, a_2, ..., a_n \rangle$ and $B = \langle b_1, b_2, ..., b_m \rangle$, find the longest sequence $c_1, ..., c_k$ that is a subsequence of both A and B.

When dealing with DP problems on pairs of sequences, a natural subproblem is to solve the problem for all *prefixes* of A and B. For the subsequence problem, some reasoning about what a common subsequence is leads to a recurrence expressed in this way. Basically, we can do a case analysis on the last letter of the strings A and B. If the last letter of A is not part of a longest increasing subsequence, we can simply ignore it, and solve the problem on the two strings where the last letter of A is removed. A similar case is applicable when the last letter of B is not part of a longest increasing subsequence. A single case remains – when both the last letter of A and the last letter of B are part of a longest increasing subsequence. In this case, we argue that these two letters must correspond to the same letter c_i in the common subsequence. In particular, they must correspond to the final character of the subsequence (by the definition of a subsequence). Thus, whenever the two final letters are equal, we may have the case that they are the last letter of the subsequence, and that the remainder of the subsequence is the longest common subsequence of A and B with the final letter removed.

This yields a simple recursive formulation, which takes $\Theta(|A||B|)$ to evaluate (since each state takes $\Theta(1)$ to evaluate).

$$\text{lcs}(A, B, n, m) = \max \begin{cases} 0 & \text{if } n = 0 \text{ or } m = 0 \\ \text{lcs}(A, B, n-1, m) & \text{if } n > 0 \\ \text{lcs}(A, B, n, m-1) & \text{if } m > 0 \\ \text{lcs}(A, B, n-1, m-1) + 1 & \text{if } a_n = b_m \end{cases}$$

9.6.3 Set Cover

Set Cover

You are given a family of subsets $S_1, S_2, ..., S_k$ of some larger set S of size

n. Find a minimum number of subsets $S_{a_1}, S_{a_2}, ..., S_{a_l}$ such that

$$\bigcup_{i=1}^{l} S_{a_i} = S$$

i.e., *cover* the set S by taking the union of as few of the subsets S_i as possible.

For small k and large n, we can solve the problem in $\Theta(n2^k)$, by simply testing each of the 2^k covers. In the case where we have a small n but k can be large, this becomes intractable. Instead, let us apply the principle of dynamic programming. In a brute force approach, we would perform k choices. For each subset, we would try including it or excluding it. After deciding which of the first m subsets to include, what information is relevant? Well, if we consider what the goal of the problem is – covering S – it would make sense to record what elements have been included so far. This little trick leaves us with a DP of $\Theta(k2^n)$ states, one for each subset of S we might have reached, plus counting how many of the subsets we have tried to use so far. Computing a state takes $\Theta(n)$ time, by computing the union of the current cover with the set we might potentially add. The recursion thus looks like:

$$\text{cover}(C, k) = \begin{cases} 0 & \text{if } C = S \\ \min(cover(C, k+1), cover(C \cup S_k, k+1)) & \text{else} \end{cases}$$

This is a fairly standard DP solution. The interesting case occurs when n is small, but k is *really* large, say, $k = \Theta(2^n)$. In this case, our previous complexity $\Theta(nk2^n)$ turns into $\Theta(n4^n)$. Such a complexity is unacceptable for anything but very small n. To avoid this, we must rethink our DP a bit.

The second term of the recursive case of $cover(C, k)$, i.e. $cover(C \cup S_k, k+1)$, actually degenerates to $cover(C, k+1)$ if $S_k \subseteq C$. When k is large, this means many states are essentially useless. In fact, at most n of our k choices will actually result in us adding something, since we can only add a new element at most n times.

We have been in a similar situation before, when solving the backtracking problem *Basin City Surveillance* in Section 7.3. We were plagued with having many choices at each state, where a large number of them would fail. Our solution was to limit our choices to a set where we *knew* an optimal solution would be found.

Applying the same change to our set cover solution, we should instead do DP over our current cover, and only try including sets which are not subsets of the current cover. So, does this help? How many subsets are there, for a given cover C, which are not its subsets? If the size of C is m, there are 2^m subsets of C, meaning $2^n - 2^m$ subsets can add a new element to our cover.

To find out how much time this needs, we will use two facts. First of all, there are $\binom{n}{m}$ subsets of size m of a size n set. Secondly, the sum $\sum_{m=0}^{n} \binom{n}{m} 2^m = 3^m$. If you are not familiar with this notation or this fact, you probably want to take a look at Section 15.4 on binomial coefficients.

So, summing over all possible extending subsets for each possible partial C, we get:

$$\sum_{m=0}^{n} \binom{n}{m} (2^n - 2^m) = 2^n \cdot 2^n - 3^n = 4^n - 3^n$$

Closer, but no cigar. Intuitively, we still have a large number of redundant choices. If our cover contains, say, $n-1$ elements, there are 2^{n-1} sets which can extend our cover, but they all extend it in the same way. This sounds wasteful, and avoiding it probably the key to getting an asymptotic speedup.

It seems that we are missing some key function which, given a set A, can respond to the question: "is there some subset S_i, that could extend our cover with some subset $A \subseteq S$?". If we had such a function, computing all possible extensions of a cover of size m would instead take time 2^{n-m} – the number of possible extensions to the cover. Last time we managed to extend a cover in time $2^n - 2^m$, but this is exponentially better!

In fact, if we do our summing this time, we get:

$$\begin{aligned}\sum_{m=0}^{n} \binom{n}{m} 2^{n-m} &= \sum_{m=0}^{n} \binom{n}{n-m} 2^{n-m} \\ &= \sum_{m=0}^{n} \binom{n}{m} 2^m \\ &= 3^n\end{aligned}$$

It turns out our exponential speedup in extending a cover translated into an exponential speedup of the entire DP.

We are not done yet – this entire algorithm depended on the assumption of our magical "can we extend a cover with a subset A?" function. Sometimes, this function may be quick to compute. For example, if $S = \{1, 2, ..., n\}$ and the family S_i consists of all sets whose sum is less than n, an extension is possible if and only if *its* sum is also less than n. In the general case, our S_i are not this nice. Naively, one might think that in the general case, an answer to this query would take $\Theta(nk)$ time to compute, by checking if A is a subset of each of our k sets. Yet again, the same clever trick comes to the rescue.

If we have a set S_i of size m available for use in our cover. just how many possible extensions could this subset provide? Well, S_i itself only have 2^m subsets. Thus, if we for each S_i mark for each of its subsets that this is a possible extension to a cover, this precomputation only takes 3^n time (by the same sum as above).

Since both steps are $O(3^n)$, this is also our final complexity.

Exercise 9.2 — Kattis Exercises

Square Fields (Easy) – squarefieldseasy

Square Fields (Hard) – squarefieldshard

9.7 Chapter Notes

r notes

Chapter 10

Divide and Conquer

A recursive algorithm solves a problem by reducing it to smaller subproblems, hoping that their solutions can be used to solve the larger problem. So far, the subproblems we have considered have been "almost the same" as the problem at hand. We have usually recursed on a series of choices, where each recursive step made one choice, as in the change-making problem. In particular, our subproblems often overlapped – solving two different subproblems required solving a common, third subproblem. In this chapter, we will take another approach altogether, by splitting our instance into large, disjoint (or almost disjoint parts) parts – dividing it – and combining their solutions – conquering it.

10.1 Inductive Constructions

Inductive construction problems comprise a large class of divide and conquer problems. The goal is often to construct something, such as a tiling of a grid, cycles in a graph and so on. In these cases, divide and conquer algorithms aim to reduce the construction of the whole object to instead constructing smaller parts which can be combined into the final answer. Such constructions are often by-products of mathematical induction proofs of the existence of such a construction. In the following example problems, it is not initially clear that the object we are asked to construct even exists.

Grid Tiling

In a square grid of side length 2^n, one unit square is blocked (represented by coloring it black). Your task is to cover the remaining $4^n - 1$ squares with *triominos*, L-shaped tiles consisting of three squares in the following fashion. The triominos can be rotated by any multiple of $90\,\mathrm{deg}$ (Figure 10.1).

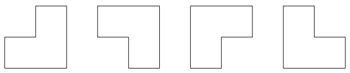


Figure 10.1: The four rotations of a triomino.

The triominos may not overlap each other, nor cover anything outside the grid. A valid tiling for $n = 2$ would be

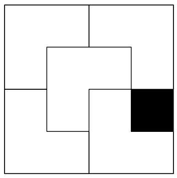


Figure 10.2: A possible tiling for $n = 2$.

Input

The input consists of three integers $1 \leq n \leq 8$, $0 \leq x < 2^n$ and $0 \leq y < 2^n$. The black square has coordinates (x, y).

Output

Output the positions and rotations of any valid tiling of the grid.

When tiling a $2^n \times 2^n$ grid, it is not immediately clear how the divide and conquer principle can be used. To be applicable, we must be able to reduce the problem into smaller instances of the same problem and combine them. The peculiar side length 2^n does hint about a possible solution. Aside from the property that $2^n \cdot 2^n - 1$ is evenly divisible by 3 (a necessary condition for a tiling to be possible), it also gives us a natural way of splitting an instance, namely into its 4 quadrants.

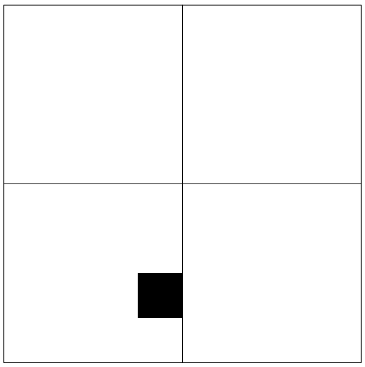


Figure 10.3: Splitting the $n = 3$ case into its four quadrants.

Each of these have the size $2^{n-1} \times 2^{n-1}$, which is also of the form we require of grids in the problem. The crux lies in that these four new grids do not comply with the input specification of the problem. While smaller and disjoint, three of them contain no black square, a requirement of the input. Indeed, a grid of this size without any black squares can not be tiled using triominos.

The solution lies in the trivial solution to the $n = 1$ case, where we can easily reduce the problem to four instances of the $n = 0$ case:

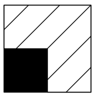


Figure 10.4: A solution to the $n = 1$ case.

In the solution, we use a single triomino which blocked a single square of each of the four quadrants. This gives us four trivial subproblems of size 1×1, where each grid has one blocked square. We can actually place such a triomino in every grid by placing it in the center (the only place where a triomino may cover three quadrants at once).

After this transformation, we can now apply the divide and conquer principle. We split the grid into its four quadrants, each of which now contain one black square. This allows us to recursively solve four new subproblems. At some point, this recursion will finally reach the base case of a 1×1 square, which

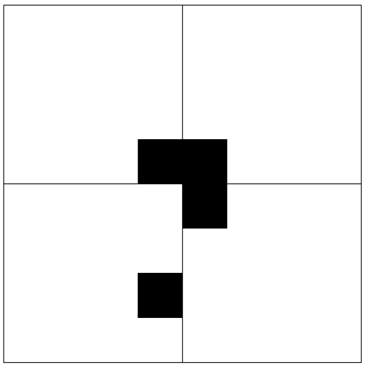


Figure 10.5: Placing a triomino in the corners of the quadrants without a black square.

must already be filled.

Algorithm 10.1: Grid Tiling

```
procedure TILE($N$, $(B_x, B_y)$, $(T_x, T_y)$)
    if $N = 0$ then
        return
    $mid \leftarrow 2^{N-1}$
    $blocked \leftarrow \{(0,0), (\mathrm{mid}-1, 0), (\mathrm{mid}-1, \mathrm{mid}-1), (0, \mathrm{mid}-1)\}$
    if $B_x \geq \mathrm{mid}$ and $B_y \geq \mathrm{mid}$ then
        $blockedQuad \leftarrow$ TOP_RIGHT
    if $B_x < \mathrm{mid}$ and $B_y \geq \mathrm{mid}$ then
        $blockedQuad \leftarrow$ TOP_LEFT
    if $B_x < \mathrm{mid}$ and $B_y < \mathrm{mid}$ then
        $blockedQuad \leftarrow$ BOTTOM_LEFT
    if $B_x \geq \mathrm{mid}$ and $B_y < \mathrm{mid}$ then
        $blockedQuad \leftarrow$ BOTTOM_RIGHT
    place($T_x + \mathrm{mid}, T_y + \mathrm{mid}, \mathrm{blockedQuad}$)
    tile($N - 1, \mathrm{blocked}[0], T_x + mid, T_y + mid$)
    tile($N - 1, \mathrm{blocked}[1], T_x, T_y + mid$)
    tile($N - 1$, blocked[2], $T_x$, $T_y$)
    tile($N - 1$, blocked[3], $T_x + mid$, $T_y$)
```

The time complexity of the algorithm can be computed easily if we use the fact that each call to tile only takes $\Theta(1)$ time except for the four recursive calls. Furthermore, each call places exactly one tile on the board. Since there are $\frac{4^n-1}{3}$ tiles to be placed, the time complexity must be $\Theta(4^n)$. This is asymptotically optimal, since this is also the size of the output.

Exercise 10.1

It is possible to tile such a grid with triominos colored red, blue and green such that no two triominos sharing an edge have the same color. Prove this fact, and give an algorithm to generate such a coloring.

Divisible Subset

Let $n = 2^k$. Given a set A of $2n - 1$ integers, find a subset S of size exactly n such that

$$\sum_{x \in S} x$$

is a multiple of n.

Input

The input contains an integer $1 \le n \le 2^{15}$ that is a power of two, followed by the $2n - 1$ elements of A.

Output

Output the n elements of S.

When given a problem, it is often a good idea to solve a few small cases by hand. This applies especially to this kind of construction problems, where constructions for small inputs often shows some pattern or insight into how to solve larger instances. The case $n = 1$ is not particularly meaningful, since it is trivially true (any integer is a multiple of 1). When $n = 2$, we get an insight which might not seem particularly interesting, but is key to the problem. We are given $2 \cdot 2 - 1 = 3$ numbers, and seek two numbers whose sum is even. Given three numbers, it must have either two numbers which both are even, or two odd numbers. Both of these cases yield a pair with an even sum.

It turns out that this construction generalizes to larger instances. Generally, it is easier to do the "divide" part of a divide and conquer solution first, but in this problem we will do it the other way around. The recursion will follow quite naturally after we attempt to find a way in combining solutions to the smaller instance to a larger one.

We will lay the the ground work for a reduction of the case $2n$ to n. First, assume that we could solve the problem for a given n. The larger instance then contains $2(2n - 1) = 4n - 1$ numbers, of which we seek $2n$ numbers whose sum is a multiple of $2n$. This situation is essentially the same as for the case $n = 2$, except everything is scaled up by n. Can we scale our solution up as well?

If we have three **sets of n numbers** whose respective sums are all **multiples of n**, we can find **two sets of n numbers** whose total sum is **divisible by $2n$**. This construction essentially use the same argument as for $n = 2$. If the three subsets have sums an, bn, cn and we wish to find two whose sum is a multiple of $2n$, this is the same as finding two numbers of a, b, c whose sum is a multiple of 2. This is possible, according to the case $n = 2$.

A beautiful generalization indeed, but we still have some remnants of wishful thinking we need to take care of. The construction assumes that, given $4n - 1$ numbers, we can find three sets of n numbers whose sum are divisible by n. We have now come to the recursive aspect of the problem. By assumption, we could solve the problem for n. This means we can pick any $2n-1$ of our $4n-1$ numbers to get our first subset. The subset uses up n of our $4n - 1$ numbers, leaving us with only $3n - 1$ numbers. We keep going, and pick any $2n - 1$ of these numbers and recursively get a second subset. After this, $2n - 1$ numbers are left, exactly how many we need to construct our third subset.

The division of the problem was thus into *four* parts. Three subsets of n numbers, and one set of $n - 1$ which we throw away. Coming up with such a division essentially required us to solve the combination part first with the generalizing of the case $n = 2$.

Algorithm 10.2: Divisible Subset

```
void fillWith(hashset<int>& toFill, hashset<int>& from, int size) {
  while (sz(from) < size) {
    from.insert(toFill.begin());
    toFill.erase(toFill.begin());
  }
}

hashset<int> divisbleSubset(int k, hashset<int> A) {
  if (k == 1) return nums;

  hashset<int> part;
  // Find three subsets of size k/2 with sums divisible by k/2
  fillWith(part, A, k - 1);
  hashset<int> pa = divisibleSubset(k / 2, A);
  A.erase(all(pa));

  fillWith(part, A, k - 1);
  hashset<int> pb = divisibleSubset(k / 2, A);
  A.erase(all(pb));

  fillWith(part, A, k - 1);
  hashset<int> pc = divisibleSubset(k / 2, A);
  A.erase(all(pc));

  // Choose two who sum to k/2
  int as = accumulate(all(pa), 0);
  int bs = accumulate(all(pa), 0);
  int cs = accumulate(all(pa), 0);

  hashset<int> ans;
  if ((as + bs) % k == 0) {
    ans.insert(all(pa));
    ans.insert(all(pb));
  } else if ((as + cs) % k == 0) {
    ans.insert(all(pa));
    ans.insert(all(pc));
  } else {
    ans.insert(all(pb));
    ans.insert(all(pc));
  }
  return ans;
}
```

This complexity is somewhat more difficult to analyze. Now, each call to divisibleSubset takes linear time to n, and makes 3 recursive calls with $n/2$. Thus, the complexity obeys the recurrence $T(n) = 3T(n/2) + \Theta(n)$. By the master theorem, this has complexity $\Theta(n^{\log_2 3}) \approx \Theta(n^{1.6})$.

Exercise 10.2

What happens if we, when solving the problem for some k, construct $k - 1$ pairs of integers whose sum are even, throw away the remaining element, and scale the problem down by 2 instead? What is the complexity then?

Exercise 10.3

The problem can be solved using a similar divide and conquer algorithm for *any* k, not just those which are powers of two[1]. In this case, those k which are prime numbers can be treated as base cases. How is this done for composite k? What is the complexity?

Exercise 10.4

The knight piece in chess can move in 8 possible ways (moving 2 steps in any one direction, and 1 step in one of the two perpendicular directions). A closed tour exists for an 8×8 grid.

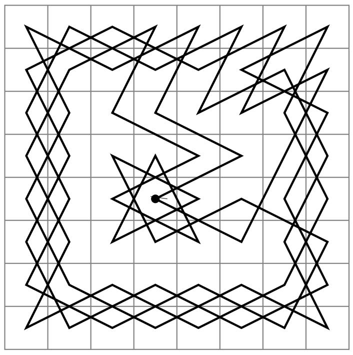


Figure 10.6: A closed tour on an 8×8 grid.

Give an algorithm to construct a tour for any $2^n \times 2^n$ grid with $n \geq 3$.

[1]This result is known as the Erdős–Ginzburg–Ziv theorem

Exercise 10.5

An n-bit *Gray code* is a sequence of all 2^n bit strings of length n, such that two adjacent bit strings differ in only one position. The first and last strings of the sequence are considered adjacent. Possible Gray codes for the first few n are

$$n = 1\text{: } 0\ 1$$

$$n = 2\text{: } 00\ 01\ 11\ 10$$

$$n = 3\text{: } 000\ 010\ 110\ 100\ 101\ 111\ 011\ 001$$

Give an algorithm to construct an n-bit Gray code for any n.

Exercise 10.6 — Kattis Problems

Bell Ringing – bells

Hamiltonian Hypercube – hypercube

10.2 Merge Sort

Merge sort is a sorting algorithm which uses divide and conquer. It is rather straightforward, and works by recursively sorting smaller and smaller parts of the array. When sorting an array by *dividing it into parts* and combining their solution, there is an obvious candidate for how to perform this partitioning. Namely, splitting the array into two halves and sorting them. When splitting an array in half repeatedly, we will eventually reach a rather simple base case. An array containing a single element *is already sorted*, so it is trivially solved. If we do so recursively, we get the recursion tree in Figure 10.7. Coding this recursive split is easy.

When we have sorted the two halves, we need to combine them to get a sorted version of the entire array. The procedure to do this is based on a simple insight. If an array A is partitioned into two smaller arrays P_1 and P_2, the smallest value of A must be either the smallest value of P_1 or the smallest value of P_2. This insight gives rise to a simple iterative procedure, where we repeatedly compare the smallest values of P_1 and P_2, extract the smaller one of them, and append it to our sorted array.

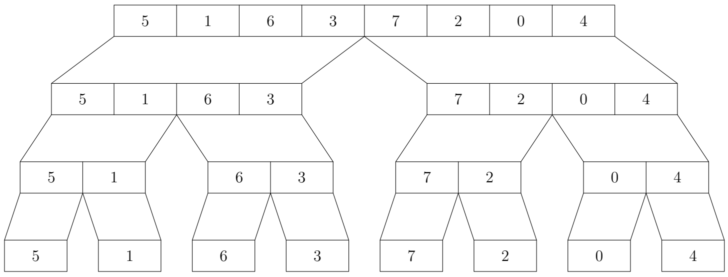


Figure 10.7: The recursion tree given when performing a recursive split of the array $[5, 1, 6, 3, 7, 2, 0, 4]$.

Algorithm 10.3: Merge Sort

```cpp
void sortVector(vector<int>& a, int l, int r){
  int m = (l + r)/2;
  sortVector(a, l, m); // sort left half
  sortVector(a, m, r); // sort right half

  //combine the answers
  vector<int> answer;
  int x = l;
  int y = m;
  while(x < m || y < r){
    if(x == m || (y < r && a[y] < a[x])){
      answer.push_back(a[y]);
      y++;
    } else {
      answer.push_back(a[x]);
      x++;
    }
  }
    for (int i = l; i < r; ++i) {
        a[i] = answer[i - l];
    }
}
```

To compute the complexity, consider the recursion tree in Figure 10.7. We make one call with 8 elements, two calls with 4 elements, and so on. Further, the combining procedure takes $\Theta(l)$ time for a call with l elements. In the general case of $n = 2^k$ elements, this means merge sort takes time

$$\sum_{i=0}^{k} 2^i \cdot \Theta(2^{k-i}) = \Theta(k2^k)$$

Since $k = \log_2 n$, this means the complexity is $\Theta(n \log n)$.

Exercise 10.7

Our complexity analysis assumed that the length of the array is a power of 2. The complexity is the same in the general case. Prove this fact.

Exercise 10.8

Given an array A of size n, we call the pair $i < j$ an *inversion* of A if $A[i] > A[j]$. Adapt the merge sort algorithm to count the number of inversions of an array in $\Theta(n \log n)$.

10.3 Binary Search

The *binary search* is a common component of other solution. Given a number L and a **non-decreasing** function $f : \mathbb{R} \to \mathbb{R}$, we wish to find the greatest x such that $f(x) \leq L$. Additionally, we need two numbers *lo* and *hi*, such that $f(lo) \leq L < f(hi)$.

It is not difficult to see how we solve this problem. Consider the number $mid = \frac{lo+hi}{2}$. If $f(mid) \leq L$, then we know that the answer must lie somewhere in the interval $[mid, hi)$. On the other hand, $L < f(mid)$ gives us a better upper bound on the answer, which must be contained in $[lo, mid)$. Computing $f(mid)$ allowed us to halve the interval in which the answer can be.

We can repeat this step until we get close to x.

Algorithm 10.4: Binary Search

```
const double precision = 1e-7;

```

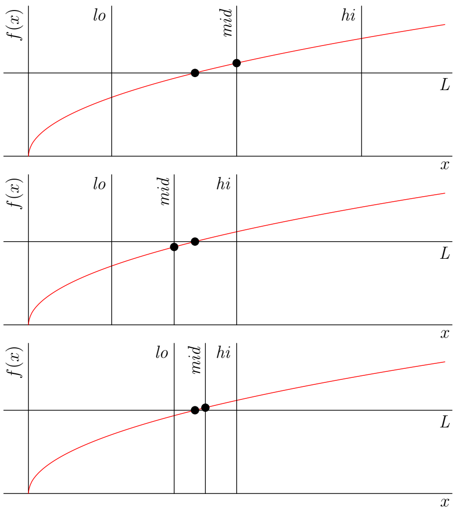


Figure 10.8: Two iterations of binary search.

```
double binarySearch(double lo, double hi, double lim) {
  while (hi - lo > precision) {
    double mid = (lo + hi) / 2;
    if (lim < f(mid)) hi = mid;
    else lo = mid;
  }
  return lo;
}
```

Notice that we are actually computing an approximation of x within some given precision (10^{-7} in the example implementation), but this is often useful enough.

Competitive Tip

Remember that the double-precision floating point type only have a precision of about 10^{15}. If the limits in your binary search are on the order of 10^x, this means that using a binary search precision of something smaller than 10^{x-15} may cause an infinite loop. This happens because the difference between *lo* and the next possible double is actually larger than your precision.

As an example, the following parameters cause our binary search with precision 10^{-7} to fail.

```cpp
double f(double x) {
  return 0;
}

double lo = 1e12;
double hi = nextafter(lo, 1e100);
binarySearch(lo, hi, 0);
```

An alternative when dealing with limit precision is to perform binary search a fixed number of iterations:

```cpp
double binarySearch(double lo, double hi, double lim) {
  rep(i,0,60) {
    double mid = (lo + hi) / 2;
    if (lim < f(mid)) hi = mid;
    else lo = mid;
  }
  return lo;
}
```

The complexity of binary search depends on how good of an approximation we want. Originally, the interval we are searching in has length $hi - lo$. After halving the interval c times, it has size $\frac{hi-lo}{2^c}$. If we binary search until our interval has some size p, this means we must choose c such that

$$\frac{hi - lo}{2^c} \leq p$$

$$\frac{hi - lo}{p2^c} \leq 1$$

$$\frac{hi - lo}{p} \leq 2^c$$

$$\log_2 \frac{hi - lo}{p} \leq c$$

For example, if we have an interval of size 10^9 which we wish to binary search down to 10^{-7}, this would require $\log_2 10^{16} = 54$ iterations of binary search.

Now, let us study some applications of binary search.

10.3.1 Optimization Problems

Cutting Hot Dogs

The finals of the Swedish Olympiad in Informatics is soon to be arranged. During the competition the participants must have a steady supply of hot dogs to get enough energy to solve the problems. Being foodies, the organizing committee couldn't just *buy* ready-to-cook hot dogs – they have to make them on their own!

The organizing committee has prepared N long rods of hot dog. These rods have length $a_1, a_2, ..., a_N$ centimeters. It is now time to cut up these rods into actual hot dogs. A rod can be cut into any number k of hot dogs using $k-1$ cuts. Note that parts of one rod cannot be combined with parts of another rod, due to the difference in taste. It is allowed to leave leftovers from a rod that will not become a hot dog.

In total, the contest has M participants. Each contestant should receive a single hot dog, and all of their hot dogs should be of the same length. What is the maximal hot dog length L the committee can use to cut M hot dogs of length L?

Input

The first line contains two integers $1 \leq N \leq 10\,000$ and $1 \leq M \leq 10^9$.

The next line contains N real numbers $0 < a_1, a_2, ..., \leq 10^6$, the length of the hot dog rods in centimeters.

Output

Output a single real number – the maximal hot dog length possible in centimeters. Any answer with a relative or absolute error of 10^{-6} is acceptable.

This problem is not only an optimization problem, but a *monotone* one. The monotonicity lies in that while we only ask for a certain maximal hot dog length, all lengths below it would also work (in the sense of being able to have M hot dogs cut of this length), while all lengths above the maximal length produce less than M hot dogs. Monotone optimization problems makes it possible to remove the optimization aspect by inverting the problem. Instead of asking ourselves what the maximum length is, we can instead ask how many hot dogs $f(x)$ can be constructed from a given length x. After this inversion, the problem is now on the form which binary search solves: we wish to find the greatest x such that $f(x) = M$ (replacing $\leq$ with $=$ is equivalent in the cases where we know that $f(x)$ assume the value we are looking for). We know that this length is at most $\max_i a_i \leq 10^6$, which gives us the interval $(0, 10^6]$ to search in.

What remains is to actually compute the function $f(x)$. In our case, this can be done by considering just a single rod. If we want to construct hot dogs of length x, we can get at most $\lfloor \frac{a_i}{x} \rfloor$ hot dogs from a rod of length a_i. Summing this for every rod gives us our solution.

Algorithm 10.5: Cutting Hot Dogs

```
procedure CountRods(lengths $A$, minimum length $M$)
    $dogs \leftarrow 0$
    for each $l \in A$ do
        $dogs \leftarrow dogs + \lfloor l/M \rfloor$
    return dogs
procedure HotDogs(lengths $A$, participants $M$)
    $L \leftarrow 0, H \leftarrow 10^6$
    while $H - L \leftarrow 10^{-7}$ do
        $mid \leftarrow (L + H)/2$
        if CountRods$(A, mid) < M$ then
            $H \leftarrow mid$
        else
            $L \leftarrow mid$
    output $L$
```

The key to our problem was that the number of hot dogs constructible with a length x was monotonically decreasing with x. It allowed us to perform binary search on the answer, a powerful technique which is a component of many optimization problems. In general, it is often easier to determine *if* an answer is acceptable, rather than computing a maximal answer.

10.3.2 Searching in a Sorted Array

The classical application of binary search is to find the position of an element x in a sorted array A of length n. Applying binary search to this is straightforward. At first, we know nothing about location of the element – its position could be anyone of $[0, n)$. So, we consider the middle element, $\mathtt{mid} = \lfloor \frac{n}{2} \rfloor$, and compare $A[\mathtt{mid}]$ to x. Since A is sorted, this leaves us with three cases:

- $A[\mathtt{mid}] = x$ – and we are done
- $x < A[\mathtt{mid}]$ – since the array is sorted, any occurrence of x must be to the left of $\mathtt{mid}$
- $A[\mathtt{mid}] < x$ – by the same reasoning, x can only lie to the right of $\mathtt{mid}$.

The last two cases both halve the size of the sub-array which x could be inside. Thus, after doing this halving $\log_2 n$ times, we have either found x or can conclude that it is not present in the array.

Algorithm 10.6: Search in Sorted Array

```
procedure SEARCH(array $A$, target $x$)
    $L \leftarrow 0, H \leftarrow |A|$
    while $H - L > 0$ do
        $mid \leftarrow \lfloor (L + H)/2 \rfloor$
        if $A[mid] = x$ then
            return $mid$
        else if $x < A[mid]$ then
            $H = mid$
        else
            $L = mid + 1$
    return $-1$
```

Competitive Tip

When binary searching over discrete domains, care must be taken. Many bugs have been caused by improper binary searches[2].

The most common class of bugs is related to the endpoints of your interval (i.e. whether they are inclusive or exclusive). Be explicit regarding this, and take care that each part of your binary search (termination condition, midpoint selection, endpoint updates) use the same interval endpoints.

Exercise 10.9 — Kattis Problems

Ballot Boxes – ballotboxes

10.3.3 Generalized Binary Search

Binary search can also be used to find *all* points where a monotone function changes value (or equivalently, all the intervals on which a monotone function is constant). Often, this is used in problems on large sequences (often with $n = 100\,000$ elements), which can be solved by iterating through all contiguous sub-sequences in $\Theta(n^2)$ time.

Or Max

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Given is an array A of integers. Let

$$B(i, k) = A[i] \mid A[i+1] \mid ... \mid A[i+k-1]$$

i.e. the bitwise or of the k consecutive numbers starting with the i'th,

$$M(i, k) = \max\{A[i], A[i+1], ..., A[i+k-1]\}$$

[2]In fact, for many years the binary search in the standard Java run-time had a bug: `http://bugs.java.com/bugdatabase/view_bug.do?bug_id=6412541`

i.e. the maximum of the k consecutive numbers starting with the i'th, and

$$S(i,k) = B(i,k) + M(i,k)$$

For each $1 \le k \le n$, find the maximum of $S(i,k)$.

Input

The first line contains the length $1 \le n \le 10^5$ of A.

The next and last line contains the n values of A ($0 \le A[i] < 2^{16}$), separated by spaces.

Output

Output n integers, the maximum values of $S(i,k)$ for $k = 1, 2, ..., n$.

As an example, consider the array in Figure 10.9. The best answer for $k = 1$ would be $S(0,1)$, with both maximal element and bitwise or 5, totaling 10. For $k = 2$, we have $S(6,2) = 7 + 4 = 11$.

$i=0$	$i=1$	$i=2$	$i=3$	$i=4$	$i=5$	$i=6$	$i=7$	$i=8$	$i=9$
5	1	4	2	2	0	4	3	1	2
101	001	100	010	010	000	100	011	001	010

Figure 10.9: Example array, with the numbers additionally written in binary.

This problem can easily be solved in $\Theta(n^2)$, by computing every $S(i,k)$ iteratively. We can compute all the $B(i,k)$ and $M(i,k)$ using the recursions

$$B(i,k) := \begin{cases} 0 & \text{if } k = 0 \\ B(i,k-1) \mid A[i+k-1] & \text{if } k > 0 \end{cases}$$

$$M(i,k) = \begin{cases} 0 & \text{if } k = 0 \\ \max\{M(i,k-1), A[i+k-1]\} & \text{if } k > 0 \end{cases}$$

by looping over k, once we fix an i. With $n = 100\,000$, this approach is too slow.

The difficulty of the problem lies in $S(i, k)$ consisting of two basically unrelated parts – the maximal element and the bitwise or of a segment. When maximizing sums of unrelated quantities that put constraints on each other, brute force often seems like a good idea. This is basically what we did in the Buying Books problem (Section 7.4), where we minimized the sum of two parts (postage and book costs) which constrained each other (buying a book forced us to pay postage to its store) by brute forcing over one of the parts (the set of stores to buy from). Since the bitwise or is much more complicated than the maximal element – it is decided by an entire interval rather than a single element – we are probably better of doing brute force over the maximal element. Our brute force will consist of fixing which element is our maximal element, by assuming that $A[m]$ is the maximal element.

With this simplification in hand, only the bitwise or remains. We could now solve the problem by looping over all the left endpoints of the interval and all the right endpoints of the interval. At a first glance, this seems to actually worsen the complexity. Indeed, this takes quadratic time for each m (on average), resulting in a cubic complexity.

This is where we use our new technique. It turns out that, once we fix m, there are only a few possible values for the bitwise or of the intervals containing the m'th element, Any such interval $A[l], A[l+1], ..., A[m-1], A[m], A[m+1], ..., A[r-1], A[r]$ can be split into two parts: one to the left, $A[l], A[l+1], ..., A[i-1], A[i]$, and one to the right, $A[i], A[i+1], ..., A[r-1], A[r]$. The bitwise or of either of these two parts is actually a monotone function (in their length), and can only assume at most 16 different values!

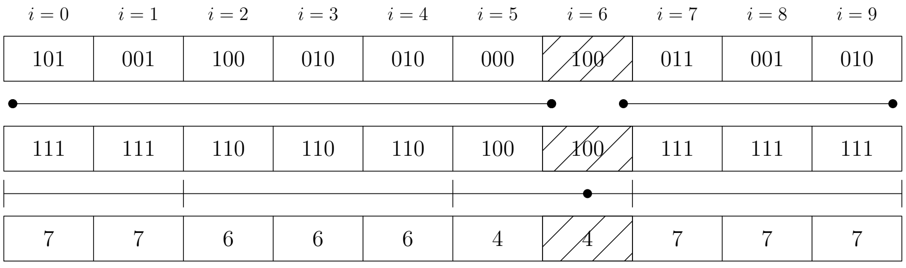

Figure 10.10: The bitwise or of the left and right parts, with an endpoint in $m = 6$

Studying Figure 10.10 gives a hint about why. The first row shows the binary values of the array, with $m = 6$ (our presumed maximal element) marked. The second row shows the binary values of the bitwise or of the interval $[i, m]$ or $[m, i]$ (depending on whether m is the right or left endpoint). The third line shows the decimal values of the second row.

For example, when extending the interval $[2, 6]$ (with bitwise or 110) to the left, the new bitwise or will be $110|001$. This is the only way the bitwise or can change – when the new value includes bits which so far have not been set. Obviously, this can only happen at most 16 times, since the values in A are bounded by 2^{16}.

For a given m, this gives us a partition of all the elements, by the bitwise or of the interval $[m, i]$. In Figure 10.10, the left elements will be partitioned into $[0, 1]$, $[2, 4]$, $[5, 6]$. The right elements will be partitioned into $[6, 6]$, $[7, 9]$. These partitions are everything we need to compute the final.

For example, if we pick the left endpoint from the part $[2, 4]$ and the right endpoint from the part $[7, 9]$, we would get a bitwise or that is $6 \mid 7 = 7$, of a length between 4 and 8, together with the 4 as the presumed maximal element. For each maximal element, we get at most $16 \cdot 16$ such choices, totaling less than $256N$ such choices. From these, we can compute the final answer using a simple sweep line algorithm.

10.4 Karatsuba's algorithm

Karatsuba's algorithm was developed by Russian mathematician Anatoly Karatsuba and published in the early 1960's. It is one of the earliest examples of a divide and conquer algorithm, and is used to quickly multiply large numbers. While multiplying small numbers (i.e. those that fit in the integer types of your favorite programming language) is considered to be a $\Theta(1)$ operation, this is not the case for arbitrarily large integers. We will look at Karatsuba as a way of multiplying polynomials, but this can easily be extended to multiplying integers.

Polynomial Multiplication

Given two n-degree polynomials (where n can be large) $p(x) = \sum_{i=0}^{n} x^i a_i$

and $q(x) = \sum_{i=0}^{n} x^i b_i$ compute their product

$$(pq)(x) = \sum_{i=0}^{2n} x^i (\sum_{j=0}^{i} a_j b_{i-j})$$

The naive multiplication algorithm evaluates this using $\Theta(n^2)$ multiplications (e.g. by two nested loops).

It turns out we can do this faster, using a recursive transformation. If we split the numbers p and q into their upper and lower $k = \frac{n}{2}$ coefficients (if n is odd, we pad the polynomials with a leading zero), so that $p(x) = p_l(x)x^k + p_r(x)$ and $q(x) = q_l(x)x^k + q_r(x)$, their product is equal to

$$\begin{aligned}(pq)(x) &= (p_l(x)x^k + p_r(x))(q_l(x)x^k + q_r(x)) \\ &= p_l(x)q_l(x)x^n + (p_l(x)q_r(x) + p_r(x)q_l(x))x^k + p_r(x)q_r(x)\end{aligned}$$

This formula requires multiplying 4 pairs of k-degree polynomials instead, which we can recursively compute, resulting in the time complexity recurrence $T(n) = 4T(\frac{n}{2}) + \Theta(n)$. Using the master theorem gives us the solution $T(n) = \Theta(n^2)$, which is no faster than the naive multiplication.

However, we can compute $p_l(x)q_r(x) + p_r(x)q_l(x)$ using only one multiplication instead of two. Both of these terms are part of the expansion of pq, which is only one multiplication. That particular multiplication is on n-degree polynomials, but it is not difficult to see how we can reduce it to a single k-degree multiplication. We simply throw away the multiplicative factors that makes $p_l x^k + p_r$ and $q_l x^k + q_r$ an n-degree polynomials:

$$(p_l(x)+p_r(x))(q_l(x)+q_r(x)) = p_l(x)q_l(x)+p_l(x)q_r(x)+p_r(x)q_l(x)+p_r(x)q_r(x)$$

so that

$$p_l(x)q_r(x)+p_r(x)q_l(x) = (p_l(x)+p_r(x))(q_l(x)+p_r(x))-p_l(x)q_l(x)-p_r(x)q_r(x)$$

This means we only need to compute three k-degree multiplications: $(p_l(x) + p_r(x))(q_l(x) + q_r(x)), p_l(x)q_l(x), p_r(x), q_r(x)$ Our time complexity recurrence is then reduced to $T(n) = 3T(\frac{n}{2}) + O(n)$, which by the master theorem is $\Theta(n^{\log_2 3}) \approx \Theta(n^{1.585})$.

Exercise 10.10

Polynomial Multiplication 2 – polymul2

10.5 Chapter Notes

Chapter 11

Data Structures

Solutions to algorithmic problems consists of two constructs – algorithms and ***data structures***. Data structures are used to organize the data that the algorithms operate on. For example, the array is such an algorithm.

Many data structures has been developed to handle particular common operations we need to perform on data quickly. In this chapter, we will study a few such structures.

11.1 Disjoint Sets

In the *Connectivity Problem*, we want to determine whether two vertices in the graph are in the same connected component. This problem can be solved using a Depth-First Search (Section 12.2). For now, we will instead focus on an extension of this problem called the *Dynamic Connectivity Problem, Additions only*[1], where we may also alter the graph by adding edges.

[1]The Dynamic Connectivity problem where edges may also be removed can be solved by a data structured called a *Link-Cut tree*, which is not discussed in this book.

Dynamic Connectivity, Additions Only

Given a graph G which initially consists of V disconnected vertices, you will receive Q queries of two types:

1. take two vertices v and w, and add an edge between them
2. determine whether vertices v and w are currently in the same component

This problem can easily be solved in $O(Q^2)$, by after each query performing a DFS to partition the graph into its connected components. Since the graph has at most Q edges, a DFS takes $O(Q)$ time.

We can improve this by explicitly computing the connected components at each step. Originally, we have V components of a single vertex each. When adding an edge between two vertices that are in different components, these components will now merge. Note that it is irrelevant which vertices we are adding an edge between – it is only important what components the vertices belong to. When merging two connected components to one, we iterate through all the vertices of one component and add them to the other. Since we make at most V joins of different components, and the components involved contain at most V vertices, these queries only take $O(V^2)$ time. Determining whether two vertices are in the same component can then be done in $O(V)$, leaving us with a total complexity of $O(V(V+Q))$. We can speed this up further by using a simple look-up table $\mathrm{comp}[v]$ for the vertices, which stores some identifier for the component a vertex is in. We can then respond to a connectivity query in $\Theta(1)$ by comparing the value of $\mathrm{comp}[v]$ and $\mathrm{comp}[w]$. Our complexity is then $O(V^2+Q)$ instead.

Finally, we will use a common trick to improve the complexity to $O(V\log V + Q)$ instead. Whenever we merge two components of size a and b, we can do this in $O(\min(a,b))$ instead of $O(a+b)$ by merging the smaller component into the larger component. Any individual vertex can be part of the smaller component at most $O(\log V)$ times. Since the total size of a component is always at least twice the size of the smaller component, this means that if a vertex is merged as part of the smaller component k times the new component size must be at least 2^k. This cannot exceed V, meaning $k \leq \log_2 V$. If we sum this up for every vertex, we arrive at the $O(V\log V + Q)$ complexity.

Algorithm 11.1: Disjoint Set

```
struct DisjointSets {

  vector<vector<int>> components;
  vector<int> comp;
  DisjointSets(int elements) : components(elements), comp(elements) {
    iota(all(comp), 0);
    for (int i = 0; i < elements; ++i) components[i].push_back(i);
  }

  void unionSets(int a, int b) {
    a = comp[a]; b = comp[b];
    if (a == b) return;
    if (components[a].size() < components[b].size()) swap(a, b);
    for (int it : components[b]) {
      comp[it] = a;
      components[a].push_back(it);
    }
  }

};
```

A somewhat faster[2] version of this structure instead performs the merges of components lazily. When merging two components, we do not update $comp[v]$ for every vertex in the smaller component. Instead, if a and b are the representative vertices of the smaller and the larger component, we only merge a by setting $comp[a] = b$. However, we still need to perform the merges. Whenever we try to find the component a vertex lies in, we perform all the merges we have stored so far.

Algorithm 11.2: Improved Disjoint Set

```
struct DisjointSets {

  vector<int> comp;
  DisjointSets(int elements) : comp(elements, -1) {}

  void unionSets(int a, int b) {
    a = repr(a); b = repr(b);
    if (a == b) return;
```

[2]With regards to actual time, not asymptotically.

```
    if (-comp[a] < -comp[b]) swap(a, b);
    comp[a] += comp[b];
    comp[b] = a;
  }

  bool is_repr(int x) { return comp[x] < 0; }

  int repr(int x) {
    if (is_repr(x)) return x;
    while (!is_repr(comp[x])) {
      comp[x] = comp[comp[x]];
    }
    return comp[x];
  }

};
```

However, it turns out we can sometimes perform many merges at once. Consider the case where we have k merges lazily stored for some vertex v. Then, we can perform *all* the merges of v, $comp[v]$, $comp[comp[v]]$, $\ldots$ at the same time since they all have the same representative: the representative of v.

Algorithm 11.3: Performing Many Merges

```
int repr(int x) {
  if (comp[x] < 0) return x;
  int par = comp[x];
  comp[x] = repr(par);
  return comp[x];
}
```

Intuitively, this should be faster. After all, we would be performing performing at least $k + (k-1) + (k-2) + \cdots = O(k^2)$ merges in $O(k)$ time, only for those vertices. If there were more vertices part of the components merged, this number grows even more.

It turns out that this change improves the complexity asymptotically.

11.2 Range Queries

Problems often ask us to compute some expression based on some interval of an array. The expressions are usually easy to compute in $\Theta(\mathit{len})$ where *len* is the length of the interval. We will now study some techniques that trade much faster query responses for a bit of memory and precomputation time.

11.2.1 Prefix Precomputation

Interval Sum

Given a sequence of integers $a_0, a_1, \dots, a_{N-1}$, you will be given Q queries of the form $[L, R)$. For each query, compute $S(L, R) = a_L + a_{L+1} + \cdots + a_{R-1}$.

Computing the sums naively would require $\Theta(N)$ worst-case time per query if the intervals are large, for a total complexity of $\Theta(NQ)$. If $Q = \Omega(N)$ we can improve this to $\Theta(N^2 + Q)$ by *precomputing* all the answers. To do this in quadratic time, we use the recurrence

$$S(L,R) = \begin{cases} 0 & \text{if } L = R \\ S(L, R-1) + a_{R-1} & \text{otherwise} \end{cases}$$

Using this recurrence we can compute the sequence $S(L, L), S(L, L+1), S(L, L+2), \dots, S(L, N)$ in average $\Theta(N)$ time for every L. This gives us the $\Theta(N^2 + Q)$ complexity.

If the function we are computing has an inverse, we can speed this precomputation up a bit. Assume that we have computed the values $P(R) = a_0 + a_1 + \cdots + a_{R-1}$, i.e. the prefix sums of a_i. Since this function is invertible (with inverse $-P(R)$), we can compute $S(L, R) = P(R) - P(L)$. Basically, the interval $[L, R)$ consists of the prefix $[0, R)$ with the prefix $[0, L)$ removed. As addition is invertible, we could simply remove the latter prefix $P(L)$ from the prefix $P(R)$ using subtraction. Indeed, expanding this expression shows us that

$$\begin{aligned} P(R) - P(L) &= (a_0 + a_1 + \cdots + a_{R-1}) - (a_0 + a_1 + \cdots + a_{L-1}) \\ &= a_L + \cdots + a_{R-1} = S(L, R) \end{aligned}$$

Algorithm 11.4: Interval Sums

```
procedure PREFIXES(sequence $A$)
    $P \leftarrow new\ int[|A| + 1]$
    for $i = 0$ to $|A| - 1$ do
        $P[i + 1] \leftarrow P[i] + A[i]$
    return $P$
procedure INTERVALSUM(interval $[L, R)$, prefix table $P$)
    return $P[R] - P[L]$
```

This same technique works for any invertible operation.

Exercise 11.1

The above technique does not work straight-off for non-commutative operations. How can it be adapted to this case?

11.2.2 Sparse Tables

The case where a function does not have an inverse is a bit more difficult.

Interval Minimum

Given a sequence of integers $a_0, a_1, \ldots, a_{N-1}$, you will be given Q queries of the form $[L, R)$. For each query, compute the value

$$M(L, R) = \min(a_L, a_{L+1}, \ldots, a_{R-1})$$

Generally, you cannot compute the minimum of an interval based only on a constant number of prefix minimums of a sequence. We need to modify our approach. If we consider the naive approach, where we simply answer the queries by computing it explicitly, by looping over all the $R - L$ numbers in the interval, this is $\Theta(len)$. A simple idea will improve the time used to answer queries by a factor 2 compared to this. If we precompute the minimum of every *pair* of adjacent elements, we cut down the number of elements we need to check in half. We can take it one step further, by using this information to precompute the minimum of all subarrays of four elements, by taking the minimum of two pairs. By repeating this procedure for very power of two, we will end up with a table $m[l][i]$ containing the minimum of the interval $[l, l + 2^i)$, computable in $\Theta(N \log N)$.

Algorithm 11.5: Sparse Table

```
vector<vi> ST(const vi& A) {
  vector<vi> ST(__builtin_popcount(sz(A)), sz(A));
  ST[0] = A;
  rep(len,1,ST.size()) {
    rep(i,0,n - (1 << len) + 1) {
      ST[len][i] = max(ST[len - 1][i], ST[len - 1][i + 1 << (len - 1)]);
    }
  }
  return ST;
}
```

Given this, we can compute the minimum of an entire interval in logarithmic time. Consider the binary expansion of the length $len = 2^{k_1} + 2^{k_2} + \cdots + 2^{k_l}$. This consists of at most $\log_2 len$ terms. However, this means that the intervals

$$[L, L + 2^{k_1})$$
$$[L + 2^{k_1}, L + 2^{k_1} + 2^{k_2})$$
$$\ldots$$
$$[L + 2^{k_1} + \cdots + 2^{k_{l-1}}, L + len)$$

together cover $[L, L + \mathrm{len})$. Thus we can compute the minimum of $[L, L + len)$ as the minimum of $\log_2 len$ intervals.

Algorithm 11.6: Sparse Table Querying

```
int rangeMinimum(const vector<vi>& table, int L, int R) {
  int len = R - L;
  int ans = std::numeric_limits<int>::max();
  for (int i = sz(table) - 1; i >= 0; --i) {
    if (len & (1 << i)) {
      ans = min(ans, table[i][L]);
      L += 1 << i;
    }
    }
    return ans;
  }
```

This is $\Theta((N+Q)\log N)$ time, since the preprocessing uses $\Theta(N \log N)$ time and each query requires $\Theta(\log Q)$ time. This structure is called a *Sparse Table*, or sometimes just the *Range Minimum Query* data structure.

We can improve the query time to $\Theta(1)$ by using that the min operation is idempotent, meaning that $\min(a, a) = a$. Whenever this is the case (and the operation at hand is commutative), we can use just two intervals to cover the entire interval. If 2^k is the largest power of two that is at most $R-L$, then

$$[L, L+2^k)$$

$$[R-2^k, R)$$

covers the entire interval.

```
int rangeMinimum(const vector<vi>& table, int L, int R) {
  int maxLen = 31 - __builtin_clz(b - a);
  return min(jmp[maxLen][L], jmp[maxLen][R - (1 << maxLen)]);
}
```

While most functions either have inverses (so that we can use the prefix precomputation) or has idempotent (so that we can use the $\Theta(1)$ sparse table), some functions do not. In such cases (for example matrix multiplication), we must use the logarithmic querying of the sparse table.

11.2.3 Segment Trees

The most interesting range queries occur on *dynamic* sequences, where values can change.

Dynamic Interval Sum

Given a sequence of integers $a_0, a_1, \ldots, a_{N-1}$, you will be given Q queries. The queries are of two types:

1. Given an interval $[L, R)$, compute $S(L, R) = a_L + a_{L+1} + \cdots + a_{R-1})$.

2. Given an index i and an integer v, set $a_i := v$.

To solve the dynamic interval problem, we will use a similar approach as the general sparse table. Using a sparse table as-is for the dynamic version, we would need to update $\Theta(N)$ intervals, meaning the complexity would be $\Theta(\log N)$ for interval queries and $\Theta(N)$ for updates. It turns out the sparse table as we formulated it contains an unnecessary redundancy.

If we accept using $2 \log N$ intervals to cover each query instead of $\log N$, we can reduce memory usage (and precomputation time!) to $\Theta(N)$ instead of $\Theta(\log N)$. We will use the same decomposition as in merge sort (Section 10.2). In Figure 11.1, you can see this decomposition, with an example of how a certain interval can be covered. In this context, the decomposition is called a *segment tree*.

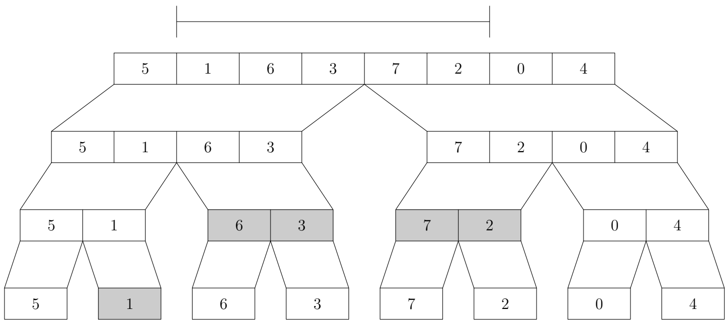

Figure 11.1: The $2N - 1$ intervals to precompute.

Usually, this construction is represented as a flat, 1-indexed array of length $2^{\lceil \log_2 N \rceil}$. The extraneous are set to some sentinel value that does not affect queries (i.e. 0 in the case of sum queries). From this point, we assume N to be a power of two, with the array padded by these sentinel values.

Algorithm 11.7: Segment Tree Construction

```
procedure MakeTree(sequence $A$)
    $tree \leftarrow$ new int[$2|N|$]
    for $i = |N|$ to $2|N| - 1$ do
```

```
        tree[i] ← $A[i - |N|]$
    for $i = |N| - 1$ to 1 do
        tree[i] ← tree[$2 \cdot i$] + tree[$2 \cdot i + 1$]
    return P
```

In the construction, we label each interval $1, 2, 3, \ldots$ in order, meaning the entire interval will have index 1, the two halves indices 2, 3 and so on. This means that the two halves of the interval numbered i will have indices $2i$ and $2i + 1$, which explains the precomputation loop in Algorithm 11.7.

We can compute the sum of each of these intervals in $\Theta(1)$, assuming the sum of all the smaller intervals have already been computed, since each interval is composed by exactly two smaller intervals (except the length 1 leaves). The height of this tree is logarithmic in N.

Note that any particular element of the array is included in $\log N$ intervals – one for each size. This means that updating an element requires only $\log N$ intervals to be updated, which means the update time is $\Theta(\log N)$ instead of $\Theta(N)$ which was the case for sparse tables.

Algorithm 11.8: Segment Tree Update

```
procedure UpdateTree(tree T, index i, value v)
    index ← $i + N$
    tree[index] ← $v$
    while index $\neq 0$ do
        index ← index/2
        tree[index] ← tree[$2 \cdot$ index] + tree[$2 \cdot$ index $+ 1$]
```

It is more difficult to construct an appropriate cover if the interval we are to compute the sum of. A recursive rule can be used. We start at the interval $[0, N)$. One of three cases must now apply:

- We are querying the entire interval $[0, N)$
- We are querying an interval that lies in either $[0, \frac{N}{2})$ or $[\frac{N}{2}, N)$
- We are querying an interval that lies in both $[0, \frac{N}{2})$ or $[\frac{N}{2}, N)$

In the first case, we are done (and respond with the sum of the current interval). In the second case, we perform a recursive call on the half of the interval that the query lies in. In the third case, we make the same recursive construction for both the left and the right interval.

Since there is a possibility we perform two recursive calls, we might think that the worst-case complexity of this query would be $\Theta(N)$ time. However, the calls that the third call results in will have a very specific form – they will always have one endpoint in common with the interval in the tree. In this case, the only time the recursion will branch is to one interval that is entirely contained in the query, and one that is not. The first call will not make any further calls. All in all, this means that there will me at most two branches of logarithmic height, so that queries are $O(\log N)$.

Algorithm 11.9: Segment Tree Query

```
procedure QueryTree(tree $T$, index $i$, query $[L, R)$, tree interval $[L', R')$)
    if $R \leq L'$ or $L > R'$ then
        return $0$
    if $L = L'$ and $R = R'$ then
        return $T[i]$
    $M = (L + R)/2$
    $lsum = \text{QueryTree}(T, 2i, [L, \min(R, M)), [L', M))$
    $rsum = \text{QueryTree}(T, 2i + 1, [\max(L, M), R), [M, R))$
    return $lsum + rsum$
```

11.3 Chapter Notes

Chapter 12

Graph Algorithms

Graph theory is probably the richest of all algorithmic areas. You are almost guaranteed to see at least one graph problem in any given contest, so it is important to be well versed in the common algorithms that operate on graphs. The most important such algorithms concern shortest paths from some vertex, which will also be our first object of study.

12.1 Breadth-First Search

One of the most common basic graph algorithms is the ***breadth-first search***. Its main usage is to find the distances from a certain vertex in an unweighted graph:

Single-Source Shortest Path, Unweighted Edges
Given an unweighted graph $G = (V, E)$ and a source vertex s, compute the shortest distances $d(s, v)$ for all $v \in V$.

For simplicity, we will first consider the problem on a grid graph, where the unit squares constitute vertices, and vertices which share an edge are connected. Additionally, some squares are blocked (and do not contain a vertex). An example can be seen in Figure 12.1.

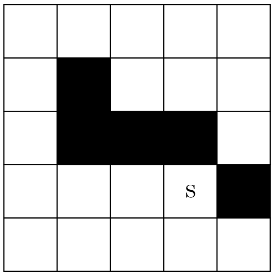

Figure 12.1: An example grid graph, with source marked s.

Let us solve this problem inductively. First of all, what vertices have distance 0? Clearly, this can only be the source vertex s itself. This seems like a reasonable base case, since the problem is about shortest paths from s. Then, what vertices have distance 1? These are exactly those with a path consisting of a single edge from s, meaning they are the neighbors of s (marked in Figure 12.2.

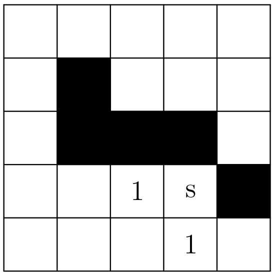

Figure 12.2: The square with distance 1 from the source.

If a vertex v should have distance 2, it must be a neighbor of a vertex u with distance 1 (except for the starting vertex). This is also a sufficient condition, since we can construct a path of length 2 simply by extending the path of any neighbor of distance 1 with the edge (u, v).

In fact, this reasoning generalizes to any particular distance, i.e., that all the vertices that have exactly distance k are those that have a neighbor of distance $k - 1$ but no neighbor to a vertex with a smaller distance. Using this, we can

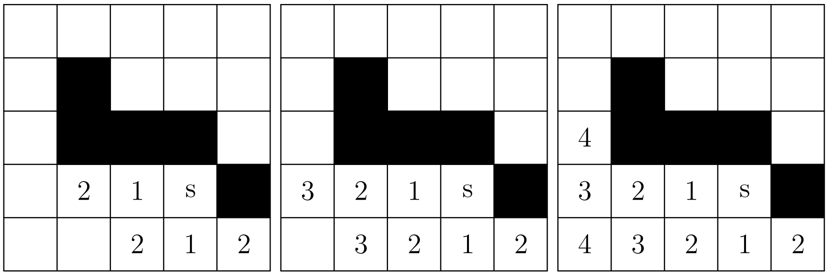

Figure 12.3: The squares with distance 2, 3 and 4.

construct an algorithm to solve the problem. Initially, we set the distance of s to 0. Then, for every $dist = 1, 2, \dots$, we mark all vertices that have a neighbor with distance $dist - 1$ as having $dist$. This algorithm is called the ***breadth-first search***.

Exercise 12.1

Use the BFS algorithm to compute the distance to every square in the following grid:

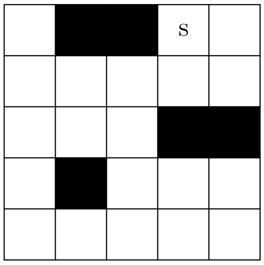

Figure 12.4

We can implement this the following way:

Algorithm 12.1: Breadth-First Search

```
procedure BREADTHFIRSTSEARCH(vertices $V$, vertex $s$)
```

```
    $distances \leftarrow$ new int[|V|]
    fill $distances$ with $\infty$
    $curDist \leftarrow 0$
    $curDistVertices \leftarrow$ new vector
    $curDistVertices.\text{add}(s)$
    $distances[s] = curDist$
    while $curDistVertices \neq \emptyset$ do
        $nCurDist = curDist + 1$
        $nCurDistVertices \leftarrow$ new vector
        for $from \in curDistVertices$ do
            for $v \in from.\text{neighbours}$ do
                if $distances[v] = \infty$ then
                    $nCurDistVertices.\text{add}(v)$
                    $distances[v] = nCurDist$
        $curDist = nCurDist$
        $curDistVertices = nCurDistVertices$
    return $distances$
```

Each vertex is added to *nCurDistVertices* at most once, since it is only pushed if $distances[v] = \infty$ whereupon it is immediately set to something else. We then iterate through every neighbor of all these vertices. In total, the number of all neighbours is $2E$, so the algorithm in total uses $\Theta(V + E)$ time.

Usually, the outer loop are often coded in another way. Instead of maintaining two separate vectors, we can merge them into a single queue:

Algorithm 12.2: Breadth-First Search, Variant

```
while $curDistVertices \neq \emptyset$ do
    $from \leftarrow curDistVertices.\text{front}()$
    $curDistVertices.\text{pop}()$
    for $from \in curDistVertices$ do
        for $v \in from.\text{neighbours}$ do
            if $distances[v] = \infty$ then
                $curDistVertices.\text{add}(v)$
                $distances[v] = distances[from] + 1$
```

The order of iteration is equivalent to the original order.

Exercise 12.2

Prove that the shorter way of coding the BFS loop (Algorithm 12.2) is equivalent to the longer version (Algorithm 12.1).

In many problems the task is to find a shortest path between some pair of vertices where the graph is given *implicitly*:

8-puzzle

In the *8-puzzle*, 8 tiles are arranged in a 3×3 grid, with one square left empty. A move in the puzzle consists of sliding a tile into the empty square. The goal of the puzzle is to perform some moves to reach the target configuration. The target configuration has the empty square in the bottom right corner, with the numbers in order $1, 2, 3$, $4, 5, 6$, $7, 8$ on the three lines.

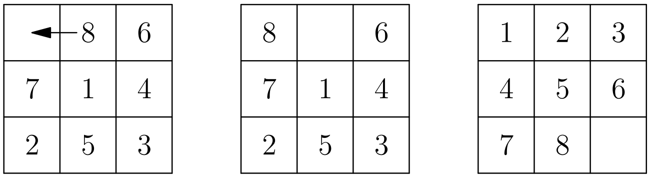

Figure 12.5: An example 8-puzzle, with a valid move. The rightmost puzzle shows the target configuration.

Given a puzzle, determine how many moves are required to solve it, or if it cannot be solved.

This is a typical BFS problem, characterized by a starting state (the initial puzzle), some transitions (the moves we can make), and the task of finding a short sequence of such transitions to some goal state. We can model such problems using a graph. The vertices are then the possible arrangements of the tiles in the grid, and an edge connects two states if the differ by a single move. A sequence of moves from the starting state to the target configuration then represents a path in this graph. The minimum number of moves required is thus the same as the distance between those vertices in the graph, meaning we can use a BFS.

In such a problem, most of the code is usually concerned with the representation of a state as a vertex, and generating the edges that a certain vertex is adjacent to. When an implicit graph is given, we generally do not compute the entire graph explicitly. Instead, we use the states from the problems as-is, and generate the edges of a vertex only when it is being visited in the breadth-first search. In the 8-puzzle, we can represent each state as a 3×3 2D-vector. The difficult part is generating all the states that we can reach from a certain state.

Algorithm 12.3: Generating 8-puzzle Moves

```
typedef vector<vi> Puzzle;

vector<Puzzle> edges(const Puzzle& v) {
  int emptyRow, emptyCol;
  rep(row,0,3)
    rep(col,0,3)
      if (v[row][col] == 0) {
        emptyRow = row;
        emptyCol = col;
      }
  vector<Puzzle> possibleMoves;
  auto makeMove = [&](int rowMove, int colMove) {
    int newRow = row + rowMove;
    int newCol = col + colMove;
    if (newRow >= 0 && newCol >= 0 && newRow < 3 && newCol < 3) {
      Puzzle newPuzzle = v;
      swap(newPuzzle[emptyRow][emptyCol], newPuzzle[newRow][newCol]);
      possibleMoves.spush_back(newPuzzle);
    }
  };
  makeMove(-1, 0);
  makeMove(1, 0);
  makeMove(0, -1);
  makeMove(0, 1);
  return possibleMoves;
}
```

With the edge generation in hand, the rest of the solution is a normal BFS, slightly modified to account for the fact that our vertices are no longer numbered $0, \ldots, V-1$. We can solve this by using e.g. maps instead.

Algorithm 12.4: 8-puzzle BFS

```
int puzzle(const Puzzle& S, const Puzzle& target) {
  map<Puzzle, int> distances;
  distances[S] = 0;
  queue<Puzzle> q;
  q.push(S);
  while (!q.empty()) {
    const Puzzle& cur = q.front(); q.pop();
    int dist = distances[cur];
    if (cur == target) return dist;
    for (const Puzzle& move : edges(cur)) {
      if (distances.find(move) != distances.end()) continue;
      distances[move] = dist + 1;
      q.push(move);
    }
  }
  return -1;
}
```

Exercise 12.3 — Kattis Exercises

Button Bashing – buttonbashing

12.2 Depth-First Search

The depth-first search is an analogue to the breadth-first search that visits vertices in another order. Similarly to how the BFS grows the set of visited vertices using a wide frontier around the source vertex, the depth-first search proceeds its search by, at every step, trying to plunge deeper into the graph. This order is called the depth-first order. More precisely, the search starts at some source vertex s. Then, any neighbor of s is chosen to be the next vertex v. Before visiting any other neighbor of s, we first visit any of the neighbours of v, and so on.

Implementing the depth-first search is usually done with a recursive function, using a vector *seen* to keep track of visited vertices:

Algorithm 12.5: Depth-First Search

```
procedure DEPTH-FIRST SEARCH(vertex $at$, adjacency list G)
    if $seen[at]$ then
        return
    $seen[at] = $ true
    for $neighbour \in G[at]$ do
        dfs($neighbour$, G)
```

In languages with limited stack space, it is possible to implement the DFS iteratively using a stack instead, keeping the vertices which are currently open in it.

Due to the simplicity of coding the DFS compared to a BFS, it is usually the algorithm of choice in problems where we want to visit all the vertices.

Coast Length

KTH Challenge 2011 – Ulf Lundström

The residents of Soteholm value their coast highly and therefore want to maximize its total length. For them to be able to make an informed decision on their position in the issue of global warming, you have to help them find out whether their coastal line will shrink or expand if the sea level rises. From height maps they have figured out what parts of their islands will be covered by water, under the different scenarios described in the latest IPCC report on climate change, but they need your help to calculate the length of the coastal lines.

You will be given a map of Soteholm as an $N \times M$ grid. Each square in the grid has a side length of 1 km and is either water or land. Your goal is to compute the total length of sea coast of all islands. Sea coast is all borders between land and sea, and sea is any water connected to an edge of the map only through water. Two squares are connected if they share an edge. You may assume that the map is surrounded by sea. Lakes and islands in lakes are not contributing to the sea coast.

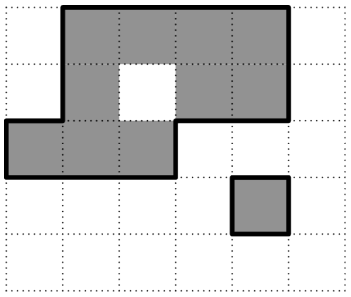

Figure 12.6: Gray squares are land and white squares are water. The thick black line is the sea coast.

We can consider the grid as a graph, where all the water squares are vertices, and two squares have an edge between them if they share an edge. If we surround the entire grid by an water tiles (a useful trick to avoid special cases in this kind of grid problems), the sea consists exactly of those vertices that are connected to these surrounding water tiles. This means we need to compute the vertices which lie in the same connected component as the sea – a typical DFS task[1]. After computing this component, we can determine the coast length by looking at all the squares which belong to the sea. If such a square share an edge with a land tile, that edge contributes 1 km to the coast length.

Algorithm 12.6: Coast Length

```
const vpi moves = {pii(-1, 0), pii(1, 0), pii(0, -1), pii(0, 1)};

int coastLength(const vector<vector<bool>>& G) {
  int H = sz(G) + 4;
    W = sz(G[0]) + 4;
  vector<vector<bool>> G2(H, vector<bool>(W, true));
  rep(i,0,sz(G)) rep(j,0,sz(G[i])) G2[i+2][j+2] = G[i][j];
  vector<vector<bool>> sea(H, vector<bool>(W));

  function<void(int, int)> floodFill = [&](int row, int col) {
    if (row < 0 || row >= H|| col < 0 || col >= W) return;
    if (sea[row][col]) return;
```

[1]This particular application of DFS, i.e. computing a connected area in a 2D grid, is called a *flood fill*.

```
    sea[row][col] = true;
    trav(move, moves) floodFill(row + move.first, col + move.second);
  };
  dfs(0, 0);

  int coast = 0;
  rep(i,1,sz(G)+1) rep(j,1,sz(G[0])+1) {
    if (sea[i][j]) continue;
    trav(move, moves) if (!sea[i + move.first][j + move.second]) coast++;
  }
  return coast;
}
```

Exercise 12.4 — Kattis Exercises

Mårten's DFS – martensdfs

12.3 Weighted Shortest Path

The theory of computing shortest paths in the case of weighted graphs is a bit more rich than the unweighted case. Which algorithm to use depends on three factors:

- The number of vertices.
- Whether edge weights are non-negative or not.
- If we seek shortest paths only from a single vertex or between all pairs of vertices.

There are mainly three algorithms used: *Dijkstra's Algorithm*, the *Bellman-Ford* algorithm, and the *Floyd-Warshall* algorithm.

12.3.1 Dijkstra's Algorithm

Dijkstra's Algorithm can be seen as an extension of the breadth-first search that works for weighted graphs as well.

Single-Source Shortest Path, non-negative weights
Given a weighted graph $G = (V, E)$ where all weights are non-negative and a source vertex s, compute the shortest distances $d(s, v)$ for all $v \in V(G)$.

It has a similar inductive approach, where we iteratively compute the shortest distances to all vertices in ordered by distance. The difference lies in that we do not immediately know when we have found the shortest path to a vertex. For example, the shortest path from a neighbour to the source vertex may now use several other vertices in its shortest path to s (Figure TODO).

image

However, can this be the case for *every* vertex adjacent to s? In particular, can the neighbour to s with the smallest edge weight W to s have a distance smaller than w? This is never the case in Figure TODO, and actually holds in general. Assume that this is not the case. In Figure TODO, this hypothetical scenario is shown. Any such path must still pass through some neighbour u of s. By assumption, the weight of the edge (s, u) must be larger than W (which was the minimal weight of the edges adjacent to s). This reasoning at least allows us to find the shortest distance to one other vertex.

12.3.2 Bellman-Ford

Single-Source Shortest Path, non-negative weights
Given a weighted graph $G = (V, E)$ where all weights are non-negative and a source vertex s, compute the shortest distances $d(s, v)$ for all $v \in V(G)$.

When edges can have negative weights, the idea behind Dijkstra's algorithm no longer works. It is very much possible that a negative weight edge somewhere else in the graph could be used to construct a shorter path to a vertex which was already marked as completed. However, the concept of relaxing an edge is still very much applicable and allows us to construct a slower, inductive solution.

Initially, we know the shortest distances to each vertex, assuming we are allowed to traverse 0 edges from the source. Assuming that we know these values when allowed to traverse up to k edges, can we find the shortest paths that traverse up to $k+1$ edges? This way of thinking is similar to how to solved the BFS problem. Using a BFS, we computed the vertices at distance $d + 1$ by taking the neighbours of the vertices at distance d Similarly, we can find the shortest path to a vertex v that traverse up to $k + 1$ edges, by attempting to extend the shortest paths using k edges from the neighbours of v. Letting $D(k, v)$ be the shorter distance to v by traversing up to k edges, we arrive at the following recursion:

$$D(k, v) = \min \begin{cases} 0 & \text{if } v = s \\ D(k-1, v) & \text{if } k > 0 \\ \min_{e=(u,v)\in E} D(k-1, u) + W(e) & \text{if } k > 0 \end{cases}$$

Algorithm 12.7: Bellman-Ford

```
procedure BellmanFord(vertices $V$, edges $E$, vertex $s$)
    $D \leftarrow$ new int[$|V|$][$|V| + 1$]
    fill $D$ with $\infty$
    $D[0][s] \leftarrow 0$
    for $k = 1$ to $|V|$ do
        $D[k] = D[k-1]$
        for $e = (u, v) \in E$ do
            $D[k][v] = \min(D[k][v], D[k-1][u] + W(e)$
    return $D$
```

All in all, the states $D(v, i)$ for a particular i takes time $\Theta(|E|)$ to evaluate. To compute the distance $d(s, v)$, we still need to know what the maximum possible k needed to arrive at this shortest path could be. It turns out that this could potentially be infinite, in the case where the graph contains a negative-weight cycle. Such a cycle can be exploited to construct arbitrarily short paths.

However, of no such cycle exists, $k = |V|$ will be sufficient. If a shortest path uses more than $|V|$ edges, it must contain a cycle. If this cycle is not of negative weight, we may simply remove it to obtain a path of at most the same length. Thus, the algorithm takes $O\Theta(|V||E|)$.

Exercise 12.5

Bellman-Ford can be adapted to instead use only $\Theta(V)$ memory, by only keeping a current know shortest path and repeatedly relaxing every edge. Sketch out the pseudo code for such an approach, and prove its correctness.

Exercise 12.6

We may terminate Bellman-Ford earlier without loss of correctness, in case $D[k] = D[k-1]$. How can this fact be used to determine whether the graph in question contains a negative-weight cycle?

12.3.3 Floyd-Warshall

All-Pairs Shortest Paths

Given a weighted graph $G = (V, E)$, compute the shortest distance $d(u, v)$ for **every** pair of vertices u, v.

The Floyd-Warshall algorithm is a remarkably short method to solve the all-pairs shortest paths problem. It basically consists of three nested loops containing a single statement:

Algorithm 12.8: Floyd-Warshall

```
procedure FLOYD-WARSHALL(distance matrix D)
    for $k = 0$ to $|V| - 1$ do
        for $i = 0$ to $|V| - 1$ do
            for $j = 0$ to $|V| - 1$ do
```

```
                $D[i][j] = \min(D[i][j], D[i][k] + D[k][j])$
    return $D$
```

Initially, the distance matrix D contains the distances of all the edges in E, so that $D[i][j]$ is the weight of the edge (i, j) if such an edge exists, ∞ if there is no edge between i and j or 0 if $i = j$. Note that if multiple edges exists between i and j, $D[i][j]$ must be given the minimum weight of them all. Additionally, if there is a self-loop (i.e. an edge from i to i itself) of negative weight, $D[i][i]$ must be set to this value.

To see why this approach works, we can use the following invariant proven by induction. After the k'th iteration of the loop, $D[i][j]$ will be at most the minimum distance between i and j that uses vertices $0, 1, \ldots, k-1$. Assume that this is true for a particular k. After the next iteration, there are two cases for $D[i][j]$. Either there is no shorter path using vertex k than those using only vertices $0, 1, \ldots, k-1$. In this case, $D[i][j]$ will fulfill the condition by the induction assumption. If there is a shorter path between i and j if we use the vertex k, this must have length $D[i][k] + D[k][j]$, since $D[i][k]$ and $D[k][j]$ both contain the shortest paths between i and k, and k and j using vertices $0, 1, \ldots, k-1$. Since we set $D[i][j] = \min(D[i][j], D[i][k] + D[k][j])$ in the inner loop, we will surely find this path too in this iteration. Thus, the statement is true after the $k+1$'th iteration too. By induction, it is true for $k = |V|$, meaning $D[i][j]$ contains at most the minimum distance between i and j using any vertex in the graph.

12.4 Minimum Spanning Tree

Using the depth-first search, we were able to find a subtree of a connected graph which spanned the entire set of vertices. A particularly important such spanning tree is the minimum spanning tree.

Minimum Spanning Tree

We say that the weight of a spanning tree is the sum of the weights of its edges. A ***minimum spanning tree*** is a spanning tree whose weight is minimal.

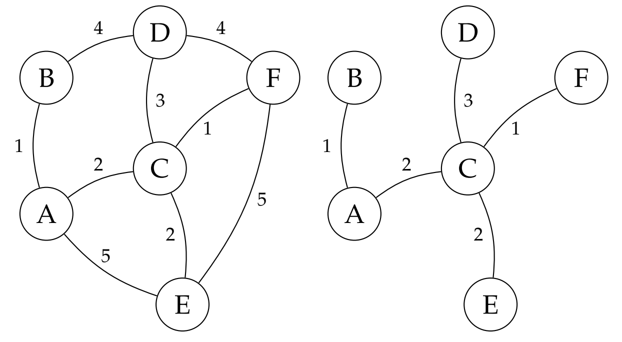

Figure 12.7: A graph with a corresponding minimum spanning tree.

Given a weighted graph, find a minimum spanning tree.

Mainly two algorithms are used to solve the Minimum Spanning Tree (MST) problem: either ***Kruskal's Algorithm*** which is based on the Union-Find data structure, or ***Prim's Algorithm*** which is an extension of Dijkstra's Algorithm. We will demonstrate Kruskal's, since it is by far the most common of the two.

Kruskal's algorithm is based on a greedy, incremental approach that reminds us of the Scheduling problem (Section 8.3). In the Scheduling problem, we tried to find any interval that we could prove to be part of an optimal solution, by considering various extremal cases. Can we do the same thing when finding a minimum spanning tree?

First of all, if we can always find such an edge, we are essentially done. Given an edge (a, b) that we know is part of a minimum spanning tree, we can contract the two vertices a and b to a single vertex ab, with all edges adjacent to the two vertices. Any edges that go between contracted vertices are ignored. An example of this process in action be be seen in Figure 12.8. Note how the contraction of an edge reduces the problem to finding an MST in a smaller graph.

A natural extremal case to consider is the edge with the minimum weight. After all, we are trying to minimize the edge sum. Our proof is similar in structure to the Scheduling problem as well by using a swapping argument.

Assume that a minimum-weight edge $\{a, b\}$ with weight w is not part of any

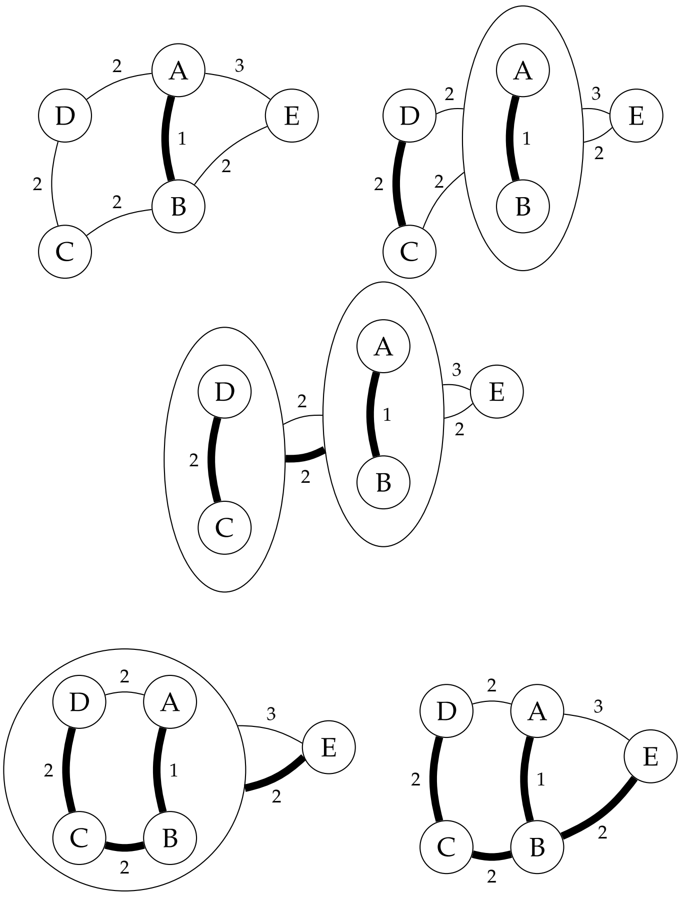

Figure 12.8: Incrementally constructing a minimum spanning tree by merging

minimum spanning tree. Then, consider the spanning tree with this edge appended. The graph will then contain exactly one cycle. In a cycle, any edge can be removed while maintaining connectivity. This means that if any edge $\{c, d\}$ on this cycle have a weight w' larger weight than w, we can erase it. We will thus have replaced the edge $\{c, d\}$ by $\{a, d\}$, while changing the weight of the tree by $w - w' < 0$, reducing the sum of weights. Thus, the tree was improved by using the minimum-weight edge, proving that it could have been part of the tree.

Exercise 12.7

What happens if all edges on the cycle that appears have weight w? Is this a problem for the proof?

When implementing the algorithm, the contraction of the edge added to the minimum spanning tree is generally not performed explicitly. Instead, a disjoint set data structure is used to keep track of which subsets of vertices have been contracted. Then, all the original edges are iterated through in increasing order of weight. An edge is added to the spanning tree if and only if the two endpoints of the edge are not already connected (as in Figure 12.8).

Algorithm 12.9: Minimum Spanning Tree

```
procedure MinimumSpanningTree(vertices $V$, edges $E$)
    sort $E$ by increasing weight
    $uf \leftarrow$ new DisjointSet($V$)
    $mst \leftarrow$ new Graph
    for each edge $\{a, b\} \in E$ do
        if not $uf$.sameSet($a, b$) then
            $mst$.append($a, b$)
            $uf$.join($a, b$)
    return $mst$
```

The complexity of this algorithm is dominated by the sorting (which is $O(E \log V)$), since operations on the disjoint set structure is $O(\log V)$.

12.5 Chapter Notes

Chapter 13

Maximum Flows

This chapter studies so called *flow networks*, and algorithms we use to solve the so-called *maximum flow* and *minimum cut* problems on such networks. Flow problems are common algorithmic problems, particularly in ICPC competitions (while they are out-of-scope for IOI contests). They are often hidden behind statements which seem unrelated to graphs and flows, especially the *minimum cut* problem.

Finally, we will end with a specialization of maximum flow on the case of bipartite graphs (called *bipartite matching*).

13.1 Flow Networks

Informally, a flow network is a directed graph that models any kind of network where paths have a fixed capacity, or throughput. For example, in a road network, each road might have a limited throughput, proportional to the number of lanes on the road. A computer network may have different speeds along different connections due to e.g. the type of material. These natural models are often use when describing a problem that is related to flows. A more formal definition is the following.

Definition 13.1 — Flow Network
A ***flow network*** is a special kind of **directed** graph (V, E, c), where each edge e is given a non-negative ***capacity*** $c(e)$. Two vertices are designated the ***source*** and the ***sink***, which we will often abbreviate to S and T.

In Figure 13.1, you can see an example of a flow network.

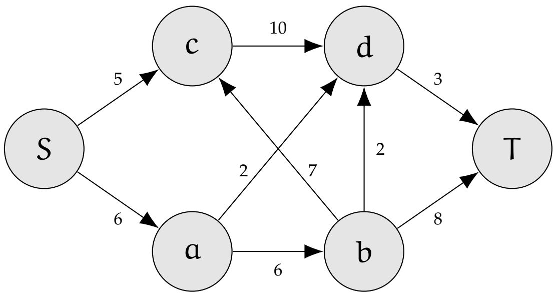

Figure 13.1: An example flow network.

In such a network, we can assign another value to each edge, that models the current throughput (which generally does not need to match the capacity). These values are what we call flows.

Definition 13.2 — Flow
A ***flow*** is a function $f : E \to \mathbb{R}_{\geq 0}$, associated with a particular flow network (V, E, c). We call a flow f ***admissible*** if:

- $0 \leq f(e) \leq c(e)$ – the flow does not exceed the capacity
- For every $v \in V \{S, T\}$, $\sum_{e \in \mathtt{in}(v)} f(e) = \sum_{e \in \mathtt{out}(v)}$ – flow is conserved for each vertex, possibly except the source and sink.

The ***size*** of a flow is defined to be the value

$$\sum_{v \in \mathrm{out}(S)} f(v) - \sum_{v \in \mathrm{in}(S)} f(v)$$

In a computer network, the flows could e.g. represent the current rate of transfer through each connection.

Exercise 13.1

Prove that the size of a given flow also equals

$$\sum_{v \in \text{in}(T)} f(v) - \sum_{v \in \text{out}(T)} f(v)$$

i.e. the excess flow out from S must be equal to the excess flow in to T.

In Figure 13.2, flows have been added to the network from Figure 13.1.

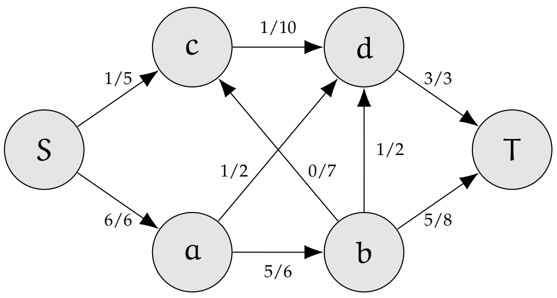

Figure 13.2: An example flow network, where each edge has an assigned flow. The size of the flow is 8.

Given such a flow, we are generally interested in determining the flow of the largest size. This is what we call the *maximum flow* problem. The problem is not only interesting on its own. Many problems which we study might initially seem unrelated to maximum flow, but will turn out to be reducible to finding a maximum flow.

Maximum Flow

Given a flow network (V, E, c, S, T), construct a maximum flow from S to T.

Input

A flow network.

Output

Output the maximal size of a flow, and the flow assigned to each edge in one such flow.

Exercise 13.2

The flow of the network in Figure 13.2 is not maximal – there is a flow of size 9. Find such a flow.

Before we study problems and applications of maximum flow, we will first discuss algorithms to solve the problem. We can actually solve the problem greedily, using a rather difficult insight, that is hard to prove but essentially gives us the algorithm we will use. It is probably one of the more complex standard algorithms that is in common use.

13.2 Edmonds-Karp

There are plenty of algorithms which solve the maximum flow problem. Most of these are too complicated to be implemented to be practical. We are going to study two very similar classical algorithms that computes a maximum flow. We will start with proving the correctness of the *Ford-Fulkerson* algorithm. Afterwards, a modification known as *Edmonds-Karp* will be analyzed (and found to have a better worst-case complexity).

13.2.1 Augmenting Paths

For each edge, we define a *residual flow* $r(e)$ on the edge, to be $c(e) - f(e)$. The residual flow represents the additional amount of flow we may push along an edge.

In Ford-Fulkerson, we associate every edge e with an additional *back edge* $b(e)$ which points in the reverse order. Each back edge is originally given a flow and capacity 0. If e has a certain flow f, we assign the flow of the back-edge $b(e)$ to be $-f$ (i.e. $f(b(e)) = -f(e)$. Since the back-edge $b(e)$ of e has capacity 0, their residual capacity is $r(b(e)) = c(b(e)) - f(b(e)) = 0 - (-f(e)) = f(e)$.

Intuitively, the residual flow represents the amount of flow we can add to a certain edge. Having a back-edge thus represents "undoing" flows we have added to a normal edge, since increasing the flow along a back-edge will decrease the flow of its associated edge.

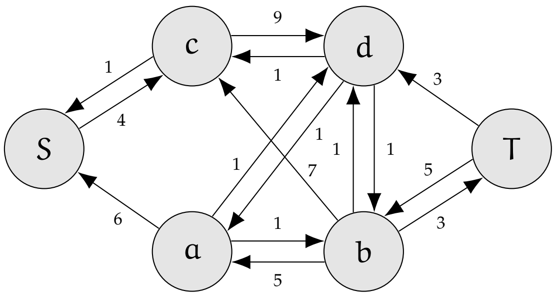

Figure 13.3: The residual flows from the network in Figure 13.2.

The basis of the Ford-Fulkerson family of algorithms is the *augmenting path*. An augmenting path is a path from S to T in the network consisting of edges $e_1, e_2, ..., e_l$, such that $r(e_i) > 0$, i.e. every edge along the path has a residual flow. Letting m be the minimum residual flow among all edges on the path, we can increase the flow of every such edge with m.

In Figure 13.3, the path S, c, d, b, T is an augmenting path, with minimum residual flow 1. This means we can increase the flow by 1 in the network, by:

- Increasing the flow from S to c by 1
- Increasing the flow from c to d by 1
- Decreasing the flow from b to d by 1 (since (d, b) is a back-edge, augmenting the flow along this edge represents removing flow from the original edge)
- Increasing the flow form d to T

The algorithm for augmenting a flow using an augmenting path is implemented in pseudo code on Algorithm 13.1.

Algorithm 13.1: Augmenting a Flow

```
procedure AUGMENT(path P)
    $inc \leftarrow \infty$
    for $e \in P$ do
        $inc \leftarrow \min(inc, c(e) - f(e))$
    for $e \in P$ do
        $f(e) \leftarrow f(e) + inc$
        $f(b(e)) \leftarrow f(b(e)) - inc$
    return $inc$
```

Performing this kind of augmentation on an admissible flow will keep the flow admissible. A path must have either zero or two edges adjacent to any vertex (aside from the source and sink). One of these will be an incoming edge, and one an outgoing edge. Increasing the flow of these edges by the same amount conserves the equality of flows between in-edges and out-edges, meaning the flow is still admissible.

This means that a flow can be maximum only if it contains no augmenting paths. It turns out this is also a necessary condition, i.e. a flow is maximum if it contains no augmenting path. Thus, we can solve the maximum flow problem by repeatedly finding augmenting paths, until no more exists.

13.2.2 Finding Augmenting Paths

The most basic algorithms based on augmenting paths is the *Ford-Fulkerson* algorithm. It uses a simple DFS to find the augmenting paths. For integer flows, where the maximum flow has size m Ford-Fulkerson may require up to $O(Em)$ time. In the worst case, a DFS takes $\Theta(E)$ time to find a path from S to T, and one augmenting path may contribute only a single unit of flow. For non-integral flows, there are instances where Ford-Fulkerson may not even terminate (nor converge to the maximum flow).

Algorithm 13.2: Finding an Augmenting Path by DFS

```
procedure AUGMENTINGPATH(flow network $(V, E, c, f, S, T)$)
    $\text{bool}[]\ seen \leftarrow new\ \text{bool}[|V|]$
```

```
        Stack stack ← new Stack
        found ← DFS(S, T, f, c, seen, stack)
        if found then
            return stack
        return Nil
    procedure DFS(vertex at, sink T, flow f, capacity c, path p)
        p.push(at)
        if at = T then
            return true
        for every out-edge e = (at, v) from at do
            if f(e) < c(e) then
                if DFS(v, T, f, c, p) then
                    return true
        p.pop()
        return false
```

An improvement to this approach is simply to use a BFS instead. This is what is called the *Edmonds-Karp* algorithm. The BFS looks similar to the Ford-Fulkerson DFS, and is modified in the same way (i.e. only traversing those edges where the flow $f(e)$ is smaller than the capacity $c(e)$. The resulting complexity is instead $O(VE^2)$ (which is tight in the worst case).

13.3 Applications of Flows

We will now study a number of problems which are reducible to finding a maximum flow in a network. Some of these problems are themselves considered to be standard problems.

Maximum-Flow with Vertex Capacities

In a flow network, each vertex v additionally have a limit C_v on the amount of flow that can go through it, i.e.

$$\sum_{e \in in(v)} f(e) \leq C_v$$

Find the maximum flow subject to this additional constraint.

This is nearly the standard maximum flow problem, with the addition of vertex capacities. We are still going to use the normal algorithms for maximum flow. Instead, we will make some minor modifications to the network. The additional constraint given is similar to the constraint placed on an edge. An edge has a certain amount of flow passing through it, implying that the same amount must enter and exit the edge. For this reason, it seems like a reasonable approach to reduce the vertex capacity constraint to an ordinary edge capacity, by forcing all the flow that passes through a vertex v with capacity C_v through a particular edge.

If we partition all the edges adjacent to v into incoming and outgoing edges, it becomes clear how to do this. We can split up v into two vertices v_{in} and v_{out}, where all the incoming edges to v are now incoming edges to v_{in} and the outgoing edges instead become outgoing edges from v_{out}. If we then add an edge of infinite capacity from v_{in} to v_{out}, we claim that the maximum flow of the network does not change. All the flow that passes through this vertex must now pass through this edge between v_{in} and v_{out}. This construction thus accomplish our goal of forcing the vertex flow through a particular edge. We can now enforce the vertex capacity by changing the capacity of this edge to C_v.

Maximum Bipartite Matching

Given a bipartite graph, a ***bipartite matching*** is a subset of edges in the graph, such that no two edges share an endpoint. Determine the matching containing the maximum number of edges.

The maximum bipartite matching problem is probably the most common reduction to maximum flow in use. Some standard problems additionally reduce to bipartite matching, making maximum flow even more important. Although there are others ways of solving maximum bipartite matching than a reduction to flow, this is what how we are going to solve it.

How can we find such a reduction? In general, we try to find some kind of graph structure in the problem, and model what it "means" for an edge to have flow pushed through it. In the bipartite matching problem, we are already given a graph. We also have a target we wish to maximize – the size of the matching – and an action that is already associated with edges – including it in the matching. It does not seem unreasonable that this is how we wish to model the flow, i.e. that we want to construct a network based on this graph where pushing flow along one of the edges means that we include the edge in the matching. No two selected edges may share an endpoint, which brings only a minor complication. After all, this condition is equivalent to each of the vertices in the graph having a vertex capacity of 1. We already know how to enforce vertex capacities from the previous problem, where we split each such vertex into two, one for in-edges and one for out-edges. Then, we added an edge between them with the required capacity. After performing this modification on the given graph, we are still missing one important part of a flow network. The network does not yet have a source and sink. Since we want flow to go along the edges, from one of the parts to another part of the graph, we should place the source at one side of the graph and the sink at the other, connecting the source to all vertices on one side and all the vertices on the other side to the sink.

Minimum Path Cover

In a directed, acyclic graph, find a minimum set of vertex-disjoint paths that includes every vertex.

This is a difficult problem to derive a flow reduction to. It is reduced to bipartite matching in a rather unnatural way. First of all, a common technique must be used to get introduce a bipartite structure into the graph. For each vertex, we split it into two vertices, one in-vertex and one out-vertex. Note that this graph still have the same minimum path covers as the original graph.

Now, consider any path cover of this new graph, where we ignore the added edges. Each vertex is then adjacent to at most a single edge, since paths are vertex-disjoint. Additionally, the number of paths are equal to the number of in-edges that does not lie on any path in the cover (since these vertices are the origins of the paths). Thus, we wish to select a maximum subset of the original edges. Since the subgraph containing only these edges is now bipartite, the problem reduces to bipartite matching.

Exercise 13.3

The minimum path cover reduction can be modified slightly to find a *minimum cycle cover* in a directed graph instead. Construct such a reduction.

13.4 Chapter Notes

The Edmonds-Karp algorithm was originally published in 1970 by Yefim Dinitz. The paper by Edmonds and Karp

paper

Chapter 14

Strings

In computing, much of the information we process is text. Therefore, it should not come as a surprise that many common algorithms and problems focus concerns text strings. In this chapter, we will study some of the common string algorithms and data structures.

14.1 Tries

The *trie* (also called a *prefix tree*) is the most common string-related data structure. It represents a set of words as a rooted tree, where every prefix of every word is a vertex, with children from a prefix P to all strings Pc which are also prefixes of a word. If two words have a common prefix, the prefix only appears once as a vertex. The root of the tree is the empty prefix. The trie is very useful when we want to associate some information with prefixes of strings and quickly get the information from neighboring strings.

The most basic operation of the trie is the insertion of strings, which may be implemented as follows.

Algorithm 14.1: Trie

```
struct Trie {
  map<char, Trie> children;
  bool isWord = false;

  void insert(const string& s, int pos) {
    if (pos != sz(s)) children[s[pos]].insert(s, pos + 1);
    else isWord = true;
  }

};
```

We mark those vertices which corresponds to the inserted word using a boolean flag `isWord`. Many problems essentially can be solved by very simple usage of a trie, such as the following IOI problem.

Type Printer

International Olympiad in Informatics 2008

You need to print N words on a movable type printer. Movable type printers are those old printers that require you to place small metal pieces (each containing a letter) in order to form words. A piece of paper is then pressed against them to print the word. The printer you have allows you to do any of the following operations:

- Add a letter to the end of the word currently in the printer.
- Remove the last letter from the end of the word currently in the printer. You are only allowed to do this if there is at least one letter currently in the printer.
- Print the word currently in the printer.

Initially, the printer is empty; it contains no metal pieces with letters. At the end of printing, you are allowed to leave some letters in the printer. Also, you are allowed to print the words in any order you like. As every operation requires time, you want to minimize the total number of operations.

Your task is to output a sequence of operations that prints all the words using the minimum number of operations needed.

Input

The first line contains the number of words $1 \leq N \leq 25\,000$. The next N lines contain the words to be printed, one per line. Each word is at most 20 letters long and consist only of lower case letters `a`-`z`. All words will be distinct

Output

Output a sequence of operations that prints all the words. The operations should be given in order, one per line, starting with the first. Adding a letter `c` is represented by outputting `c` on a line. Removing the last letter of the current word is represented by a `-`. Printing the current word is done by outputting `P`.

Let us start by solving a variation of the problem, where we are not allowed to leave letters in the printer at the end. First of all, are there actions that never make sense? For example, what sequences of letters will ever appear in the type writer during an optimal sequence of operations? Clearly we never wish to input a sequence that is not a prefix of a word we wish to type. For example, if we input $abcdef$ and this is not a prefix of any word, we must at some point erase the last letter f, without having printed any words. But then we can erase the entire sequence of operations between inputting the f and erasing the f, without changing what words we print.

On the other hand, every prefix of a word we wish to print must at some point appear on the type writer. Otherwise, we would not be able to reach the word we wish to print. Therefore, the partial words to ever appear on the type printer are exactly the prefixes of the words we wish to print – strongly hinting at a trie-based solution.

If we build the trie of all words we wish to print, it contains as vertices exactly those strings which will appear as partial words on the printer. Furthermore, the additions and removals of letters form a sequence of vertices that are connected by edges in this trie. We can move either from a prefix P to a prefix Pc, or from a prefix Pc to a prefix P, which are exactly the edges of a trie. The goal is then to construct the shortest possible tour starting at the root of the trie and passing through all the vertices of the trie.

Since a trie is a tree, any such trail must pass through every edge of the trie at least twice. If we only passed through an edge once, we can never get back to the root since every edge disconnects the root from the endpoint of the edge further away from the root. It is actually possible to construct a trail which passes through every edge exactly twice (which is not particularly difficult if you attempt this task by hand). As it happens, the depth-first search of a tree passes through an edge exactly twice – once when first traversing the edge to an unvisited vertex, and once when backtracking.

The problem is subtly different once we are allowed to leave some letters in the printer at the end. Clearly, the only difference between an optimal sequence when letters may remain and an optimal sequence when we must leave the printer empty is that we are allowed to skip some trailing removal operations. If the last word we print is S, the difference will be exactly $|S|$ "-" operations. An optimal solution will therefore print the longest word last, in order to "win" as many "-" operations as possible. We would like this last word to be the longest word *of all the ones we print* if possible. In fact, we can order our DFS such that this is possible. First of all, our DFS starts from the root and the longest word is $s_1 s_2 \dots s_n$. When selecting which order the DFS should visit the children of the root in, we can select the child s_1 last. Thus, all words starting with the letter s_1 will be printed last. When visiting s_1, we use the same trick and visit the child $s_1 s_2$ last of the children of s_1, and so on. This guarantees S to be the last word to be printed.

Note that the solution requires no additional data to be stored in the trie – the only modification to our basic trie is the DFS.

Algorithm 14.2: Typewriter

```
struct Trie {
  ...

  void dfs(int depth, const string& longest) {
    trav(it, children)
      if (it->first != longest[depth])
        dfs2(depth, longest, it->first);
    dfs2(depth, longest, longest[depth]);
  }

  void dfs2(int depth, const string& longest, char output) {
    cout << output << endl;
    if (isWord) cout << "P" << endl;
    children[output]->dfs(depth + 1, longest);
    if (longest[depth] != output) {
        cout << "-" << endl;
      }
    }
  };
```

Generally, the uses of tries are not this simple, where we only need to construct the trie and fetch the answer through a simple traversal. We often need to augment tries with additional information about the prefixes we insert. This is when tries start to become really powerful. The next problem requires only a small augmentation of a trie, to solve a problem which looks complex.

Rareville

In Rareville, everyone must have a distinct name. When a new-born baby is to be given a name, its parents must first visit *NAME*, the Naming Authority under the Ministry of Epithets, to have its name approved. The authority has a long list of all names assigned to the citizens of Rareville. When deciding whether to approve a name or not, a case officer uses the following procedure. They start at the first name in the list, and read the first letter of it. If this letter matches the first letter of the proposed name, they proceed to read the next letter in the word. This is repeated for every letter of the name *in the list*. After reading a letter from the word, the case officer can sometime determine that this could not possibly be the same name as the proposed one. This happens if either

- the next letter in the proposed name did not match the name in the list
- there was no next letter in the proposed name
- there was no next letter in the name in the list

When this happen, the case officer starts over with the next name in the list, until exhausting all names in the list. For each letter the case officer reads (or attempts to read) from a name in the list, one second pass.

Currently, there are N people in line waiting to apply for a name. Can you determine how long time the decision process will take for each person?

Input

The first line contains integers $1 \leq D \leq 200\,000$ and $1 \leq N \leq 200\,000$, the size of the dictionary and the number of people waiting in line. The next D lines contains one lowercase name each, the contents of the dictionary. The next N lines contains one lowercase name each, the names the people in line wish to apply with. The total size of the lists is at most 10^6 letters.

Output

For each of the N names, output the time (in seconds) the case officer needs to decide on the application.

The problem clearly relates to prefixes in some way. Given a dictionary word A and an application for a name B, the case officer needs to read letters from A corresponding to the longest common prefix of A and B, plus 1. Hence, our solution will probably be to consider all the prefixes of each proposed name, which is exactly what tries are good at.

Instead of thinking about this process one name a time, we use a common trie technique and look at the transpose of this problem, i.e. for every i, how many names C_i have a longest common prefix of length *at least* i when handling the application for a name S? This way, we have transformed the problem from being about D individual processes to $|S|$ smaller problems which treats the dictionary as unified group of strings. Then, we will have to read $C_0 + C_1 + \cdots + C_{|S|}$ letters.

Now, the solution should be clear. We augment the trie vertex for a particular prefix p with the number of strings P_p in the list that start with this prefix. Initially, an empty trie has $P_p = 0$ for every p. Whenever we insert a new word $W = w_1 w_2 \ldots$ in the trie, we need to increment $P_{w_1}, P_{w_1 w_2}, \ldots$, to keep all the P_p correct, since we have added a new string which have those prefixes. Then, we have that $C_i = P_{s_1 s_2 \ldots s_i}$, so that we can compute all the numbers P_i by following the word S in the trie. The construction of the trie is linear in the number of characters we insert, and responding to a query is linear in the length of the proposed name.

Algorithm 14.3: Rareville

```
struct Trie {
  map<char, Trie> children;
  int P = 0;
  void insert(const string& s, int pos) {
    P++;
    if (pos != sz(s)) children[s[pos]].insert(s, pos + 1);
  }

  int query(const string& s, int pos) {
    int ans = P;
    if (pos != sz(s)) {
      auto it = children.find(s[pos]);
      if (it != children.end) ans += it->second.query(s, pos + 1);
    }
    return ans;
  }
};
```

14.2 String Matching

A common problem on strings – both in problem solving and real life – is that of searching. Not only do we need to check whether e.g. a set of strings contain some particular string, but also if one string contain another one as a substring. This operation is ubiquitous; operating systems allow us to search the contents of our files, and our text editors, web browsers and email clients all support substring searching in documents. It should come as no surprise that string matching is part of many string problems.

String Matching

Find all occurrences of the pattern P as a substring in the string W.

We can solve this problem naively in $O(|W| \cdot |P|)$. If we assume that an occurrence of P starts at position i in W, we can compare the substring $W[i...i+|P|-1]$ to P in $O(|P|)$ time by looping through both strings, one character at a time.

Algorithm 14.4: Naive String Matching

```
procedure StringMatching(pattern $P$, string $W$)
    $answer \leftarrow$ new vector
    for outer: $i$ from $0$ to $|W| - |P|$ do
        for $j$ from $0$ to $|P| - 1$ do
            if $P[j]! = W[i + j]$ then
                start next iteration of outer
        $answer.\text{append}(i)$
    return answer
```

Intuitively, we should be able to do better. With the naive matching, our problem is basically that we can perform long stretches of partial matches for every position. Searching for the string $a^{\frac{n}{2}}$ in the string a^n takes $O(n^2)$ time, since each of the $\frac{n}{2}$ positions where the pattern can appear requires us to look ahead for $\frac{n}{2}$ characters to realize we made a match. On the other hand, if we manage to find a long partial match of length l starting at i, we *know* what the next l letters of W are – they are the l first letters of P. With some cleverness, we should be able to exploit this fact, hopefully avoiding the need to scan them again when we attempt to find a match starting at $i + 1$.

For example, assume we have $P = bananarama$. Then, if we have performed a partial match of $banana$ at some position i in W but the next character is a mismatch (i.e., it is not an r), we know that no match can begin at the next 5 characters. Since we have matched $banana$ at i, we have that $W[i+1...i+5] = anana$, which does not contain a b.

As a more interesting example, take $P = abbaabborre$. This pattern has the property that the partial match of $abbaabb$ actually contains as a prefix of P itself as a suffix, namely abb. This means that if at some position i get this partial match but the next character is a mismatch, we can not immediately skip the next 6 characters. It is possible that the entire string could have been $abbaabbaabborre$. Then, an actual match (starting at the fifth character) overlaps our partial match. It seems that if we find a partial match of length 7 (i.e. $abbaabb$), we can only skip the first 4 characters of the partial match.

For every possible partial match of the pattern P, how many characters are we able to skip if we fail a k-length partial match? If we could precompute such a table, we should be able to perform matching in linear time, since we would only have to investigate every character of W once. Assume the next possible match is l letters forward. Then the new partial match must consist of the last

$k - l$ letters of the partial match, i.e. $P[l \dots k-1]$. But a partial match is just a prefix of P, so we must have $P[l \dots k-1] = P[0 \dots l-1]$. In other word, for every given k, we must find the longest suffix of $P[0 \dots K-1]$ that is also a prefix of P (besides $P[0 \dots k-1]$ itself, of course).

We can compute these suffixes rather easily in $O(n^2)$. For each possible position for the next possible match l, we perform a string matching to find all occurrences of prefixes of P within P.

Algorithm 14.5: Longest Suffix Computation

```
procedure LongestSuffixes(pattern P)
    T ← new int[|P| + 1]
    for l from 1 to |P| − 1 do
        matchLen ← 0
        while l + matchLen ≤ |W| do
            if P[l]! = P[matchLen] then
                break
            matchLen ← matchLen + 1
            T[l + matchLen] = matchLen
    return T
```

A string such as $P = \mathtt{bananarama}$, where no partial match could possibly contain a new potential match, this table would simply be:

P	b	a	n	a	n	a	r	a	m	a
T	0	0	0	0	0	0	0	0	0	0

When $P = \mathtt{abbaabborre}$, the table instead becomes:

P	a	b	b	a	a	b	b	o	r	r	e
T	0	0	0	1	1	2	3	0	0	0	0

With this precomputation, we can now perform matching in linear time. The matching is similar to the naive matching, except we can now use this precomputed table to determine whether there is a new possible match somewhere within the partial match.

Algorithm 14.6: String Matching using Longest Suffixes

```
procedure StringMatching(pattern P, text $W$)
    $matches \leftarrow$ new vector
    $T \leftarrow$ LongestSuffixes$(P)$
    $pos \leftarrow 0, match \leftarrow 0$
    while $pos + match < |W|$ do
        if $match < |P|$ and $W[pos + match] = P[match]$ then
            $match \leftarrow match + 1$
        else if $match = 0$ then
            $pos \leftarrow pos + 1$
        else
            $pos \leftarrow pos + match - T[match]$
            $match \leftarrow T[match]$
        if $match = |P|$ then
            $matches.\text{append}(match)$
    return $matches$
```

In each iteration of the loop, we see that either *match* is increased by one, or *match* is decreased by $match - T[match]$ and *pos* is increased by the same amount. Since *match* is bounded by P and *pos* is bounded by $|W|$, this can happen at most $|W| + |P|$ times. Each iteration takes constant time, meaning our matching is $\Theta(|W| + |P|)$ time.

While this is certainly better than the naive string matching, it is not particularly helpful when $|P| = \Theta(|W|)$ since we need an $O(|P|)$ preprocessing. The solution lies in how we computed the table of suffix matches, or rather, the fact that it is entirely based on string matching itself. We just learned how to use this table to perform string matching in linear time. Maybe we can use this table to extend itself and get the precomputation down to $O(|P|)$? After all, we are looking for occurrences of prefixes of P in P itself, which is exactly what string matching does. If we modify the string matching algorithm for this purpose, we get what we need:

Algorithm 14.7: Improved Longest Suffix Computation

```
procedure LongestSuffixes(pattern P)
    $T \leftarrow$ new int$[|P| + 1]$
    $pos \leftarrow 1, match \leftarrow 0$
    while $pos + match < |P|$ do
```

```
            if $P[pos + match] = P[match]$ then
                $T[pos + match] \leftarrow match + 1$
                $match \leftarrow match + 1$
            else if $match = 0$ then
                $pos \leftarrow pos + 1$
            else
                $pos \leftarrow pos + match - T[match]$
                $match \leftarrow T[match]$
            if $match = |P|$ then
                $matches.\text{append}(match)$
    return $T$
```

Using the same analysis as for the improved string matching, this precomputation is instead $\Theta(|P|)$. The resulting string matching then takes $\Theta(|P| + |W|)$.

This string matching algorithm is called the ***Knuth-Morris-Pratt*** (KMP) algorithm.

Competitive Tip

Most programming languages have functions to find occurrences of a certain string in another. However, they mostly use the naive $O(|W||P|)$ procedure. Be aware of this and code your own string matching if you need it to perform in linear time.

14.3 Hashing

Hashing is a concept most familiar from the hash table data structure. The idea behind the structure is to compress a set S of elements from a large set to a smaller set, in order to quickly determine memberships of S by having a direct indexing of the smaller set into an array (which has $\Theta(1)$ look-ups). In this section, we are going to look at hashing in a different light, as a way of speeding up comparisons of data. When comparing two pieces of data a and b of size n for equality, we need to use $\Theta(n)$ time in the worst case since every bit of data must be compared. This is fine if we perform only a single comparison. If we instead wish to compare many pieces of data, this becomes an unnecessary bottleneck. We can use the same kind of hashing as with hash tables, by defining a "random" function $H(x) : S \to \mathbb{Z}_n$ such that $x \neq y$ implies $H(x) \neq H(y)$ with high probability. Such a function allows us to perform comparisons in $\Theta(1)$ time (with linear preprocessing), by reducing the comparison of arbitrary data to small integers (we often choose n to be on the order of 2^{32} or 2^{64} to get constant-time comparisons). The trade-off lies in correctness, which is compromised in the unfortunate event that we perform a comparison $H(x) = H(y)$ even though $x \neq y$.

FriendBook

Swedish Olympiad in Informatics 2011, Finals

FriendBook is a web site where you can chat with your friends. For a long time, they have used a simple "friend system" where each user has a list of which other users are their "friends". Recently, a somewhat controversial feature was added, namely a list of your "enemies". While the friend relation will always be mutual (two users must confirm that they wish to be friends), enmity is sometimes one-way – a person A can have an enemy B, who – by plain animosity – refuse to accept A as an enemy.

Being a poet, you have lately been pondering the following quote.

A friend is someone who dislike the same people as yourself.

Given a FriendBook network, you wonder to what extent this quote applies. More specifically, for how many pairs of users is it the case that they are either friends with identical enemy lists, or are not friends and does not have identical enemy lists?

Input

The first line contains an integer $2 \leq N \leq 5000$, the number of friends on FriendBook. N lines follow, each containing n characters. The c'th character on the r'th line S_{rc} species what relation person r has to person c. This character is either

`V` – in case they are friends.

`F` – if r thinks of c as an enemy.

`.` – r has a neutral attitude towards c.

S_{ii} is always `.`, and S_{ij} is `V` if and only if S_{ji} is `V`.

Output

Output a single integer, the number of pairs of persons for which the quote holds.

This problem lends itself very well to hashing. It is clear that the problem is about comparisons – indeed, we are to count the number of pairs of persons who are either friends and have equal enemy lists or are not friends and have unequal enemy lists. The first step is to extract the enemy lists E_i for each person i. This will be a N-length string, where the j'th character is `F` if person j is an enemy of person i, and `.` otherwise. Basically, we remove all the friendships from the input matrix. Performing naive comparisons on these strings would only give us a $O(N^3)$ time bound, since we need to perform N^2 comparisons of enemy lists of length N bounded only by $O(N)$ in the worst case. Here, hashing comes to our aid. By instead computing $h_i = H(E_i)$ for every i, comparisons of enemy lists instead become comparisons of the integers h_i – a $\Theta(1)$ operation – thereby reducing the complexity to $\Theta(N^2)$.

Alternative solutions exist. For example, we could instead have sorted all the enemy lists, after which we can perform a partitioning of the lists by equality in $\Theta(N^2)$ time. However, this takes $O(N^2 \log N)$ time with naive sorting (or $O(N^2)$ if radix sort is used, but it is more complex) and is definitely more complicated to code than the hashing approach. Another option is to insert all the strings into a trie, simplifying this partitioning and avoiding the sorting altogether. This is better, but still more complex. While it would have the same complexity, the constant factor would be significantly worse compared to the hashing approach.

This is a common theme among string problems. While most string problems can be solved without hashes, solutions using them tend to be simpler.

The true power of string hashing is not this basic preprocessing step where we can only compare two strings. Another hashing technique allows us to compare arbitrary substring of a string in constant time.

Definition 14.1 — Polynomial Hash

Let $S = s_1 s_2 \dots s_n$ be a string. The *polynomial hash* $H(S)$ of S is the number

$$H(S) = (s_1 p^{n-1} + s_2 p^{n-2} + \dots + s_{n-1} p + s_n) \bmod M$$

As usual when dealing with strings in arithmetic expressions, we take s_i to be some numeric representation of the character, like its ASCII encoding. In C++, `char` is actually a numeric type and is thus usable as a number when using polynomial hashes.

Polynomial hashes have many useful properties.

Theorem 14.1 — Properties of the Polynomial Hash
If $S = s_1 \dots s_n$ is a string and c is a single character, we have that

1. $H(S||c) = (pH(S) + H(c)) \bmod M$
2. $H(c||S) = (H(S) + H(c)p^n) \bmod M$
3. $H(s_2 \dots s_n) = (H(S) - H(s_1)p^{n-1}) \bmod M$
4. $H(s_1 \dots s_{n-1}) = (H(S) - H(s_n))p^{-1} \bmod M$
5. $H(s_l s_{l+1} \dots s_{r-2} s_{r-1}) = (H(s_1 \dots s_{R-1}) - H(s_1 - S_{L-1})p^{R-L}) \bmod M$

Exercise 14.1

Prove the properties of Theorem 14.1

Exercise 14.2

How can we compute the hash of $S||T$ in $O(1)$ given the hashes of the strings S and T?

Properties 1-4 alone allow us to append and remove characters from the beginning and end of a hash in constant time. We refer to this property as polynomial hashes being *rolling*. This property allows us to String Matching problem with a single pattern (Section 14.2) with the same complexity as KMP, by computing the hash of the pattern P and then rolling a $|P|$-length hash through the string we are searching in. This algorithm is called the ***Rabin-Karp*** algorithm.

Property 5 allows us to compute the hash of any substring of a string in constant time, provided we have computed the hashes $H(S_1), H(s_1s_2), \dots, H(s_1s_2\dots s_n)$ first. Naively this computation would be $\Theta(n^2)$, but property 1 allows us to compute them recursively, resulting in $\Theta(n)$ precomputation.

Radio Transmission

Baltic Olympiad in Informatics 2009

Given is a string S. Find the shortest string L, such that S is a substring of the infinite string $T = \dots LLLLL \dots$.

Input

The first and only line of the input contains the string S, with $1 \le |S| \le 10^6$.

Output

Output the string L. If there are multiple strings L of the shortest length, you can output any of them.

Assume that L has a particular length l. Then, since T is periodic with length l, S must be too (since it is a substring of T). Conversely, if S is periodic with some length l, can can choose as $L = s_1s_2\dots s_l$. Thus, we are actually seeking the smallest l such that S is periodic with length l. The constraints this puts on S are simple. We must have that

$$s_1 = s_{l+1} = s_{2l+1} = \dots$$

$$s_2 = s_{l+2} = s_{2l+2} = \dots$$

$$\dots$$

$$s_l = s_{2l} = s_{3l} = \dots$$

Using this insight as-is gives us a $O(|S|^2)$ algorithm, where we first fix l and then verify if those constraints hold. The idea is sound, but a bit slow. Again, the problematic step is that we need to perform many slow, linear-time comparisons. If we look at what comparisons we actually perform, we are actually comparing two substrings of S with each other:

$$s_1s_2\dots s_{n-l+1} = s_{l+1}s_{l+2}\dots s_n$$

Thus we are actually performing a linear number of substring comparisons, which we now know are actually constant-time operations after linear preprocessing. Hashes thus gave us a $\Theta(N)$ algorithm.

Algorithm 14.8: Radio Transmission

```
H lh = 0, Rh = 0;
int l = 0;
for (int i = 1; i <= n; ++i) {
  Lh = (Lh * p + S[i]) % M;
  Rh = (S[n - i + 1] * p^(i - 1) + Rh) % M;
  if (Lh == Rh) {
    l = i;
  }
}
cout << n - l << endl;
```

Polynomial hashes are also a powerful tool to compare something against a large number of strings using hash sets. For example, we could actually use hashing as a replacement for Aho-Corasick. However, we would have to perform one pass of rolling hash for each different pattern length. If the string we are searching in is N and the sum of pattern lengths are P, this is not $O(N + P)$ however. If we have k different pattern lengths, their sum must be at least $1 + 2 + \cdots + k = \Theta(k^2)$, so $k = O(\sqrt{P})$.

Substring Range Matching

Petrozavodsk Winter Training Camp 2015

Given N strings $s_1, s_2, \ldots, s_N$ and a list of queries of the form L, R, S, answer for each such query the number of strings in $s_L, s_{L+1}, \ldots, s_R$ which contain S as a substring.

Input

The first line contains $1 \leq N \leq 50\,000$ and the number of queries $0 \leq Q \leq 100\,000$. The next N lines contains the strings $s_1, s_2, \ldots, s_N$, one per line. The next Q lines contains one query each. A query is given by the integers $1 \leq L \leq R \leq N$ and a string S.

The sum of $|S|$ over all queries is at most $20\,000$. The lengths $|s_1| + |s_2| + \cdots + |s_N|$ is at most $50\,000$.

Output

For each query L, R, S, output a line with the answer to the query.

Let us focus on how to solve the problem where every query has the same string S. In this case, we would first find which of the strings s_i that S is contained in using polynomial hashing. To respond to a query, could for example keep a set of all the i where s_i was an occurrence together with how many smaller s_i contained the string (i.e. some kind of partial sum). This would allow us to respond to a query where $L = 1$ using a upper bound in our set. Solving queries of the form $[1, R]$ is equivalent to general intervals however, since the interval $[L, R]$ is simply the interval $[1, R]$ with the interval $[1, L - 1]$ removed. This procedure would take $\Theta(\sum |s_i|)$ time to find the occurrences of S, and $O(Q \log N)$ time to answer the queries.

When extending this to the general case where our queries may contain different S, we do the same thing but instead find the occurrences of all the patterns of the same length p simultaneously. This can be done by keeping the hashes of those patterns in a map, to allow for fast look-up of our rolling hash. Since there can only be at most $\sqrt{20\,000} \approx 140$ different pattern lengths, we must perform about $140 \cdot 50\,000 \approx 7\,000\,000$ set look-ups, which is feasible.

Algorithm 14.9: Substring Range Matching

```
int countInterval(int upTo, const set<pii>& s) {
  auto it = s.lower_bound(pii(upTo + 1, 0));
  if (it == s.begin()) return 0;
  return (--it)->second;
}

int main() {
  int N, Q;
  cin >> N >> Q;
  vector<string> s(N);
  rep(i,0,N) cin >> s[i];

  map<int, set<string>> patterns;

  vector<tuple<int, int, string>> queries;
  rep(i,0,Q) {
    int L, R;
    string S;
    cin >> L >> R >> S;
    queries.emplace_back(L, R, S);
    patterns[sz(s)].insert(S);
  }

  map<H, set<pii>> hits;
  trav(pat, patterns) {
    rep(i,0,N) {
      vector<H> hashes = rollHash(s[i], pat.first);
      trav(h, hashes)
        if (pat.second.count(h))
          hits[h].emplace(i, sz(hits[h]) + 1);
    }
  }

  trav(query, queries) {
    H h = polyHash(get<2>(query));
    cout << countInterval(R, hits[h]) - countInterval(L-1, hits[h]) << endl;
  }
}
```

Exercise 14.3

Hashing can be used to determine which of two substrings are the lexicographically smallest one. How? Extend this result to a simple $\Theta(n \log S + S)$ construction of a suffix array, where n is the number of strings and S is the length of the string.

14.3.1 The Parameters of Polynomial Hashes

Until now, we have glossed over the choice of M and p in our polynomial hashing. These choices happen to be important. First of all, we want M and p to be relatively prime. This ensures p has an inverse modulo M, which we use when erasing characters from the end of a hash. Additionally, $p^i \bmod M$ have a smaller period when p and M share a factor.

We wish M to be sufficiently large, to avoid hash collisions. If we compare the hashes of c strings, we want $M = \Omega(\sqrt{c})$ to get a reasonable chance at avoiding collisions. However, this depends on how we use hashing. p must be somewhat large as well. If p is smaller than the alphabet, we get trivial collisions such as $H(10) = H(p)$.

Whenever we perform rolling hashes, we must have $(M-1)p < 2^{64}$ if we use 64-bit unsigned integers to implement hashes. Otherwise, the addition of a character would overflow. If we perform substring hashes, we instead need that $(M-1)^2 < 2^{64}$, since we perform multiplication of a hash and an arbitrary power of p. When using 32-bit or 128-bit hashes, these limits change correspondingly. Note that the choice of hash size depends on how large an M we can choose, which affect collision rates.

One might be tempted to choose $M = 2^{64}$ and use the overflow of 64-bit integers as a cheap way of using hashes modulo 2^{64}. This is a bad idea, since it is possible to construct strings which are highly prone to collisions.

Definition 14.2 — Thue-Morse Sequence
Let the binary sequence τ_i be defined as

$$\tau_i = \begin{cases} 0 & \text{if } i = 0 \\ \tau_{i-1}\overline{\tau_{i-1}} & \text{if } i > 0 \end{cases}$$

The *Thue-Morse* sequence is the infinite sequence τ_i as $i \to \infty$.

This sequence is well-defined since τ_i is a prefix of τ_{i-1}, meaning each recursive step only append a string to the sequence. It starts 0, 01, 0110, 01101001, 0110100110010110.

Exercise 14.4

Prove that τ_{2i} is a palindrome.

Theorem 14.2 For a polynomial hash H with an odd p, $2^{\frac{n(n+1)}{2}} \mid H(\overline{\tau_n}) - H(\tau_n)$.

Proof. We will prove this by induction on n. For $n = 0$, we have $1| \mid H(\overline{\tau_n}) - H(\tau_n)$ which is vacuously true.

In our inductive step, we have that

$$H(\tau_n) = H(\tau_{n-1} \| \overline{\tau_{n-1}}) = p^{2^{n-1}} \cdot H(\overline{\tau_{n-1}}) + H(\tau_{n-1})$$

and

$$H(\overline{\tau_n}) = H(\overline{\tau_{n-1}} \| \tau_{n-1}) = p^{2^{n-1}} \cdot H(\tau_{n-1}) + H(\overline{\tau_{n-1}})$$

Then,

$$\begin{aligned} H(\overline{\tau_n}) - H(\tau_n) &= p^{2^{n-1}}(H(\tau_{n-1}) - H(\overline{\tau_{n-1}})) + (H(\overline{\tau_{n-1}}) - H(\tau_{n-1})) \\ &= (p^{2^{n-1}} - 1)(H(\tau_{n-1}) - H(\overline{\tau_{n-1}})) \end{aligned}$$

Note that $p^{2^{n-1}} - 1 = (p^{2^{n-2}} - 1)(p^{2^{n-2}} + 1)$ If p is odd, the second factor is divisible by 2. By expanding $p^{2^{n-2}}$, we can prove that $p^{2^{n-1}}$ is divisible by 2^n.

Using our induction assumption, we have that

$$2^n \cdot 2^{\frac{(n-1)n}{2}} \mid (p^{2^{n-1}} - 1)(H(\tau_{n-1}) - H(\overline{\tau_{n-1}}))$$

But $2^n \cdot 2^{\frac{(n-1)n}{2}} = 2^{\frac{n(n+1)}{2}}$, proving our statement. □

This means that we can construct a string of length linear in the bit size of M that causes hash collisions if we choose M as a power of 2, explaining why it is a bad choice.

14.3.2 2D Polynomial Hashing

Polynomial hashing can also be applied to pattern matching in grids, by first performing polynomial hashing on all rows of the grid (thus reducing the grid to a sequence) and then on the columns.

Surveillance

Swedish Olympiad in Informatics 2016, IOI Qualifiers

Given a matrix of integers $A = (a_{r,c})$ find all occurrences of another matrix $P = (p_{r,c})$ in A which may differ by a constant C. An occurrence (i, j) means that $a_{i+r,j+c} = p_{r,c} + C$ where C is a constant.

If we assume that $C = 0$, the problem is reduced to simple 2D pattern matching, which is easily solved by hashing. The requirement that such a pattern should be invariant to addition by a constant is a bit more complicated.

How would we solve this problem in one dimension, i.e. when $r = 1$? In this case, we have that a match on column j would imply

$$a_{1,j} - p_{1,1} = c$$

$$\dots$$

$$a_{1,j+n-1} - p_{1,n} = c$$

Since c is arbitrary, this means the only condition is that

$$a_{1,j} - p_{1,1} = \dots = a_{1,j+n-1} - p_{1,n} = c$$

Rearranging this gives us that

$$a_{1,j} - a_{1,j+1} = p_{1,1} - p_{1,2}$$

$$a_{1,j+1} - a_{1,j+2} = p_{1,2} - p_{1,3}$$

$$\dots$$

By computing these two sequences of the adjacent differences of elements $a_{1,i}$ and $r_{1,j}$, we have reduced the problem to substring matching and can apply hashing. In 2D, we can do something similar. For a match (i, j), it is sufficient that this property holds for every line and every column in the match. We can then find matches using two 2D hashes.

Exercise 14.5 — Kattis Exercise

Chasing Subs — chasingsubs

14.4 Chapter Notes

rabin karp paper

KMP

hashing

Chapter 15

Combinatorics

Combinatorics deals with various discrete structures, such as graphs and permutations. In this chapter, we will mainly study the branch of combinatorics known as *enumerative combinatorics* – the art of counting. We will count the number of ways to choose K different candies from N different candies, the number of distinct seating arrangements around a circular table, the sum of sizes of all subsets of a set and many more objects. Many combinatorial counting problems are based on a few standard techniques which we will learn in this chapter.

15.1 The Addition and Multiplication Principles

The ***addition principle*** states that, given a finite collection of **disjoint** sets $S_1, S_2, \ldots, S_n$, we can compute the size of the union of all sets by simply adding up the sizes of our sets, i.e.

$$|S_1 \cup S_2 \cup \cdots \cup S_n| = |S_1| + |S_2| + \cdots + |S_n|$$

Example 15.1 Assume we have 5 different types of chocolate bars (the set C), 3 different types of bubble gum (the set G), and 4 different types of lollipops (the set L). These form three disjoint sets, meaning we can compute the total number of snacks by summing up the number of snacks of the different types. Thus, we have $|C| + |G| + |L| = 5 + 3 + 4 = 12$ different snacks.

Later on, we will see a generalization of the addition principle that handles cases where our sets are not disjoint.

The ***multiplication principle***, on the other hand, states that the size of the Cartesian product $S_1 \times S_2 \times \cdots \times S_n$ equals the product of the individual sizes of these sets, i.e.

$$|S_1 \times S_2 \times \cdots \times S_n| = |S_1| \cdot |S_2| \cdots |S_n|$$

Example 15.2 Assume that we have the same sets of candies C, G and L as in Example 15.1. We want to compose an entire dinner out of snacks, by choosing one chocolate bar, one bubble gum and a lollipop. The multiplication principles tells us that, modeling a snack dinner as a tuple $(c, g, l) \in C \times G \times L$, we can form our dinner in $5 \cdot 3 \cdot 4 = 60$ ways.

The addition principle is often useful when we solve counting problems by case analysis.

Example 15.3 How many four letter words consisting of the letters a, b, c and d contain exactly two letters a?

There are six possible ways to place the two letters a:

$$aa\_\_$$
$$a\_a\_$$
$$a\_\_a$$
$$\_aa\_$$
$$\_a\_a$$
$$\_\_aa$$

For each of these ways, there are four ways of choosing the other two letters (bb, bc, cb, cc). Thus, there are $4 + 4 + 4 + 4 + 4 + 4 = 6 \cdot 4 = 24$ such words.

Let us now apply these basic principle sto solve the following problem:

Kitchen Combinatorics

Northwestern Europe Regional Contest 2015 – Per Austrin

The world-renowned Swedish Chef is planning a gourmet three-course dinner for some muppets: a starter course, a main course, and a dessert. His famous Swedish cook-book offers a wide variety of choices for each of these three courses, though some of them do not go well together (for instance, you of course cannot serve chocolate moose and sooted shreemp at the same dinner).

Each potential dish has a list of ingredients. Each ingredient is in turn available from a few different brands. Each brand is of course unique in its own special way, so using a particular brand of an ingredient will always result in a completely different dinner experience than using another brand of the same ingredient.

Some common ingredients such as pølårber may appear in two of the three chosen dishes, or in all three of them. When an ingredient is used in more than one of the three selected dishes, Swedish Chef will use the same brand of the ingredient in all of them.

While waiting for the meecaroo, Swedish Chef starts wondering: how many different dinner experiences are there that he could make, by different choices of dishes and brands for the ingredients?

Input

The input consists of:

- five integers r, s, m, d, n, where $1 \leq r \leq 1\,000$ is the number of different ingredients that exist, $1 \leq s, m, d \leq 25$ are the number of available starter dishes, main dishes, and desserts, respectively, and $0 \leq n \leq 2\,000$ is the number of pairs of dishes that do not go well together.
- r integers $b_1, \ldots, b_r$, where $1 \leq b_i \leq 100$ is the number of different brands of ingredient i.
- $s + m + d$ dishes – the s starter dishes, then the m main dishes, then the d desserts. Each dish starts with an integer $1 \leq k \leq 20$

denoting the number of ingredients of the dish, and is followed by k distinct integers $i_1, \ldots, i_k$, where for each $1 \leq j \leq k$, $1 \leq i_j \leq r$ is an ingredient.

- n pairs of incompatible dishes.

Output

If the number of different dinner experiences Swedish Chef can make is at most 10^{18}, then output that number. Otherwise, output "`too many`".

The solution is a similar addition-multiplication principle combo as used in Example 15.3. First off, we can simplify the problem considerably by brute forcing over the coarsest component of a dinner experience, namely the courses included. Since there are at most 25 dishes of every type, we need to check up to $25^3 = 15\,625$ choices of dishes. By the addition principle, we can compute the number of dinner experiences for each such three-course dinner, and then sum them up to get the answer. Some pairs of dishes do not go well together. At this stage in the process we exclude any triple of dishes that include such a pair. We can perform this check in $\Theta(1)$ time if we save the incompatible dishes in 2D boolean vectors, so that e.g. badStarterMain$[i][j]$ determines if starter i is incompatible with main dish j.

For a given dinner course consisting of starter a, main dish b and dessert c, only the **set** of ingredients of three dishes matters since the chef will use the same brand for an ingredient even if it is part of two dishes. The next step is thus to compute this set by taking the union of ingredients for the three included dishes. This step takes $\Theta(k_a + k_b + k_c)$. Once this set is computed, the only remaining task is to choose a brand for each ingredient. Assigning brands is an ordinary application of the multiplication principle, where we multiply the number of brands available for each ingredient together.

15.2 Permutations

A ***permutation*** of a set S is an ordering of all the elements in the set. For example, the set $\{1, 2, 3\}$ has 6 permutations:

123	132
213	231
312	321

Our first "real" combinatorial problem will be to count the number of permutations of an n-element set S. When counting permutations, we use the multiplication principle. We will show a procedure that can be used to construct permutations one element at a time. Assume that the permutation is the sequence $\langle a_1, a_2, \dots, a_n \rangle$. The first element of the permutation, a_1, can be assigned any of the n elements of S. Once this assignment has been made, we have $n - 1$ elements we can choose to be a_2 (any element of S except a_1). In general, when we are to select the $(i + 1)$'th value a_{i+1} of the permutation, i elements have already been included in the permutation, leaving $n - i$ options for a_{i+1}. Using this argument for all n elements of the sequence, we can construct a permutation in $n \cdot (n - 1) \cdots 2 \cdot 1$ ways (by the multiplication principle).

This number is so useful that it has its own name and notation.

Definition 15.1 — Factorial
The ***factorial*** of n, where n is a non-negative integer, denoted $n!$, is defined as the product of the first n positive integers, i.e.

$$n! = 1 \cdot 2 \cdots n = \prod_{i=1}^{n} i$$

For $n = 0$, we use the convention that the empty product is 1.

This sequence of numbers thus begin 1, 1, 2, 6, 24, 120, 720, 40 320, 362 880, 3 628 800, 39 916 800 for $n = 0, 1, 2, \dots, 11$. It is good to know the magnitudes of these numbers, since they are frequent in time complexities when doing brute force over permutations. Asypmtotically, the grow as $n^{\Theta(n)}$. More precisely, the well-used *Stirling's formula*[1] gives the approximation

$$n! = \sqrt{2\pi n}\left(\frac{n}{e}\right)^n\left(1 + O\left(\frac{1}{n}\right)\right)$$

Exercise 15.1

In how many ways can 8 persons be seated around a round table, if we consider cyclic rotations of a seating to be different? What if we consider cyclic rotations to be equivalent?

Exercise 15.2 — Kattis Problems

n'th permutation – nthpermutation

Name That Permutation – namethatpermutation

15.2.1 Permutations as Bijections

The word *permutation* has roots in Latin, meaning "to change completely". We are now going look at permutations in a very different light, which gives some justification to the etymology of the word.

Given a set such as $[5]$, we can fix some ordering of its elements such as $\langle 1, 2, 3, 4, 5\rangle$. A permutation $\pi = \langle 1, 3, 4, 5, 2\rangle$ of this set can then be seen as a movement of these elements. Of course, this same movement can be applied to any other 5-element set with a fixed permutation, such as $\langle a, b, c, d, e\rangle$ being transformed to $\langle a, c, d, e, b\rangle$. This suggests that we can consider permutation as a "rule" which describes how to move – *permute* – the elements.

Such a movement rule can also be described as a function $\pi : [n] \to [n]$, where $\pi(i)$ describes what element should be placed at position i. Thus, the permutation $\langle 1, 3, 4, 5, 2\rangle$ would have $\pi(1) = 1$, $\pi(2) = 3$, $\pi(3) = 4$, $\pi(4) = 5$, $\pi(5) = 2$.

[1]Named after James Stirling (who have other important combinatorial objects named after him too), but stated already by his contemporary Abraham de Moivre.

$$\begin{array}{c|ccccc} i & 1 & 2 & 3 & 4 & 5 \\ & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\ \pi(i) & 1 & 3 & 4 & 5 & 2 \end{array}$$

Since each element is mapped to a different element, the function induced by a permutation is actually a bijection. By interpreting permutations as function, all the theory from functions apply to permutations too.

We call $\langle 1, 2, 3, 4, \ldots, n\rangle$ the *identity permutation*, since the function given by the identity permutation is actually the identity function. As a function, we can also consider the composition of two permutations. Given two permutations, α and β, their composition $\alpha\beta$ is also a permutation, given by $\alpha\beta(k) = \alpha(\beta(k))$. If we let $\sigma = \langle 5, 4, 3, 2, 1\rangle$ the composition with $\pi = \langle 1, 3, 4, 5, 2\rangle$ from above would then be

$$\begin{array}{c|ccccc} i & 1 & 2 & 3 & 4 & 5 \\ & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\ \pi(i) & 1 & 3 & 4 & 5 & 2 \\ & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\ \sigma\pi(i) & 5 & 3 & 2 & 1 & 4 \end{array}$$

This is called *multiplying* permutations, i.e. $\sigma\pi$ is the product of σ and π. If we multiply a permutation π by itself n times, we call the resulting product π^n.

An important property regarding the multiplication of permutations follows from their functional properties, namely their associativity. We have that the permutation $(\alpha\beta)\gamma = \alpha(\beta\gamma)$, so we will take the liberty of dropping the parentheses and writing $\alpha\beta\gamma$.

Exercise 15.3 — Kattis Problems

Permutation Product – permutationproduct

Permutations also have inverses, which are just the inverses of their functions. The permutation $\pi = \langle 1, 3, 4, 5, 2\rangle$ which we looked at in the beginning thus have the inverse given by

$$\pi^{-1}(1) = 1 \qquad \pi^{-1}(3) = 2 \qquad \pi^{-1}(4) = 3 \qquad \pi^{-1}(5) = 4 \qquad \pi^{-1}(2) = 5$$

written in permutation notation as $\langle 1, 5, 2, 3, 4\rangle$. Since this is the functional inverse, we expect $\pi^{-1}\pi = \text{id}$.

$$\begin{array}{c|ccccc}
i & 1 & 2 & 3 & 4 & 5 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi(i) & 1 & 3 & 4 & 5 & 2 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi^{-1}\pi(i) & 1 & 2 & 3 & 4 & 5
\end{array}$$

Exercise 15.4 — Kattis Problems

Permutation Inverse – permutationinverse

A related concept is that of the ***cycle decomposition*** of a permutation. If we start with an element i and repeatedly apply a permutation on this element (i.e. take $i, \pi(i), \pi(\pi(i)), \ldots$) we will at some point find that $\pi^k(i) = i$, at which point we will start repeating ourselves.

$$\begin{array}{c|ccccc}
i & 1 & 2 & 3 & 4 & 5 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi(i) & 2 & 1 & 4 & 5 & 3 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi^2(i) & 1 & 2 & 5 & 3 & 4 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi^3(i) & 2 & 1 & 3 & 4 & 5 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi^4(i) & 1 & 2 & 4 & 5 & 3 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi^5(i) & 2 & 1 & 5 & 3 & 4 \\
 & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\
\pi^6(i) & 1 & 2 & 3 & 4 & 5
\end{array}$$

We call the k distinct numbers of this sequence the *cycle* of i. For π, we have two cycles: $(1, 2)$ and $(3, 4, 5)$. Note how $\pi(1) = 2$ and $\pi(2) = 1$ for the first cycle, and $\pi(3) = 4, \pi(4) = 5, \pi(5) = 3$. It gives us an alternative way of writing it, namely as the concatenation of its cycles: $(1, 2)(3, 4, 5)$.

To compute the cycle decomposition of a permutation π, we repeatedly pick any element of the permutation which is currently not a part of a cycle, and compute the cycle it is in using the method described above. Since we will consider every element exactly once, this procedure is $\Theta(n)$ for n-element permutations.

Exercise 15.5 — Kattis Problems

Cycle Decomposition – cycledecomposition

Given a permutation π, we define its ***order***, denoted $\operatorname{ord}\pi$, as the size of the set $\{\pi, \pi^2, \pi^3, \dots\}$. For all permutations except for the identity permutation, this is the smallest integer $k > 0$ such that π^k is the identity permutation. In our example, we have that $\operatorname{ord}\pi = 6$, since π^6 was the first power of π that was equal to the identity permutation. How can we quickly compute the order of π?

The maximum possible order of a permutation happens to grow rather quickly (it is $e^{(1+o(1))\sqrt{n \log n}}$ in the number of elements n). Thus, trying to compute the order by computing π^k for every k until π^k is the identity permutation is too slow. Instead, we can use the cycle decomposition. If a permutation has a cycle $(c_1, c_2, \dots c_l)$, we know that

$$\pi^l(c_1) = c_1, \pi^l(c_2) = c_2, \dots, \pi^l(c_l) = c_l$$

by the definition of the cycle composition. Additionally, this means that $(\pi^l)^k(c_1) = (\pi^{lk})(c_1) = c_1$. Hence, any power of π that is a multiple of l will act as the identity permutation *on this particular cycle*.

This fact gives us an upper bound on the order of π. If its cycle decomposition has cycles of length $l_1, l_2, \dots, l_m$, the smallest positive number that is the multiple of every l_i is $\operatorname{lcm}(l_1, l_2, \dots, l_m)$. The permutation $\pi = \langle 2, 1, 4, 5, 3\rangle$ had two cycles, one of length 2 and 3. Its order was $\operatorname{lcm}(2, 3) = 2 \cdot 3 = 6$. This is also a lower bound on the order, a fact that uses the following fact which is left as an exercise:

Exercise 15.6

Prove that if π has a cycle of length l, we must have $l \mid \operatorname{ord}\pi$.

Exercise 15.7 — Kattis Problems

Order of a Permutation – permutationorder

Dance Reconstruction

Nordic Collegiate Programming Contest 2013 – Lukáš Poláček

Marek loves dancing, got really excited when he heard about the coming wedding of his best friend Miroslav. For a whole month he worked on a special dance for the wedding. The dance was performed by N people and there were N marks on the floor. There was an arrow from each mark to another mark and every mark had exactly one incoming arrow. The arrow could be also pointing back to the same mark.

At the wedding, every person first picked a mark on the floor and no 2 persons picked the same one. Every 10 seconds, there was a loud signal when all dancers had to move along the arrow on the floor to another mark. If an arrow was pointing back to the same mark, the person at the mark just stayed there and maybe did some improvised dance moves on the spot.

Another wedding is now coming up a year later, and Marek would like to do a similar dance. He found two photos from exactly when the dance started and when it ended. Marek also remembers that the signal was triggered K times during the time the song was played, so people moved K times along the arrows.

Given the two photos, can you help Marek reconstruct the arrows on the floor? On the two photos it can be seen for every person to which position he or she moved. Marek numbered the people in the first photo from 1 to N and then wrote the number of the person whose place they took in the second photo.

Marek's time is running out, so he is interested in any placement of arrows that could produce the two photos.

Input

Two integers $2 \leq N \leq 10\,000$ and $1 \leq K \leq 10^9$. Then, N integers $1 \leq a_1, \ldots, a_N \leq N$, denoting that dancer number i ended up at the place of dancer number a_i. Every number between 1 and N appears exactly once in the sequence a_i.

Output

If it is impossible to find a placement of arrows such that the dance performed K times would produce the two photos, print "`Impossible`". Otherwise print N numbers on a line, the i'th number denoting to which person the arrow leads from person number i.

The problem can be rephrased in terms of permutations. First of all, the dance corresponds so some permutation π of the dancers, given by where the arrows pointed. This is the permutation we seek in the problem. We are given the permutation a, so we seek a permutation π such that $\pi^K = a$.

When given permutation problems of this kind, we should probably attack it using cycle decompositions in some way. Since the cycles of π are all independent of each other under multiplication, it is a good guess that the decomposition can simplify the problem. The important question is then how a cycle of π is affected when taking powers. For example, a cycle of 10 elements in π would decompose into two cycles of length 5 in π^2, and five cycles of length 2 in π^5. The general case involves the divisors of l and K:

Exercise 15.8

Prove that a cycle of length l in a permutation π decomposes into $\gcd(l, K)$ cycles of length $\frac{l}{\gcd(l,K)}$ in π^K.

This suggests our first simplification of the problem: to consider all cycles of π^K partitioned by their lengths. By Exercise 15.8, cycles of different lengths are completely unrelated in the cycle decomposition of π^K.

The result also gives us a way to "*reverse*" the decomposition that happens to the cycles of π. Given $\frac{l}{m}$ cycles of length m in π^K, we can combine them into a l-cycle in π in the case where $m \cdot \gcd(l, K) = l$. By looping over every possible cycle length l (from 1 to N), we can then find all possible ways to combine cycles of π^K into larger cycles of π. This step takes $\Theta(N \log(N + K))$ due to the GCD computation.

Given all the ways to combine cycles, a knapsack problem remains for each cycle length of π^K. If we have a cycles of length l in π^K, we want to partition them into sets of certain sizes (given by by previous computation). This step takes $\Theta(a \cdot c)$ ways, if there are c ways to combine a-length cycles.

Once it has been decided what cycles are to be combined, only the act of computing a combination of them remains. This is not difficult on a conceptual level, but is a good practice to do on your own (the solution to Exercise 15.8 basically outlines the reverse procedure).

15.3 Ordered Subsets

A variation of the permutation counting problem is to count the number of ordered sequences containing *exactly* k distinct elements, from a set of n. We can compute this by first consider the permutations of the entire set of n elements, and then group together those whose k first elements are the same. Taking the set $\{a, b, c, d\}$ as an example, it has the permutations:

abcd	**ba**cd	**ca**bd	**da**bc
abdc	**ba**dc	**ca**db	**da**cb
acbd	**bc**ad	**cb**ad	**db**ac
acdb	**bc**da	**cb**da	**db**ca
adbc	**bd**ac	**cd**ab	**dc**ab
adcb	**bd**ca	**cd**ba	**dc**ba

Once we have chosen the first k elements of a permutation, there are $(n-k)!$ ways to order the remaining $n-k$ elements. Thus, we must have divided our $n!$ permutations into one group for each ordered k-length sequence, with each group containing $(n-k)!$ elements. To get the correct total, this means there must be $\frac{n!}{(n-k)!}$ such groups – and k-length sequences.

We call these objects ***ordered*** ***k-subsets*** of an n-element set, and denote the number of such ordered sets by

$$P(n,k) = \frac{n!}{(n-k)!}$$

Note that this number can also be written as $n \cdot (n-1) \cdots (n-k+1)$, which hints at an alternative way of computing these numbers. We can perform the ordering and choosing of elements at the same time. The first element of our sequence can be any of the n elements of the set. The next element any but the first, leaving us with $n-1$ choices, and so on. The difference to the permutation is that we stop after choosing the k'th element, which we can do in $(n-k+1)$ ways.

15.4 Binomial Coefficients

Finally, we are going to do away with the "ordered" part of the ordered k-subsets, and count the number of subsets of size k of an n-element size. This number is called the *binomial coefficient*, and is probably the most important combinatorial number there is.

To compute the number of k-subsets of a set of size n, we start with all the $P(n,k)$ *ordered* subsets. Any particular unordered k-subset can be ordered in exactly $k!$ different ways. Hence, there must be $\frac{P(n,k)}{k!}$ unordered subsets, by the same grouping argument we used when determining $P(n,k)$ itself.

For example, consider again the ordered 2-subsets of the set $\{a,b,c,d\}$, of which there are 12.

ab	ba	ca	da
ac	bc	cb	db
ad	bd	cd	dc

The subset $\{a,b\}$ can be ordered in 2! ways - the ordered subsets ab and ba. Since each unordered subset is responsible for the same number of ordered subsets, we get the number of unordered subsets by dividing 12 with 2!, giving us the 6 different 2-subsets of $\{a,b,c,d\}$.

ab		
ac	bc	
ad	bd	cd

Definition 15.2 — Binomial Coefficient
The number of k-subsets of an n-set is called the ***binomial coefficient***

$$\binom{n}{k} = \frac{n!}{k!(n-k)!}$$

This is generally read as "n choose k".

Note that

$$\binom{n}{k} = \frac{(n-k+1)\cdot(n-k+2)\cdots(n-1)\cdot n}{1\cdot 2\cdots(k-1)\cdot k}$$

They are thus the product of k numbers, divided by another k numbers. With this fact in mind, it does not seem unreasonable that they should be computable in $O(k)$ time. Naively, one might try to compute them by first multiplying the k numbers in the nominator, then the k numbers in the denominator, and finally divide them.

Unfortunately, both of these numbers grow quickly. Indeed, already at 21! we have outgrown a 64-bit integer. Instead, we will compute the binomial coefficient by alternating multiplications and divisions. We will start with storing $1 = \frac{1}{1}$. Then, we multiply with $n - r + 1$ and divide with 1, leaving us with $\frac{n-r+1}{1}$. In the next step we multiply with $n - r + 2$ and divide with 2, having computed $\frac{(n-r+1)\cdot(n-r+2)}{1\cdot 2}$. After doing this r times, we will be left with our binomial coefficient.

There is one big question mark from performing this procedure - why must our intermediate result always be integer? This must be true if our procedure is correct, or we will at some point perform an inexact integer division, leaving us with an incorrect intermediate quotient. If we study the partial results more closely, we see that they are binomial coefficients themselves, namely $\binom{n-r+1}{1}$, $\binom{n-r+2}{2}, \dots, \binom{n-1}{r-1}, \binom{n}{r}$. Certainly, these numbers must be integers. As we just showed, the binomial coefficients count things, and counting things tend to result in integers.

As a bonus, we discovered another useful identity in computing binomial coefficients:

$$\binom{n}{r} = \frac{n}{r}\binom{n-1}{r-1}$$

Exercise 15.9

Prove this identity combinatorially, by first multiplying both sides with r. (Hint: both sides count the number of ways to do the same two-choice process, but in different order.)

We have one more useful trick up our sleeves. Currently, if we want to compute e.g. $\binom{10^9}{10^9-1}$, we have to perform $10^9 - 1$ operations. To avoid this, we exploit a symmetry of the binomial coefficient. Assume we are working with subsets of some n-element set S. Then, we can define a bijection from the subsets of S onto itself by taking complements. Since a subset T and its complement $S \setminus T$ are disjoint, we have $|S \setminus T| = |S| - |T|$. This means that every 0-subset is mapped bijectively to every n-subset, every 1-subset to every $(n-1)$-subset, and every r-subset to every $(n-r)$-subset.

However, if we can bijectively map r-subsets to $(n-r)$-subsets, there must be equally many such subsets. Since there are $\binom{n}{r}$ subsets of the first kind and $\binom{n}{n-r}$ subsets of the second kind, they must be equal:

$$\binom{n}{r} = \binom{n}{n-r}$$

More intuitively, our reasoning is basically "choosing what r elements to include in a set is the same as choosing what $n-r$ elements to exclude". This is very useful in our example of computing $\binom{10^9}{10^9-1}$, since this equals $\binom{10^9}{1} = 10^9$. More generally, this enables us to compute binomial coefficients in $O(\min\{r, n-r\})$ instead of $O(r)$.

Exercise 15.10 — Kattis Exercises

Binomial Coefficients – binomial

Sjecista

Croatian Olympiad in Informatics 2006/2007, Contest #2

In a convex polygon with N sides, line segments are drawn between all pairs of vertices in the polygon, so that no three line segments intersect in the same point. Some pairs of these inner segments intersect, however.

For $N = 6$, this number is 15.

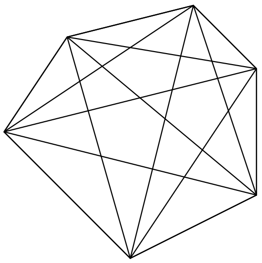

Figure 15.1: A polygon with 4 vertices.

Given N, determine how many pairs of segments intersect.

Input

The integer $3 \leq N \leq 100$.

Output

The number of pairs of segments that intersect.

The problem is a classical counting problem. If we compute the answer by hand starting at $N = 0$, we get $0, 0, 0, 0, 1, 5, 15, 35$. A quick lookup on OEIS[2] suggests that the answer is the binomial coefficient $\binom{N}{4}$. While this certainly is a legit strategy when solving problems on your own, this approach is usually not applicable at contests where access to the Internet tend to be restricted.

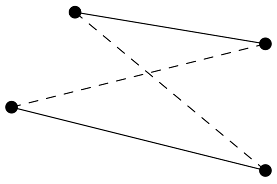

Figure 15.2: Four points taken from Figure 15.1.

[2]`https://oeis.org/A000332`

Instead, let us find some kind of bijection between the objects we count (intersections of line segments) with something easier to count. This strategy is one of the basic principles of combinatorial counting. An intersection is defined by two line segments, of which there are $\binom{N}{2}$. Does every pair of segments intersect? In Figure 15.2, two segments (the solid segments) do not intersect. However, two other segments which together have the same four endpoints *do* intersect with each other. This suggests that line segments was the wrong level of abstraction when finding a bijection. On the other hand, if we choose a set of four points, the segments formed by the two diagonals in the convex quadrilateral given by those four points will intersect at some point (the dashed segments in Figure 15.2).

Conversely, any intersection of two segments give rise to such a quadrilateral – the one given by the four endpoints of the segments that intersect. Thus there exists a bijection between intersections and quadrilaterals, meaning that there must be an equal number of both. There are $\binom{N}{4}$ such choices of quadrilaterals, meaning there are also $\binom{N}{4}$ points of intersection.

Exercise 15.11

Prove that

1) $\binom{n}{k} = \binom{n-1}{k-1} + \binom{n-1}{k}$

2) $\sum_{k=0}^{n} \binom{n}{k} = 2^n$

3) $\sum_{k=0}^{n} (-1)^k \binom{n}{k} = 0$

4) $\sum_{k=0}^{n} \binom{n}{k} 2^k = 3^n$

5) $\sum_{k=0}^{n} \left[\binom{n}{k} \left(\sum_{l=0}^{k} \binom{k}{l} 2^l\right)\right] = 4^n$

15.4.1 Dyck Paths

In a grid of width W and height H, we stand in the lower left corner at coordinates $(0, 0)$, wanting to venture to the upper right corner at (W, H). To do this, we are only allowed two different moves – we can either move one unit north, from (x, y) to $(x, y + 1)$ or one unit east, to $(x + 1, y)$. Such a path is called a ***Dyck path***.

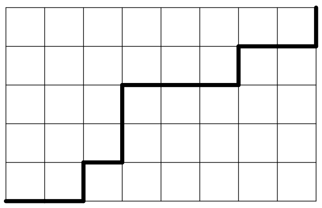

Figure 15.3: A Dyck path on a grid of width 8 and height 5.

As is the this spirit of this chapter, we ask how many Dyck paths there are in a grid of size $W \times H$. The solution is based on two facts: a Dyck path consists of exactly $H + W$ moves, and exactly H of those should be northbound moves, and W eastbound. Conversely, any path consisting of exactly $H + W$ moves where exactly H of those are northbound moves is a Dyck path.

If we consider e.g. the Dyck path in Figure 15.3, we can write down the sequence of moves we made, with the symbol N for northbound moves and E for eastbound moves:

$$\mathsf{EENENNEEEENEEN}$$

Such a sequence must consist of all $H + W$ moves, with exactly H "N"-moves. There are exactly $\binom{H+W}{H}$ such sequences, since this is the number of ways we can choose the subset of positions which should contain the N moves.

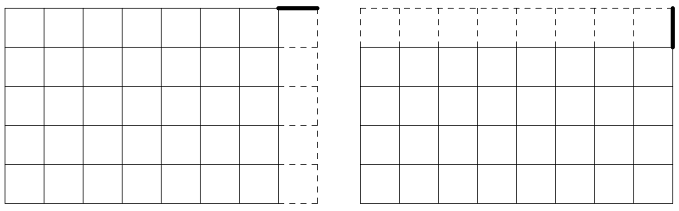

Figure 15.4: The two options for the last possible move in a Dyck path.

If we look at Figure 15.3, we can find another way to arrive at the same answer. Letting $D(W, H)$ be the number of Dyck paths in a $W \times H$ grid, some case work on the last move gives us the recurrence

$$D(W, H) = D(W - 1, H) + D(W, H - 1)$$

with base cases

$$D(0, H) = D(W, 0) = 1$$

We introduce a new function D', defined by $D'(W + H, W) = D(W, H)$. This gives us the recurrence

$$D'(W + H, H) = D'(W - 1 + H, W - 1) + D'(W + H - 1, H - 1)$$

with base cases

$$D'(0, 0) = D'(H, H) = 0$$

These relations are satisfied by the binomial coefficients (Exercise 15.11).

Exercise 15.12

Prove that $\sum_{i=0}^{n} \binom{n}{i}\binom{n}{n-i} = \binom{2n}{n}$.

While Dyck paths sometimes do appear directly in problems, they are also a useful tool to find bijections to other objects.

Sums

In how many ways can the numbers $0 \leq a_1, a_2, \ldots, a_k$ be chosen such that

$$\sum_{i=1}^{k} a_i = n$$

Input

The integers $0 \leq n \leq 10^6$ and $0 \leq k \leq 10^6$.

Output

Output the number of ways modulo $10^9 + 7$.

Given a Dyck path such as the one in Figure 15.3, what happens if we count the number of northbound steps we take at each x-coordinate? There are a total of $W + 1$ coordinates and H northbound steps, so we except this to be a sum of $W + 1$ (non-negative) variables with a sum of H. This is indeed similar to what we are counting, and Figure 15.5 shows this connection explicitly.

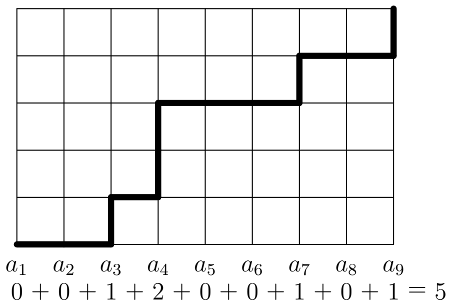

Figure 15.5: A nine-term sum as a Dyck path.

This mapping gives us a bijective mapping between sums of k terms with a sum of n, to Dyck paths on a grid of size $(k-1) \times n$. We already know how many such Dyck paths there are: $\binom{n+k-1}{n}$.

15.4.2 Catalan Numbers

A special case of the Dyck paths are the paths on a square grid that *do not cross the diagonal* of the grid. See Figure 15.6 for an example.

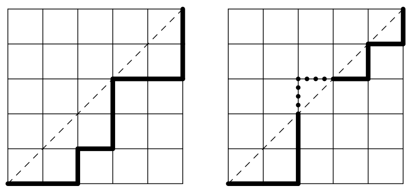

Figure 15.6: A valid path (left) and an invalid path (right).

We are now going to count the number of such paths, the most complex counting problem we have encountered so far. It turns out there is a straightforward bijection between the *invalid* Dyck paths, i.e. those who do cross the diagonal of the grid, to Dyck paths in a grid of different dimensions. In Figure 15.6, the right grid contained a path that cross the diagonal. If we take the part of the grid just after the first segment that crossed the diagonal and mirror it in the diagonal translated one unit upwards, we get the situation in Figure 15.7.

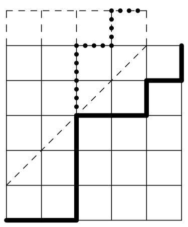

Figure 15.7: Mirroring the part of the Dyck path after its first diagonal crossing.

We claim that when mirroring the remainder of the path in this translated diagonal, we will get a new Dyck path on the grid of size $(n-1) \times (n+1)$. Assume that the first crossing is at the point (c, c). Then, after taking one step up in order to cross the diagonal, the remaining path goes from $(c, c+1)$ to (n, n). This needs $n-c$ steps to the right and $n-c-1$ steps up. When mirroring, this instead turns into $n-c-1$ steps up and $n-c$ steps right. Continuing from $(c, c+1)$, the new path must thus end at $(c+(n-c-1), c+1+(n-c)) = (n-1, n+1)$. This mapping is also bijective.

This bijection lets us count the number of paths that do cross the diagonal: they are $\binom{2n}{n+1}$. The numbers of paths that does not cross the diagonal is then $\binom{2n}{n} - \binom{2n}{n+1}$.

Definition 15.3 — Catalan Numbers

The number of Dyck paths in an $\times n$ grid is called the n'th ***Catalan number***

$$C_n = \binom{2n}{n} - \binom{2n}{n+1} = \binom{2n}{n} - \frac{n}{n+1}\binom{2n}{n} = \frac{1}{n+1}\binom{2n}{n}$$

The first few Catalan numbers[3] are $1, 1, 2, 5, 14, 42, 132, 429, 1430$.

Exercise 15.13 — Kattis Exercises

Catalan Numbers – catalan

Catalan numbers count many other objects, most notably the number of *bal-*

[3] `https://oeis.org/A000108`

anced parentheses expressions. A balanced parentheses expression is a string of $2n$ characters $s_1 s_2 \ldots s_{2n}$ of letters (and), such that every prefix $s_1 s_2 \ldots s_k$ contain *at least* as many letters (as). Given such a string, like (()())(()) we can interpret it as a Dyck path, where (is a step to the right, and) is a step upwards. Then, the condition that the string is balanced is that, for every partial Dyck path, we have taken at least as many right steps as we have taken up steps. This is equivalent to the Dyck path never crossing the diagonal, giving us a bijection between parentheses expressions and Dyck paths. The number of such parentheses expressions are thus also C_n.

15.5 The Principle of Inclusion and Exclusion

Often, we wish to compute the size of the union of a collection of sets $S_1, S_2, \ldots, S_n$, where these sets are not pairwise disjoint. For this, the *principle of inclusion and exclusion* was developed.

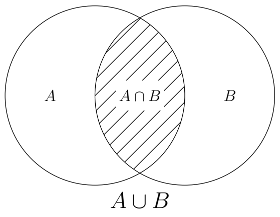

Figure 15.8: The union of two sets A and B.

Let us consider the most basic case of the principle, using two sets A and B. If we wish to compute the size of their union $|A \cup B|$, we *at least* need to count every element in A and every set in B, i.e. $|A| + |B|$. The problem with this formula is that whenever an element is in *both* A and B, we count it twice. Fortunately, this is easily mitigated: the number of elements in both sets equals $|A \cap B|$ (Figure 15.8). Thus, we see that $|A \cup B| = |A| + |B| - |A \cap B|$.

Similarly, we can determine a formula for the union of three sets $|A \cup B \cup C|$. We begin by including every element: $|A| + |B| + |C|$. Again, we have included the pairwise intersections too many times, so we remove those and get

$$|A| + |B| + |C| - |A \cap B| - |A \cap C| - |B \cap C|$$

This time, however, we are not done. While we have counted the elements which are in exactly one of the sets correctly (using the first three terms), and the elements which are in exactly two of the sets correctly (by removing the double-counting using the three latter terms), we currently do not count the elements which are in all three sets at all! Thus, we need to add them back, which gives us the final formula:

$$|A \cup B \cup C| = |A| + |B| + |C| - |A \cap B| - |A \cap C| - |B \cap C| + |A \cap B \cap C|$$

Exercise 15.14

Compute the number of integers between 1 and 1000 that are divisible by 2, 3 or 5.

From the two examples, you can probably guess formula in the general case, which we write in the following way:

$$\left|\bigcup_{i=1}^{n} S_i\right| = \sum_i |S_i| - \sum_{i<j} |S_i \cap S_j| + \sum_{i<j<k} |S_i \cap S_j \cap S_k| - \cdots + (-1)^{n+1} |S_1 \cap S_2 \cap \cdots \cap S_n|$$

From this formula, we see the reason behind the naming of the principle. We *include* every element, *exclude* the ones we double-counted, *include* the ones we removed too many times, and so on. The principle is based on a very important assumption – that it is easier to compute intersections of sets than their unions. Whenever this is the case, you might want to consider if the principle is applicable.

Derangements

Compute the number of permutations π of length N such that $\pi(i) \neq i$ for every $i = 1 \ldots N$.

This is a typical application of the principle. We will use it on those sets of permutations be where the condition is false for *at least* a particular index i If we let these sets be D_i, the set of all permutations where the condition is false is $D_1 \cup D_2 \cup \cdots \cup D_N$. This means we seek $N! - |D_1 \cup \cdots \cup D_N|$. To apply the inclusion and exclusion formula, we must be able to compute the size of intersections of the subsets of D_i. This task is simplified greatly since the intersection of k such subsets is entirely symmetrical (it does not matter for which elements the condition is false, only the number).

If we want to compute the intersection of k such subsets, this means that there are k indices i where $\pi(i) = i$. There are $N - k$ other elements, which can be arranged in $(N - k)!$ ways, so the intersection of these sets have size $(N - k)!$. Since we can choose which k elements that should be fixed in $\binom{N}{k}$ ways, the term in the formula where we compute all k-way intersections will evaluate to $\binom{N}{k}(N - k)! = \frac{N!}{k!}$. Thus, the formula can be simplified to

$$\frac{N!}{1!} - \frac{N!}{2!} + \frac{N!}{3!} - \dots$$

Subtracting this from $N!$ means that there are

$$N!(1 - 1 + \frac{1}{2!} - \frac{1}{3!} + \dots)$$

This gives us a $\Theta(N)$ algorithm to compute the answer.

It is possible to simplify this further, using some insights from calculus. We have that

$$e^{-1} = 1 - 1 + \frac{1}{2} - \frac{1}{3} + \dots$$

Then, we expect that the answer should converge to $\frac{N!}{e}$. As it happens, the answer will *always* be $\frac{N!}{e}$ rounded to the nearest integer.

Exercise 15.15

8 persons are to be seated around a circular table. The company is made up of 4 married couples, where the two members of a couple prefer not to be seated next to each other. How many possible seating arrangements are possible, assuming the cyclic rotations of an arrangement are considered equivalent?

15.6 Invariants

Many problems deal with processes which consist of many steps. During such processes, we are often interested in certain properties that never change. We call such a property an *invariant*. For example, consider the binary search algorithm to find a value in a sorted array. During the execution of the algorithm, we maintain the invariant that the value we are searching for must be contained in some given segment of the array indexed by $[lo, hi)$ at any time. The fact that this property is invariant basically constitutes the entire proof of correctness of binary search. Invariants are tightly attached to greedy algorithms, and is a common tool used in proving correctness of various greedy algorithms. They are also one of the main tools in proving impossibility results (for example when to answer *NO* in decision problems).

Permutation Swaps

Given is a permutation a_i of $\langle 1, 2, ..., N\rangle$. Can you perform exactly K *swaps*, i.e. exchanging pairs of elements of the permutation, to obtain the identity permutation $\langle 1, 2, ..., N\rangle$?

Input

The first line of input contains the size of the permutation $1 \leq N \leq 100\,000$. The next line contains N integers separated, the permutation $a_1, a_2, ..., a_N$.

Output

Output `YES` if it is possible, and `NO` if it is impossible.

First, we need to compute the minimum number of swaps needed.

Assume the cycle decomposition of the permutation consists of C cycles (see 15.2.1 for a reminder of this concept), with lengths $b_1, b_2, .., b_C$. Then, we need at least

$$S = \sum_{i=1}^{C} b_i - 1$$

swaps to return it to the identity permutation, a fact you will be asked to prove in the next section on monovariants. This gives us one necessary condition: $K \geq S$. However, this is not sufficient. A single additional condition is needed

– that S and K have the same parity! To prove this, we will look at the number of *inversions* of a permutation, one of the common invariant properties of permutations.

Given a permutation a_i, we say that the pair (i, j) is an inversion if $i < j$, but $a_i > a_j$. Intuitively, it is the number of pairs of elements that are "out of place" in relation to each other.

3	5	2	1	4	6 inversions
1	5	2	3	4	3 inversions
1	5	3	2	4	4 inversions
1	5	3	4	2	5 inversions
1	2	3	4	5	0 inversions

Figure 15.9: The number of inversions for permutations differing only by a single swap.

If we look at Figure 15.9, where we started out with a permutation and performed a number of swaps (transforming it to the identity permutation), we can spot a simple invariant. The parity of the number of swaps and the number of inversions seems to always be the same. This characterization of a permutation is called *odd* and *even* permutations depending on whether the number of inversions is odd or even. Let us prove that this invariant actually holds.

If this is the case, it is obvious why S and K must have the same parity. Since S is the number of swaps needed to transform the identity permutation to the given permutation, it must have the same parity as the number of inversions. By performing K swaps, K must have the same parity as the number of inversions. As K and S must have the same parity as the number of inversions, they must have the same parity as each other.

To see why these two conditions are sufficient, we can, after performing S swaps to obtain the identity permutation, simply swap two numbers with each other the remaining swaps. This can be done since $K - S$ will be an even number due to their equal parity.

15.7 Monovariants

Another similar tool (sometimes called a *monovariant*) instead define some kind of value $p(v)$ to the state v of each step of the process. We choose p such that it is strictly increasing or decreasing. They are mainly used to prove the finiteness of a process, in which either:

- The value function assume e.g. integer values, and is easily bounded in the direction of monotonicity (e.g. an increasing function would have an upper bound).
- The value function assume can assume any real, but there are only finitely many states the process can be in. In this case, the monovariant is used to prove that the process will never return to a previous state since this would contradict the monotonicity of p.

Let us begin with a famous problem of the first kind.

Majority Graph Bipartitioning

Given is a graph G. Find a bipartition of this graph into parts U and V, such that every vertex v has at most $\frac{|N(v)|}{2}$ neighbors in the same part as v itself.

Input

The first line of input contains integers $1 \le V \le 100$ and $0 \le E \le \frac{V(V-1)}{2}$ – the number of vertices and edges respectively. The next E lines contain two integers $0 \le a \ne b < V$, the zero-indexed numbers of two vertices that are connected by an edge. No pair of vertices will have two edges.

Output

Output N integers, one for each vertex. The i'th integer should be 1 or 2 if the i'th vertex is in the first or the second part of the partition, respectively.

As an example, consider the valid and invalid partitionings in Figure 15.10. The vertices which does not fulfill the neighbor condition are marked in gray.

Problems generally considered greedy algorithms and pure monovariant prob-

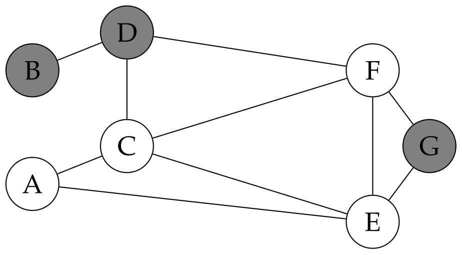

Figure 15.10: An invalid bipartitioning, where vertices B, D, G break the condition.

lems usually differ in that the choice of next action usually has less thought behind it in the monovariant problems. We will often focus not on optimally short sequences of choices as we do with greedy algorithms, but merely finding *any* valid configuration. For example, in the problem above, one might try to construct a greedy algorithm based on for example the degrees of the vertices, which seems reasonable. However, it turns out there is not enough structure in the problem to find any simple greedy algorithm to solve the problem.

Instead, we will attempt to use the most common monovariant attack. Roughly, the process follows these steps:

1. Start with any arbitrary state s.
2. Look for some kind of modification to this state, which is possible if and only if the state is not admissible. Generally, the goal of this modification is to "fix" whatever makes the state inadmissible.
3. Prove that there is some value $p(s)$ that must decrease whenever such a modification is done.
4. Prove that this value cannot decrease infinitely many times.

Using these four rules, we prove the existence of an admissible state. If (and only if) s is not admissible, by step 2 we can perform some specified action on it, which by step 3 will decrease the value $p(s)$. Step 4 usually follows from one of the two value functions discussed previously. Hence, by performing finitely many such actions, we must (by rule 4) reach a state where no such action is possible. This happens only when the state is admissible, meaning such a state must exist. The process might seem a bit abstract, but will become clear once we walk you through the bipartitioning step.

Our algorithm will work as follows. First, consider any bipartition of the graph. Assume that this graph does not fulfill the neighbor condition. Then, there must exist a vertex v which has more than $\frac{|N(v)|}{2}$ vertices in the same part as v itself. Whenever such a vertex exists, we move any of them to the other side of the partition. See Figure 15.11 of the this process.

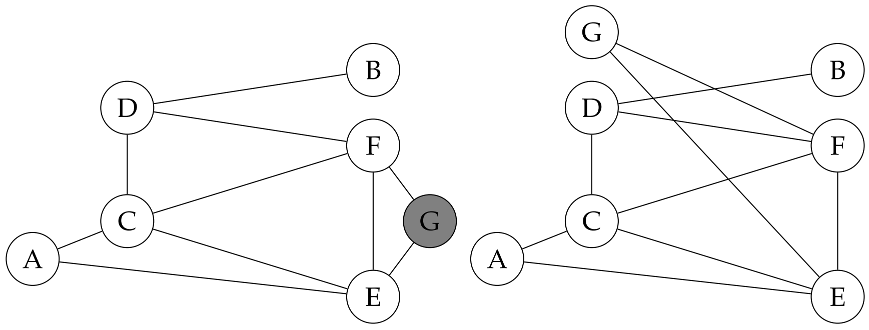

Figure 15.11: Two iterations of the algorithm, which brings the graph to a valid state.

One question remains – why does this move guarantee a finite process? We now have a general framework to prove such things, which suggests that perhaps we should look for a value function $p(s)$ which is either strictly increasing or decreasing as we perform an action. By studying the algorithm in action in Figure 15.11 we might notice that more and more edges tend to go between the two parts. In fact, this number never decreased in our example, and it turns out this is always the case.

If a vertex v has a neighbors in the same part, b neighbors in the other part, and violates the neighbor condition, this means that $a > b$. When we move v to the other part, the b edges from v to its neighbors in the other part will no longer be between the two parts, while the a edges to its neighbors in the same part will. This means the number of edges between the parts will change by $a - b > 0$. Thus, we can choose this as our value function. Since this is an integer function with the obvious upper bound of E, we complete step 4 of our proof technique and can thus conclude the final state must be admissible.

In mathematical problem solving, monovariants are usually used to prove that the an admissible state exists. However, such problems are really algorithmic problems in disguise, since they actually provide an algorithm to construct such an admissible state.

Let us complete our study of monovariants, by also showing a problem using the second value function rule.

Water Pistols

N girls and N boys stand on a large field, with no line going through three different children.

Each girl is equipped with a water pistol, and wants to pick a boy to fire at. While the boys probably will not appreciate being drenched in water, at least the girls are a fair menace – the will only fire at a single boy each. Unfortunately, it may be the case that two girls choose which boys to fire at in such a way that the water from their pistols will cross at some point. If this happens, they will cancel each other out, never hitting their targets.

Help the girls choose which boys to fire at, in such a way that no two girls fire at the same boy, and the water fired by two girls will not cross.

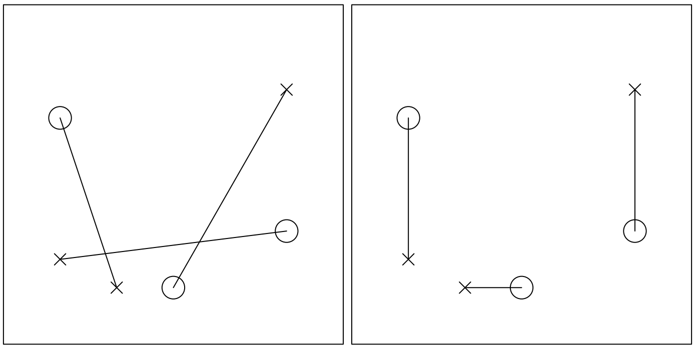

Figure 15.12: An assignment where some beams intersect (left), and an assignment where no beams intersect (right).

Input

The first line contains the integer $N \leq 200$. The next N lines contain two real numbers $-10^6 \leq x, y \leq 10^6$, separated by a space. Each line

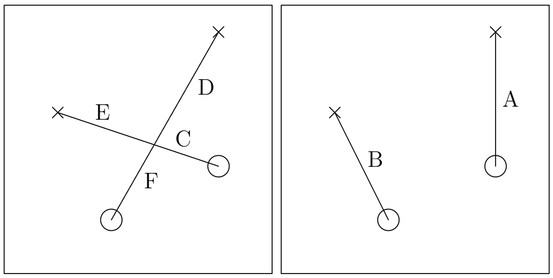

Figure 15.13: Swapping the targets of two intersecting beams.

is the coordinate (x, y) of a girl. The next and final N lines contain the coordinates of the boys, in the same format.

Output

Output N lines. The i'th line should contain the zero-indexed number of the boy which the i'th girl should fire at.

After seeing the solution to the previous problem, the solution should not come as a surprise. We start by randomly assigning the girls to one boy each, with no two girls shooting at he same boy. If this assignment contains two girls firing water beams which cross, we simply swap their targets.

Unless you are geometrically minded, it may be hard to figure out an appropriate value function. The naive value function of counting the current number of water beams crossing unfortunately fails – and might even increase after a move.

Instead, let us look closer at what happens when we switch the targets of two girls. In Figure 15.13, we see the before and after of such an example, as well as the two situations interposed. If we consider the sum of the two lengths of the water beams before the swap ($(C + D) + (E + F)$) versus the lengths after the swap ($A + B$), we see that the latter must be less than the first. Indeed, we have $A < C+D$ and $B < E+F$ by the triangle inequality, which by summing the two inequalities give the desired result. Thus the sum of all water beam lengths will decrease whenever we perform such a move. As students of algorithmics, we can make the additional note that this means the minimum-cost matching of the complete bipartite graph of girls and boys, with edges given as cost the distance between a particular girl and boy, is a valid assignment. If this was not the case, we would be able to swap two targets and decrease the cost of the matching, contradicting the assumption that it was minimum-cost. Thus, this rather mathematical proof actually ended up giving us a very simple reduction to min-cost matching.

Exercise 15.16 — Kattis Exercise

Army Division – armydivision

Bread Sorting – breadsorting

15.8 Chapter Notes

Chapter 16

Number Theory

Number theory is the study of certain properties of integers. It makes an occasional appearance within algorithmic problem solving, in the form of its subfield *computational number theory*. It is within number theory topics such as divisibility and prime numbers belong.

16.1 Divisibility

All of the number theory in this chapter relate to a single property of integers, divisibility.

Definition 16.1 — Divisibility
An integer n is ***divisible*** by an integer d if there is another integer q such that $n = dq$. We also say that d is a ***divisor*** of n.

We denote this fact with $d \mid n$.

Dividing both sides of the equality $n = dq$ with d gives us an almost equivalent definition, namely that $\frac{n}{d}$ is an integer. The difference is that the first definition admit the divisibility by 0 with 0, while the second one does not (zero division is undefined). When we speak of the divisors of a number in most contexts (as in Example 16.1), we will generally consider only the non-negative divisors. Since d is a divisor of n if and only if $-d$ is a divisor of n, this sloppiness lose little information.

Example 16.1 — Divisors of 12

The number 12 has 6 divisors – 1 ($1 \cdot 12 = 12$), 2 ($2 \cdot 6 = 12$), 3, ($3 \cdot 4 = 12$), 4 ($4 \cdot 3 = 12$), 6 ($6 \cdot 2 = 12$) and 12 ($12 \cdot 1 = 12$).

12 is not divisible by e.g. 5 – we have $\frac{12}{5} = 2 + \frac{2}{5}$, which is clearly not an integer.

Exercise 16.1

Determine the divisors of 18.

The concept of divisibility raises many questions. First and foremost – how do we check if a number is divisible by another? This question has one short and one long answer. For small numbers – those that fit inside the native integer types of a language – checking for divisibility is as simple as using the modulo operator (%) of your favorite programming language – n is divisible by d if and only if $n \bmod d = 0$. The situation is not as simple for large numbers. Some programming languages, such as Java and Python, have built-in support for dealing with large integers, but e.g. C++ does not. In Section 16.4 on modular arithmetic, we discuss the implementation of the modulo operator on large integers.

Secondly, how do we compute the divisors of a number? Every integer has at least two particular divisors called the ***trivial divisors***, namely 1 and n itself. If we exclude the divisor n, we get the ***proper divisors***. To find the remaining divisors, we can use the fact that any divisor d of n must satisfy $|d| \leq |n|$. This means that we can limit ourselves to testing whether the integers between 1 and n are divisors of n, a $\Theta(n)$ algorithm. We can do a bit better though.

Almost Perfect

Baylor Competitive Learning course – David Sturgill

A positive integer p is called a perfect number if all the proper divisors of p sum to p exactly. Perfect numbers are rare; only 10 of them are known. Perhaps the definition of perfection is a little too strict. Instead, we will consider numbers that we'll call almost perfect. A positive integer p is almost perfect if the proper divisors of p sum to a value that differs from p by no more than two.

Input

Input consists of a sequence of up to 500 integers, one per line. Each integer is in the range 2 to 10^9 (inclusive).

Output

For each input value, output the same value and then one of the following: "perfect" (if the number is perfect), "almost perfect" (if it is almost perfect but not perfect), or "not perfect" (otherwise).

In this problem, computing the divisors of the numbers of the input sequence would be way too slow, requiring upwards of 10^{11} operations. Hidden in Example 16.1 lies the key insight to speeding this up. It seems that whenever we had a divisor d, we were immediately given another divisor q. For example, when claiming 3 was a divisor of 12 since $3 \cdot 4 = 12$, we found another divisor, 4. This should not be a surprise, since our definition of divisibility (Definition 16.1)– the existence of the integer q in $n = dq$ – is symmetric in d and q, meaning divisors come in pairs $(d, \frac{n}{d})$.

Exercise 16.2

Prove that an integer has an odd number of divisors if and only if it is a perfect square (except 0, which has an infinite number of divisors).

Since divisors come in pairs, we can limit ourselves to finding one member of each such pair. Furthermore, one of the elements in each such pair must be bounded by $\sqrt{n}$. Otherwise, we would have that $n = d \cdot \frac{n}{d} > \sqrt{n} \cdot \sqrt{n} = n$, a contradiction (again, except for 0, which has $\frac{0}{d} = 0$). This limit helps us reduce the time it takes to find the divisors of a number to $\Theta(\sqrt{N})$, which allows us to solve the problem. You can see the pseudo code for this in Algorithm 16.1

Algorithm 16.1: Almost Perfect

```
procedure DIVISORS(N)
    divisors ← new list
    for i from 1 up to $i^2 \leq N$ do
        if $N \bmod i = 0$ then
            divisors.add(i)
            if $i \neq N/i$ then
                divisors.add($\frac{N}{i}$)
    return divisors

procedure ALMOSTPERFECT(N)
    divSum ← 0
    for $d \in$ Divisors(N) do
        if $d \neq N$ then
            divSum ← divSum + d
    if divSum = N then
        output "perfect"
    else if $|divSum - N| \leq 2$ then
        output "almost perfect"
    else
        output "not perfect"
```

This also happens to give us some help in answering our next question, regarding the plurality of divisors. The above result gives us an upper bound of $2\sqrt{n}$ divisors of an integer n. We can do a little better, with $O(n^{\frac{1}{3}})$ being a commonly used bound for the number of divisors when dealing with integers which fit in the native integer types.[1] For example, the maximal number of divisors of a number less than 10^3 is 32, 10^6 is 240, 10^9 is 1 344, 10^{18} is 103 680.[2]

A bound we will find more useful when solving problems concerns the *average* number of divisors of the integers between 1 and n.

[1] In reality, the maximal number of divisors of the interval $[1, n]$ grows sub-polynomially, i.e., as $O(n^{\epsilon})$ for *every* $\epsilon > 0$.

[2] Sequence A066150 from OEIS: `http://oeis.org/A066150`.

Theorem 16.1 Let $d(i)$ be the number of divisors of i. Then,

$$\sum_{i=1}^{n} d(i) \approx n \ln n$$

Proof. There are approximately $\frac{n}{i}$ integers between 1 and n divisible by i, since every i'th integer is divisible by i Thus, the number of divisors of all those integers is bounded by

$$\sum_{j=1}^{n} \frac{n}{j} = n \sum_{j=1}^{n} \frac{1}{j} \approx n \ln n$$

□

This proof also suggest a way to compute the divisors of all the integers $1, 2, ..., n$ in $\Theta(n \ln n)$ time. For each integer i, we find all the numbers divisible by i (in $\Theta(\frac{n}{i})$ time), which are $0i, 1i, 2i, \dots \lceil \frac{n}{i} \rceil i$. This is an extension of the algorithm commonly known as the ***Sieve of Eratosthenes***, an algorithm to find the objects which are our next topic of study – prime numbers.

Exercise 16.3 — Kattis Exercises

Dividing Sequence – sequence

16.2 Prime Numbers

From the concept of divisibility comes the building blocks of the integers, the famous *prime numbers*. With divisibility, we got factorizations. For example, given the number 12, we could factor it as $2 \cdot 6$, or $3 \cdot 4$, or even $2 \cdot 2 \cdot 3$. This last factorization is special, in that no matter how hard we try, it cannot be factored further. It consists only of prime numbers.

Definition 16.2 — Prime Number
An integer $p \geq 2$ is called a ***prime number*** if its only positive divisors are 1

and p.

The numbers that are *not* prime numbers are called ***composite numbers***. There are an infinite number of primes. This be proven by a simple proof by contradiction. If $p_1, p_2, ..., p_q$ are the only primes, then $P = p_1 p_2 \dots p_q + 1$ is not divisible by any prime number (and by extension has no divisors but the trivial ones), so it is not composite. However, P is larger than any prime, so it is not a prime number either, a contradiction.

Example 16.2 The first 10 prime numbers are $2, 3, 5, 7, 11, 13, 17, 19, 23, 29$. Which is the next one?

Since the prime numbers have no other divisors besides the trivial ones, a factorization consisting only of prime numbers is special.

Definition 16.3 — Prime Factorization
The ***prime factorization*** of a positive integer n is a factorization of the form $p_1^{e_1} \cdot p_2^{e_2} \cdot \dots \cdot p_k^{e_k}$, where p_i are all distinct primes. This factorization is unique, except for a reordering of the p_i.

Example 16.3 The prime factorization of 228 is $2 \cdot 2 \cdot 3 \cdot 19$.

A List Game

Spotify Challenge 2010 – Per Austrin

You are playing the following simple game with a friend:

1. The first player picks a positive integer X.
2. The second player gives a list of k positive integers $Y_1, \dots, Y_k$ such that
$$(Y_1 + 1)(Y_2 + 1) \cdots (Y_k + 1) = X$$
and gets k points.

Write a program that plays the second player.

Input

The input consists of a single integer X satisfying $10^3 \leq X \leq 10^9$, giving the number picked by the first player.

Output

Write a single integer k, giving the number of points obtained by the second player, assuming she plays as good as possible.

The problem seeks the factorization of X that contains the largest number of factors, where every factor is at least 2. This factorization must in fact be the prime factorization of X, which we will prove by contradiction. Assume that the optimal list of integers $Y_1, \ldots, Y_k$ contains a number Y_i that is composite. In this case, it can be further factored into $Y_i = ab$ with $a, b > 1$. Replacing Y_i with the numbers a and b will keep the product of the list invariant (since $Y_i = ab$), but extend the length of the list by 1, thus giving a higher-scoring sequence. The only case when this is impossible is if all the Y_i are primes, so the list we seek must indeed be the prime factorization of X.

This begs the question, how do we compute the prime factorization of a number? Mainly two different algorithms are used when computing prime factorizations: trial division and the Sieve of Eratosthenes[3]. In computing the prime factorization of a few, large numbers, trial division is used. It runs in $O(\sqrt{N})$ time, and use the same insight we used in the improved algorithm to compute the divisors of an algorithm. Since any composite number N must have a divisor less than $\sqrt{N}$, it must also have a prime divisor less than $\sqrt{N}$. Implementing this is straightforward.

The other algorithm is used to factor every number in a large interval.

Product Divisors

Given a sequence of integers $a_1, a_2, \ldots a_n$, compute the number of divisors of $A = \prod_{i=1}^{n} a_i$.

Input

Input starts with an integer $0 \leq n \leq 1\,000\,000$, the length of the sequence

[3]Many more exist, but are too complicated to be used in problem solving context, although they are very much in use in real-life situations.

a_i. The next line contains the numbers $1 \leq a_1, \ldots, a_n \leq 10^6$.

Output

Output a single integer – the number of divisors of n. Since this number can be very large, output it modulo $10^9 + 7$.

Let A have the prime factorization $A = p_1^{e_1} \cdot p_2^{e_2} \cdot \cdots \cdot p_k^{e_k}$. A divisor of A must be of the form $d = p_1^{e_1'} \cdot p_2^{e_2'} \cdot \cdots \cdot p_k^{e_k'}$, where $0 \leq e_i' \leq e_i$. This can be proven using the uniqueness of the prime factorization, and the fact that $A = dq$ for some integer q. More importantly, *any* number of this form is a divisor of A, by the same cancellation argument used when proving the uniqueness of the prime factorization.

With this in hand, we apply a simple combinatorial argument to count the number of divisors of A. Each number e_i' can take any integer value between 0 and e_i to fulfill the conditions needed to make d a divisor of A. This gives us $e_i + 1$ choices for the value of e_i'. Since each e_i' is independent, there are a total of $(e_1 + 1)(e_2 + 1) \ldots (e_k + 1)$ numbers of this form, and thus divisors of A. We are left with the problem of determining the prime factorization of A. Essentially, this is tantamount to computing the prime factorization of *every* integer between 1 and 10^6. Once this is done, we can go through the sequence a_i and tally up all primes in their factorization. Since an integer m has at most $\log_2 m$ prime factors, this step is bounded by approximately $n \log_2 10^6$ operations. This is implemented in Algorithm 16.2.

Algorithm 16.2: Product Divisors

```
procedure ProductDivisors(sequence $A$)
    list of lists *factorizations* ← $\mathtt{factorInterval}(10^6 + 1)$
    map *counts* ← $\mathtt{new\ map}$
    for each $a$ in $A$ do
        for each $p$ in *factorizations*[$a$] do
            *counts*[$p$] ← *counts*[$p$] + 1
    *ans* ← 1
    for each $(\mathtt{key}, \mathtt{value})$ in *counts* do
        *ans* ← $(ans \cdot (\mathtt{value} + 1)) \bmod (10^9 + 7)$
    return *ans*
```

As of now, the crucial step of factoring all integers in $[1..10^6]$ remains. This is the purpose of the Sieve of Eratosthenes. We have already seen the basic idea when computing the divisors of all numbers in the interval $[1...n]$ in Section 16.1. Extending this to factoring is only a matter of restricting the algorithm to finding prime divisors (Algorithm 16.3).

Algorithm 16.3: Sieve of Eratosthenes

```
procedure PRIMESIEVE(limit $N$)
    list nums ← $\mathtt{new}$ $\mathtt{list}[N]$
    for $i$ from 1 to $N-1$ do
        nums[$i$] ← $i$
    list of lists factorizations ← $\mathtt{new}$ list of lists[$N$]
    for $i$ from 2 to $i^2 \leq N$ do
        if nums[$i$]! $= i$ then
            for $j \in \{i \cdot i, i(i+1), i(i+2), ...\}$ up to $N-1$ do
                while $\mathtt{nums}[j]$ mod $i = 0$ do
                    factorizations[$j$].$\mathtt{add}(i)$
                    nums[$j$] $=$ nums[$j$]$/i$
    return factors
```

The complexity of this procedure is a bit tricky to analyze. The important part of the sieve is the inner loop, which computes the actual factors. Let us count the number of times a prime p is pushed in this loop. First of all, every p'th integer is divisible by p, which totals $\frac{n}{p}$ iterations. However, every p^2'th integer integer is divisible by p yet again, contributing an additional $\frac{n}{p^2}$ iterations, and so on. Summing this over every p which is used in the sieve gives us the bound

$$\sum_{p \leq \sqrt{n}} \left(\frac{n}{p} + \frac{n}{p^2} + \frac{n}{p^3} + ... \right) = n \sum_{p \leq \sqrt{n}} \left(\frac{1}{p} + \frac{1}{p^2} + \frac{1}{p^3} + ... \right)$$

Using the formula for the sum of a geometric series ($\frac{1}{p} + \frac{1}{p^2} + ... = \frac{p}{p-1}$) gives us the simplification

$$n \sum_{p \leq \sqrt{n}} \frac{1}{p-1} = \Theta\left(n \sum_{p \leq \sqrt{n}} \frac{1}{p} \right)$$

This last sum is out of reach to estimate with our current tools. It turns out that $\sum_{p \le n} \frac{1}{p} = O(\ln \ln n)$. With this, the final complexity becomes a simple $O(n \ln \ln \sqrt{n}) = O(n \ln \ln n)$.

It is not uncommon for an algorithm to include in its complexity the number of primes up to a certain limit n. This function is known as $\pi(n)$, the prime counting function. We have $\pi(10^3) = 168, \pi(10^6) = 78\,498, \pi(10^9) \approx 51\,000\,000$. In general, $\pi(n) \approx \frac{n}{\ln n}$ for large n.

Exercise 16.4 — Kattis Exercises

Prime Sieve – primesieve

Happy Happy Prime Prime – happyprime

Prime Path – primepathc

Perfect Pth Powers – perfectpowers

Factovisors – factovisors

Divisors – divisors

16.3 The Euclidean Algorithm

The Euclidean algorithm is one of the oldest known algorithms, dating back to Greek mathematician Euclid who wrote of it in his mathematical treatise *Elements*. It regards those numbers which are divisors two different integers, with an extension capable of solving integer equations of the form $ax + by = c$.

Definition 16.4 We call an integer d dividing both of the integers a and b a ***common divisor*** of a and b.

The greatest such integer is called the ***greatest common divisor***, or *GCD* of a and b. This number is denoted (a, b).

As always, we ask ourselves – how do we compute it?

Greatest Common Divisor

Given to integers a and b, compute (a, b).

We already know of an $O(\sqrt{a} + \sqrt{b})$ algorithm to compute (a, b), namely to enumerate *all* divisors of a and b. Two simple identities are key to the much faster Euclidean algorithm.

$$(a, 0) = |a| \tag{16.1}$$

$$(a, b) = (a - b, b) \tag{16.2}$$

Identity 16.1 is obvious. An integer a cannot have a larger divisor than $|a|$, and this is certainly a divisor of a. Identity 16.2 needs a bit more work. We can prove their equality by proving an even stronger result – that *all* common divisors of a and b are also common divisors of a and $b - a$. Assume d is a common divisor of a and b, so that $a = da'$ and $b = db'$ for integers a', b'. Then $b - a = db' - da' = d(b' - a')$, with $b' - a'$ being an integer, is sufficient for d also being a divisor of $b - a$. Hence the divisors of a and b are also divisors of a and $b - a$. In particular, their largest common divisor is the same. The application of these identities yield a recursive solution to the problem. If we wish to compute (a, b) where a, b are positive and $a > b$, we reduce the problem to a smaller one by instead computing (a, b), we compute $(a - b, b)$. This gives us a smaller problem, in the sense that $a + b$ decrease. Since both a and b are non-negative, this means we must at some point arrive at the situation where either a or b are 0. In this case, we use the base case that is Identity 16.1.

One simple but important step remains before the algorithm is useful. Note how computing $(10^9, 1)$ requires about 10^9 steps right now, since we will do the reductions $(10^9 - 1, 1), (10^9 - 2, 1), (10^9 - 3, 1)$... The fix is easy – the repeated application of subtraction of a number b from a while $a > b$ is exactly the modulo operation, meaning

$$(a, b) = (a \bmod b, b)$$

This last piece of our Euclidean puzzle complete our algorithm, and gives us a remarkably short algorithm, as seen in Algorithm 16.4.

Algorithm 16.4: Greatest Common Divisor

```
procedure GCD($A$, $B$)
    if $B = 0$ then
        return $A$
    return GCD($B$, $A \bmod B$)
```

Competitive Tip

The Euclidean algorithm exists as the built-in function `__gcd(a, b)` in C++.

Whenever dealing with divisors in a problem, the greatest common divisor may be useful. This is the case in the next problem, from the Croatian high school olympiad.

Granica

Croatian Open Competition in Informatics 2007/2008, Contest #6

Given integers $a_1, a_2, ..., a_n$, find all those numbers d such that upon division by d, all of the numbers a_i leave the same remainder.

Input

The first line contains the integer $2 \le n \le 100$, the length of the sequence a_i. The second line contains the integers n integers $1 \le a_1, a_2, \ldots, a_n \le 10^9$.

Output

Output all such integers d, separated by spaces.

What does it mean for two numbers a_i and a_j to have the same remainder when dividing by d? Letting this remainder be r we can write $a_i = dn + r$ and $a_j = dm + r$ for integers n and m. Thus, $a_i - a_j = d(n - m)$ so that d is divisor of $a_i - a_j$! This gives us a necessary condition for our numbers d. Is it sufficient? If $a_i = dn + r$ and $a_j = dm + r'$, we have $a_i - a_j = d(n - m) + (r - r')$. Since d is a divisor of $a_i - a_j$ it must be a divisor of $d(n - m) + (r - r')$ too, meaning $r - r' = 0$ so that $r = r'$ and both remainders were the same. The question then is how we compute

$$\gcd_{1 \le i < j \le n} a_i - a_j$$

which seek the greatest common divisor of many rather than just two numbers.

To our rescue comes the prime factor interpretation of divisors, namely that a divisor of a number

$$n = p_1^{e_1} \cdots p_k^{e_k}$$

is of the form

$$d = p_1^{e'_1} \cdots p_k^{e'_k}$$

where $0 \le e'_i \le e_i$. Then, the requirement for d to be a **common** divisor of n and another number

$$m = p_1^{f_1} \cdots p_k^{f_1}$$

is that $0 \le e'_i \le \min(f_i, e_i)$, with $e'_i = \min(f_i, e_i)$ giving us the GCD.

Using this interpretation of the GCD, we can extend the result can be extended to finding the GCD d of a sequence $b_1, b_2, \ldots$ Consider any prime p, such that $p^{q_i} \parallel b_i$. Then, we must have $p^{\min(q_1, q_2, \ldots)} \parallel d$. This suggests the recursion formula $d = \gcd(b_1, b_2, \ldots) = \gcd(b_1, \gcd(b_2, \ldots))$.

Algorithm 16.5: Greatest Common Divisor of Several Integers

```
procedure MultiGCD(sequence $A$)
    $gcd \leftarrow 0$
    for each $a \in A$ do
        $gcd \leftarrow \mathrm{GCD}(gcd, a)$
    return $gcd$
```

We only need one more insight to solve the problem, namely that the common divisors d of a and b are exactly the divisors of (a, b).

A related concept is given if we instead of taking the minimum of prime factors of two numbers take the maximum.

Definition 16.5 — Least Common Multiple
The ***least common multiple*** of integers a and b is the smallest integer m such that $a \mid m$ and $b \mid m$.

The computation of the LCM is basically the same as for the GCD.

A multiple d of an integer a of the form

$$a = p_1^{e_1} \cdots p_k^{e_k}$$

must be of the form

$$d = p_1^{e'_1} \cdots p_k^{e'_k}$$

where $e_i \le e'_i$.

Thus, if d is to be a common multiple of a and

$$b = p_1^{f_1} \cdots p_k^{f_1}$$

it must be that $\max(f_i, e_i) \le e'_i$, with $e'_i = \max(f_i, e_i)$ giving us the LCM. Since $\max(e_i, f_i) + \min(e_i, f_i) = e_i \cdot + f_i$, we must have that $\text{lcm}(a, b) \cdot \gcd(a, b) = ab$. This gives us the formula $\text{lcm}(a, b) = \frac{a}{\gcd(a,b)} b$ to compute the LCM. The order of operations is chosen to avoid overflows in computing the product ab.

Since max is associative just like min, the LCM operation is too, meaning

$$\text{lcm}(a, b, c, \dots) = \text{lcm}(a, \text{lcm}(b, \text{lcm}(c, \dots)))$$

Next up is the ***extended Euclidean algorithm***.

Diophantine Equation

Given integers a, b, c, find an integer solution x, y to

$$ax + by = (a, b)$$

First of all, it is not obvious such an integer solution exists. This is the case however, which we will prove constructively thus gaining an algorithm to find such a solution at the same time. The trick lies in the exact same identities used when we formulated the Euclidean algorithm. Since $(a, 0) = a$, the case $b = 0$ gives us $ax = (a, b) = a$ with the obvious solution $x = 1, y = 0$. Furthermore, we have $(a, b) = (b, a \bmod b)$. Assume we could compute a solution to $bx + (a \bmod b)y = (b, a \bmod b)$. Some rearrangement of this gives us

$$\begin{aligned} bx + (a \bmod b)y &= (b, a \bmod b) \\ bx + (a - \lfloor \frac{a}{b} \rfloor b)y &= (b, a \bmod b) \\ b(x - \lfloor \frac{a}{b} \rfloor y) + ay &= (b, a \bmod b) \\ ay + b(x - \lfloor \frac{a}{b} \rfloor y)x &= (b, a \bmod b) \\ ay + b(x - \lfloor \frac{a}{b} \rfloor y)x &= (a, b) \end{aligned}$$

meaning $(y, x - \lfloor \frac{a}{b} \rfloor y)$ would be a solution to the equation we are actually interested in.

Given the solution $[x, y]$ to the equation with coefficients $[b, a \bmod b]$ we thus get the solution $[y, x - \lfloor \frac{a}{b} \rfloor y]$ to the equation with coefficients $[a, b]$. The transformation $[b, a \bmod b] \leftrightarrow [a, b]$ happen to be the key step in the Euclidean algorithm. This suggests a recursive solution, where we first perform the ordinary Euclidean algorithm to find (a, b) and obtain the solution $[1, 0]$ to the equation $(a, b)x + 0y = (a, b)$ and then use the above trick to iteratively construct a solution to $ax + by = (a, b)$.

Example 16.4 — Extended Euclidean algorithm

Consider the equation $15x + 11y = 1$. Performing the Euclidean algorithm on these numbers we find that

$$(15, 11) = (11, 15 \bmod 11) =$$

$$(11, 4) = (4, 11 \bmod 4) =$$

$$(4, 3) = (3, 4 \bmod 3) =$$

$$(3, 1) = (1, 3 \bmod 1) =$$

$$(1, 0) = 1$$

Originally, we have the solution $[1, 0]$ to the equation with coefficients $[1, 0]$:

$$1 \cdot 1 + 0 \cdot 0 = (1, 0)$$

Using the transformation we derived gives us the solution $[0, 1 - \lfloor \frac{3}{1} 0 \rfloor] = [0, 1]$ to the equation with coefficients $[3, 1]$:

$$3 \cdot 0 + 1 \cdot 1 = (3, 1)$$

The next application gives us the solution $[1, 0 - \lfloor \frac{4}{3} \rfloor 1] = [1, -1]$ to $[4, 3]$.

$$4 \cdot 1 + 3 \cdot (-1) = (4, 3)$$

$[4, 3] \to [-1, 1 - \lfloor \frac{11}{4} \rfloor (-1)] = [-1, 3]$ which gives us

$$11 \cdot (-1) + 4 \cdot 3 = (11, 4)$$

Finally, $[-1, 3] \to [3, -1 - \lfloor \frac{15}{11} \rfloor 3] = [3, -4]$, the solution we sought

$$15 \cdot 3 + 11 \cdot (-4) = (15, 11)$$

Exercise 16.5

Find an integer solution to the equation $24x + 52y = 2$.

This gives us a single solution, but can we find all solutions? First, assume a and b are co-prime. Then, given two solutions

$$ax_1 + by_1 = 1$$

$$ax_2 + by_2 = 1$$

a simple subtraction gives us that

$$a(x_1 - x_2) + b(y_1 - y_2) = 0$$

$$a(x_1 - x_2) = b(y_2 - y_1)$$

Since a and b are co-prime, we have that

$$b \mid x_1 - x_2$$

Thus means $x_2 = x_1 + kb$ for some k. Inserting this gives us

$$a(x_1 - (x_1 + kb)) = b(y_2 - y_1)$$
$$-akb = b(y_2 - y_1)$$
$$-ak = y_2 - y_1$$
$$y_1 - ak = y_2$$

Thus, any solution must be of the form

$$(x_1 + kb, y_1 - ka) \text{ for } k \in \mathbb{Z}$$

That these are indeed solutions to the original equation can be verified by substituting x and y for these values. This result is called ***Bezout's identity***.

16.4 Modular Arithmetic

When first learning division, one is often introduced to the concept of *remainders*. For example, when diving 7 by 3, you would get "2 with a remainder of 1". In general, when dividing a number a with a number n, you would get a ***quotient*** q and a ***remainder*** r. These numbers would satisfy the identity $a = nq + r$, with $0 \leq r < b$.

Example 16.5 — Division with remainders
Consider division (with remainders) by 4 of the numbers $0, \dots, 6$ We have that

$$\frac{0}{4} = 0, \text{remainder } 0$$
$$\frac{1}{4} = 0, \text{remainder } 1$$
$$\frac{2}{4} = 0, \text{remainder } 2$$
$$\frac{3}{4} = 0, \text{remainder } 3$$
$$\frac{4}{4} = 1, \text{remainder } 0$$

$$\frac{5}{4} = 1, \text{remainder } 1$$

$$\frac{6}{4} = 1, \text{remainder } 2$$

Note how the remainder always increase by 1 when the nominator increased. As you might remember from Chapter 2 on C++ (or from your favorite programming language), there is an operator which compute this remainder called the *modulo operator*. Modular arithmetic is then the computation on numbers, where every number is taken modulo some integer n. Under such a scheme, we have that e.g. 3 and 7 are basically the same if computing modulo 4, since $3 \bmod 4 = 3 = 7 \bmod 4$. This concept, where numbers with the same remainder are treated as if they are equal is called *congruence*.

Definition 16.6 — Congruence

If a and b have the same remainder when divided by n, we say that a and b are ***congruent modulo*** n, written

$$a \equiv b \pmod{n}$$

An equivalent and in certain applications more useful definition is that $a \equiv b \pmod{n}$ if and only if $n \mid a - b$.

Exercise 16.6

What does it mean for a number a to be congruent to 0 modulo n?

When counting modulo something, the laws of addition and multiplication are somewhat altered:

+	**0**	**1**	**2**
0	0	1	2
1	1	2	$3 \equiv 0$
2	2	$3 \equiv 0$	$4 \equiv 1$

*	**0**	**1**	**2**
0	0	0	0
1	0	1	2
2	0	2	$4 \equiv 1$

When we wish to perform arithmetic of this form, we use the ***integers modulo*** n rather than the ordinary integers. These has a special set notation as well: $\mathbb{Z}_n$.

While addition and multiplication is quite natural (i.e. performing the operation as usual and then taking the result modulo n), division is a more complicated story. For real numbers, the ***inverse*** x^{-1} of a number x is defined as the number which satisfy the equation $xx^{-1} = 1$. For example, the inverse of 4 is 0.25, since $4 \cdot 0.25 = 1$. The division $\frac{a}{b}$ is then simply a multiplied with the inverse of b. The same definition is applicable to modular arithmetic:

Definition 16.7 — Modular Inverse
The ***modular inverse*** of a modulo n is the integer a^{-1} such that $aa^{-1} \equiv 1 \pmod{n}$, if such an integer exists.

Considering our multiplication table of $\mathbb{Z}_3$, we see that 0 has no inverse and 1 is its own inverse (just as with the real numbers). However, since $2 \cdot 2 = 4 \equiv 1 \pmod{3}$, 2 is actually its own inverse. If we instead consider multiplication in $\mathbb{Z}_4$, the situation is quite different.

*	**0**	**1**	**2**	**3**
0	0	0	0	0
1	0	1	2	3
2	0	2	0	2
3	0	3	2	1

Now, 2 does not even have an inverse! To determine when an inverse exists – and if so, computing the inverse – we will make use of the extended Euclidean algorithm. If $aa^{-1} \equiv 1 \pmod{n}$, we have $n \mid aa^{-1} - 1$, meaning $aa^{-1} - 1 = nx$ for some integer x. Rearranging this equation gives us $aa^{-1} - nx = 1$. We know from Section 16.3 that this has a solution if and only if $(a, n) = 1$. In this case, we can use the extended Euclidean algorithm to compute a^{-1}. Note that be Bezout's identity, a^{-1} is actually unique modulo n.

Just like the reals, modular arithmetic has a cancellation law regarding

Theorem 16.2 Assume $a \perp n$. Then $ab \equiv ac \pmod{n}$ implies $b \equiv c \pmod{n}$.

Proof. Since $a \perp n$, there is a number a^{-1} such that $aa^{-1} \equiv 1 \pmod{n}$.

$$ab \equiv ac \pmod{n}$$

with a^{-1} results in

$$aa^{-1}b \equiv aa^{-1}c \pmod{n}$$

Simplifying aa^{-1} gives us

$$b \equiv c \pmod{n}$$

□

Another common modular operation is exponentiation, i.e. computing $a^m \pmod{n}$. While this can be computed easily in $\Theta(m)$, we can actually do better using a method called ***exponentiation by squaring***. It is essentially based on the recursion

$$a^m \bmod n = \begin{cases} 1 \bmod n & \text{if } m = 0 \\ a \cdot (a^{m-1} \bmod n) \bmod n & \text{if } m \text{ odd} \\ (a^{\frac{m}{2}} \bmod n)^2 \bmod n & \text{if } m \text{ even} \end{cases}$$

This procedure is clearly $\Theta(\log_2 m)$, since applying the recursive formula for even numbers halve the m to be computed, while applying it an odd number will first make it even and then halve it in the next iteration. It is very important that $a^{\frac{m}{2}} \bmod n$ is computed only once, even though it is squared! Computing it twice causes the complexity to degrade to $\Theta(m)$ again.

16.5 Chinese Remainder Theorem

The Chinese Remainder Theorem is probably the most useful theorem in algorithmic problem solving. It gives us a way of solving certain systems of linear equations.

Theorem 16.3 — Chinese Remainder Theorem
Given a system of equations

$$\begin{aligned} x &\equiv a_1 \pmod{m_1} \\ x &\equiv a_2 \pmod{m_2} \\ \dots \\ x &\equiv a_m \pmod{m_n} \end{aligned}$$

where the numbers $m_1, \dots, m_n$ are pairwise relatively prime, there is a *unique* integer $x \pmod{\prod_{i=1}^{n} m_i}$ that satisfy such a system.

Proof. We will prove the theorem inductively. The theorem is clearly true for $n = 1$, with the unique solution $x = a_1$. Now, consider the two equations

$$\begin{aligned} x &\equiv a_1 \pmod{m_1} \\ x &\equiv a_2 \pmod{m_2} \end{aligned}$$

Let $x = a_1 \cdot m_2 \cdot (m_2^{-1} \bmod m_1) + a_2 \cdot m_1 \cdot (m_1^{-1} \bmod m_2)$, where $m_1^{-1} \bmod m_2$ is taken to be a modular inverse of m_1 modulo m_2. These inverses exist, since $m_1 \perp m_2$ by assumption. We then have that $x = a_1 \cdot m_2 \cdot (m_2^{-1} \bmod m_1) + a_2 \cdot m_1 \cdot (m_1^{-1} \bmod m_2) \equiv a_1 \cdot m_2 \cdot (m_2^{-1} \bmod m_1) \equiv a_i \pmod{m_1}$.

Since a solution exist for every a_1, a_2, this solution must be unique by the pigeonhole principle – there are $m_1 \cdot m_2$ possible values for a_1, a_2, and $m_1 \cdot m_2$ possible values for x. Thus, the theorem is also true for $n = 2$.

Assume the theorem is true for $k - 1$ equations. Then, we can replace the equations

$$\begin{aligned} x &\equiv a_1 \pmod{m_1} \\ x &\equiv a_2 \pmod{m_2} \end{aligned}$$

with another equation

$$x \equiv x* \pmod{m_1 m_2}$$

where $x*$ is the solution to the first two equations. We just proved those two equations are equivalent with regards to x. This reduces the number of equations to $k - 1$, which by assumption the theorem holds for. Thus, it also holds for k equations. □

Note that the theorem used an explicit construction of the solution, allowing us to find what the unique solution to such a system is.

Radar

KTH Challenge 2014

We say that an integer z is within distance y of an integer x modulo an integer m if

$$z \equiv x + t \pmod{m}$$

where $|t| \leq y$.

Find the smallest non-negative integer z such that it is:

- within distance y_1 of x_1 modulo m_1
- within distance y_2 of x_2 modulo m_2
- within distance y_3 of x_3 modulo m_3

Input

The integers $0 \leq m_1, m_2, m_3 \leq 10^6$. The integers $0 \leq x_1, x_2, x_3 \leq 10^6$. The integers $0 \leq y_1, y_2, y_3 \leq 300$.

Output

The integer z.

The problem gives rise to three linear equations of the form

$$z \equiv x_i + t_i \pmod{m_i}$$

where $-y_i \leq t_i \leq y_i$. If we fix all the variables t_i, the problem reduces to solving the system of equations using CRT. We could then find all possible values of z, and choose the minimum one. This requires applying the CRT construction about $2 \cdot 600^3 = 432\,000\,000$ times. Since the modulo operation involved is quite expensive, this approach would use too much time. Instead, let us exploit a useful greedy principle in finding minimal solutions.

Assume that z is the minimal answer to an instance. There are only two situations where $z - 1$ cannot be a solution as well:

- $z = 0$ – since z must be non-negative, this is the smallest possible answer
- $z \equiv x_i - y_i$ – then, decreasing z would violate one of the constraints

In the first case, we only need to verify whether $z = 0$ is a solution to the three inequalities. In the second case, we managed to change an inequality to a linear equation. By testing which of the i this equation holds for, we only need to test the values of t_i for the two other equations. This reduce the number of times we need to use the CRT to $600^2 = 360\,000$ times, a modest amount well within the time limit.

16.6 Euler's totient function

Now that we have talked about modular arithmetic, we can give the numbers which are *not* divisors to some integer n their well-deserved attention. This discussion will start with the ϕ-function.

Definition 16.8 Two integers a and b are said to be ***relatively prime*** if their only (and thus greatest) common divisor is 1. If a and b are relatively prime, we write that $a \perp b$.

Example 16.6 The numbers 74 and 22 are not relatively prime, since they are both divisible by 2.

The numbers 72 and 65 are relatively prime. The prime factorization of 72 is $2 \cdot 2 \cdot 2 \cdot 3 \cdot 3$, and the factorization of 65 is $5 \cdot 13$. Since these numbers have no prime factors in common, they have no divisors other than 1 in common.

Given an integer n, we ask ourselves how many of the integers $1, 2, \dots, n$ which are relatively prime to n.

Definition 16.9 — Euler's totient function
Euler's totient function $\phi(n)$ is defined as the number if integers $k \in [1, n]$ such that $(k, n) = 1$, i.e. those positive integers less than n which are co-prime to n.

Example 16.7 What is $\phi(12)$? The numbers $2, 4, 6, 8, 10$ all have the factor 2 in common with 12 and the numbers $3, 6, 9$ all have the factor 3 in common with 12.

This leaves us with the integers $1, 5, 7, 11$ which are relatively prime to 12. Thus, $\phi(12) = 4$.

For prime powers, $\phi(p^k)$ is easy to compute. The only integers which are not relatively prime to $\phi(p^k)$ are the multiples of p, which there are $\frac{p^k}{p} = p^{k-1}$ of, meaning

$$\phi(p^k) = p^k - p^{k-1} = p^{k-1}(p-1)$$

It turns out $\phi(n)$ has a property which is highly useful in computing certain number theoretical functions – it is ***multiplicative***, meaning

$$\phi(ab) = \phi(a)\phi(b) \text{ if } a \perp b$$

For multiplicative functions, we can reduce the problem of computing arbitrary values of the function to finding a formula only for prime powers. The reasoning behind the multiplicativity of ϕ is quite simple. Let $a' = a - \phi(a)$, i.e. the number of integers which do share a factor with a, and similarly $b' = b - \phi(b)$. Then, there will be ab' numbers between 1 and ab which share a factor with b. If x is one of the b' numbers sharing a factor with b, then so are $x, x+b, x+2b, ..., x+(a-1)b$. Similarly, there will be $a'b$ numbers between 1 and ab sharing a factor with a. However, there may be some numbers sharing both a factor with a and b. Consider two such numbers $x + ib = y + ja$, which gives $ib - ja = y - x$. By Bezout's identity, this have a single solution (i, j) modulo ab, meaning every number $x + ib$ equals exactly one number $y + ja$. Thus, there were $a'b'$ numbers sharing a factor with both a and b. This means there are $ab' + a'b - a'b'$ numbers sharing a factor with either a and b, so

$$\phi(ab) = ab - ab' - a'b + a'b' = (a - a')(b - b') = \phi(a)\phi(b)$$

and we are done.

Using the multiplicativity of ϕ we get the simple formula

$$\phi(p_1^{e_1} \dots p_k^{e_k}) = \phi(p_1^{e_1}) \cdots \phi(p_k^{e_k}) = p_1^{e_1 - 1}(p_1 - 1) \cdots p_k^{e_k - 1}(p_k - 1)$$

Computing ϕ for a single value can thus be done as quickly as factoring the number. If we wish to compute ϕ for an interval $[1, n]$ we can use the Sieve of Eratosthenes.

This seemingly convoluted function might seem useless, but is of great importance via the following theorem:

Theorem 16.4 — Euler's theorem
If a and n are relatively prime and $n \geq 1$,

$$a^{\phi(n)} \equiv 1 \pmod n$$

Proof. The proof of this theorem isn't trivial, but it is number theoretically interesting and helps to build some intuition for modular arithmetic. The idea behind the proof will be to consider the product of the $\phi(n)$ positive integers less than n which are relatively prime to n. We will call these $x_1, x_2, \dots, x_{\phi(n)}$. Since these are all distinct integers between 1 and n, they are incongruent modulo n. We call such a set of $\phi(n)$ numbers, all incongruent modulo n a ***complete residue system*** (CRS) modulo n.

Next, we will prove that $ax_1, ax_2, \dots, ax_\phi$ also form a CRS modulo n. We need to show two properties for this:

1. All numbers are relatively prime to n
2. All numbers are incongruent modulo n

We will start with the first property. Since both a and x_i are relatively prime to n, neither number have a prime factor in common with n. This means ax_i have no prime factor in common with n either, meaning the two numbers are relatively prime. The second property requires us to make use of the cancellation property of modular arithmetic (Theorem 16.2). If $ax_i \equiv ax_j \pmod{n}$, the cancellation law gives us $x_i \equiv x_j \pmod{n}$. Since all x_i are incongruent modulo n, we must have $i = j$, meaning all the numbers ax_i are incongruent as well. Thus, these numbers did indeed form a complete residue system modulo n.

If $ax_1, \dots, ax_{\phi(n)}$ form a CRS, we know every ax_i must be congruent to some x_j, meaning

$$ax_1 \cdots ax_{\phi(n)} \equiv x_1 \cdots x_{\phi(n)} \pmod{n}$$

Factoring the left hand size turns this into

$$a^{\phi(n)} x_1 \cdots x_{\phi(n)} \equiv x_1 \cdots x_{\phi(n)} \pmod{n}$$

Since all the x_i are relatively prime to n, we can again use the cancellation law, leaving

$$a^{\phi(n)} \equiv 1 \pmod{n}$$

completing our proof of Euler's theorem. □

For primes p we get a special case of Euler's theorem when since $\phi(p) = p - 1$.

Corollary 16.1 Fermat's Theorem For a prime p and an integer $a \perp p$, we have

$$a^{p-1} \equiv 1 \pmod{p}$$

Competitive Tip

By Fermat's Theorem, we also have $a^{p-2} \equiv a^{-1} \pmod{p}$ when p is prime (and $a \perp p$). This is often an easier way of computing modular inverses modulo primes than using the extended Euclidean algorithm, in particular if you already coded modular exponentiation.

Exponial

Nordic Collegiate Programming Contest 2016

Define the *exponial* of n as the function

$$\text{exponial}(n) = n^{(n-1)^{(n-2)^{\cdots^{2^{1}}}}}$$

Compute $\text{exponial}(n) \pmod{m}$.

Input

The input contains the integers $1 \le n, m \le 10^9$.

Output

Output a single integer, the value of $\text{exponial}(n) \pmod{m}$.

Euler's theorem suggests a recursive approach. Since $n^e \pmod{m}$ is periodic (in e), with a period of $\phi(m)$, maybe when computing $n^{(n-1)^{\cdots}}$ we could compute $e = (n-1)^{\cdots}$ modulo $\phi(m)$ and only then compute $n^e \pmod{m}$? Alas, this is only useful when $n \perp m$, since this is a necessary precondition for Euler's theorem. When working modulo some integer m with a prime factorization of $p_1^{e_1} \cdots p_k^{e_k}$, a helpful approach is to instead work modulo its prime powers $p_i^{e_i}$ and then combine the results using the Chinese remainder theorem. Since the prime powers of a prime factorization is relatively prime, the remainder theorem applies.

Let us apply this principle to Euler's theorem. When computing $n^e \bmod p^k$ we have two cases. Either $p \mid n$, in which case $n^e \equiv 0 \pmod{p^k}$ whenever $e \ge k$. Otherwise, $p \perp n$, and $n^e \equiv n^{e \bmod \phi(p^k)} \pmod{p^k}$ by Euler's theorem.

This suggests that if $e \ge \max(e_1, \ldots, e_k)$, we have that n^e is indeed periodic. Furthermore, e_i is bounded by $\log_2 n$, since

$$p_i^{e_i} \le n \Rightarrow$$

$$e_i \log_2(p_i) \le \log_2(N) \Rightarrow$$

$$e_i \le \frac{\log_2(N)}{\log_2(p_i)} \le \log_2(N)$$

As $p_i \geq 2$, we know that $\log_2(p_i) \geq 1$, which we used in the final inequality. Since $\log_2(10^9) \approx 30$ and $4^{3^{2^1}} \geq 30$, we can use the periodicity of n^e whenever $n \geq 5$.

$$n^{\phi(m)+\text{exponial}(n-1) \bmod \phi(m)} \bmod m$$

For $n = 4$, the exponial equals only 262144, meaning we can compute it immediately.

One final insight remains. If we use the recursive formula, i.e. first computing $e = (n-1)^{(n-2)^{\cdots}} \bmod \phi(m)$ and then $n^{\phi(m)+e \bmod \phi(m)} \bmod m$, we still have the problem that n can be up to 10^9. We would need to perform a number of exponentiations that is linear in n, which is slow for such large n. However, our modulo will actually very quickly converge to 1. While the final result is taken modulo m, the first recursive call is taken modulo $\phi(m)$. The recursive call performed at the next level will thus be modulo $\phi(\phi(m))$, and so on. That this sequence decrease very quickly is based on two facts. For even m, $\phi(m) = \phi(2)\phi(\frac{m}{2}) = \phi(\frac{m}{2}) \leq \frac{m}{2}$. For odd m, $\phi(m)$ is even. Any odd m consists only of odd prime factors, but since $\phi(p) = p - 1$ (i.e. an even number for odd primes p) and ϕ is multiplicative, $\phi(m)$ must be even. Thus $\phi(\phi(m)) \leq \frac{m}{2}$ for $m > 1$ (1 is neither even nor contains an odd prime factor). This means the modulo will become 1 in a logarithmic number of iterations, completing our algorithm.

16.7 Chapter Notes

A highly theoretical introduction to classical number theory can be found in *An Introduction to the Theory of Numbers*[10] While devoid of exercises and examples, it is very comprehensive.

A Computational Introduction to Number Theory and Algebra[20] instead takes a more applied approach, and is freely available under a Creative Commons license at the authors home page.[4].

[4]`http://www.shoup.net/ntb/`

Chapter 17

Competitive Programming Strategy

Competitive programming is what we call the mind sport of solving algorithmical problems and coding their solutions, often under the pressure of time. Most programming competitions are performed online, at your own computer through some kind of online judge system. For students of either high school or university, there are two main competitions. High school students compete in the *International Olympiad in Informatics* (IOI), and university students go for the *International Collegiate Programming Contest* (ICPC).

Different competition styles have different difficulty, problem types and strategies. In this chapter, we will discuss some basic strategy of programming competitions, and give tips on how to improve your competitive skills.

17.1 IOI

The IOI is an international event where a large number of countries send teams of up to 4 high school students to compete individually against each other during two days of competition. Every participating country has its own national selection olympiad first.

During a standard IOI contest, contestants are given 5 hours to solve 3 problems, each worth at most 100 points. These problems are not given in any particular order, and the scores of the other contestants are hidden until the end of the contest. Generally none of the problems are "easy" in the sense that it is immediately obvious how to solve the problem in the same way the first 1-2 problems of most other competitions are. This poses a large problem, in particular for the amateur. Without any trivial problems nor guidance from other contestants on what problems to focus on, how does an IOI competitor prioritize? The problem is further exacerbated by problems not having a simple binary scoring, with a submission being either accepted or rejected. Instead, IOI problems contain many so-called *subtasks*. These subtasks give partial credit for the problem, and contain additional restrictions and limits on either input or output. Some problems do not even use discrete subtasks. In these tasks, scoring is done on some scale which determines how "good" the output produced by your program is.

17.1.1 Strategy

Very few contestants manage to solve every problem fully during an IOI contest. There is a very high probability you are not one of them, which leaves you with two options – you either skip a problem entirely, or you solve some of its subtasks. At the start of the competition, you should read through every problem and *all of the subtasks*. In the IOI you do not get extra points for submitting faster. Thus, it does not matter if you read the problems at the beginning instead of rushing to solve the first problem you read. Once you have read all the subtasks, you will often see the solutions to some of the subtasks immediately. Take note of the subtasks which you know how to solve!

Deciding on which order you should solve subtasks in is probably one of the most difficult parts of the IOI for contestants at or below the silver medal level. In IOI 2016, the difference between receiving a gold medal and a silver medal was a mere 3 points. On one of the problems, with subtasks worth 11, 23, 30 and 36 points, the first silver medalist solved the third subtask, worth 30 points (a submission that possibly was a failed attempt at 100 points). Most competitors instead solved the first two subtasks, together worth 34 points. If the contestant had solved the first two subtasks instead, he would have gotten a gold medal.

The problem basically boils down to the question *when should I solve subtasks instead of focusing on a 100 point solution?* There is no easy answer to this question, due to the lack of information about the other contestants' performances. First of all, you need to get a good sense of how difficult a solution will be to implement correctly before you attempt it. If you only have 30 minutes left of a competition, it might not be a great idea to go for a 100 point solution on a very tricky problem. Instead, you might want to focus on some of the easier subtasks you have left on this or other problems. If you fail your 100 point solution which took over an hour to code, it is nice to know you did not have some easy subtasks worth 30-60 points which could have given you a medal.

Problems without discrete scoring (often called *heuristic* problems) are almost always the hardest ones to get a full score on. These problems tend to be very fun, and some contestants often spend way too much time on these problems. They are treacherous in that it is often easy to increase your score by *something*. However, those 30 minutes you spent to gain one additional point may have been better spent coding a 15 point subtask on another problem. As a general rule, go for the heuristic problem last during a competition. This does not mean to skip the problem unless you completely solve the other two, just to focus on them until you decide that the heuristic problem is worth more points if given the remaining time.

In IOI, you are allowed to submit solution attempts a large number of times, without any penalty. Use this opportunity! When submitting a solution, you will generally be told the results of your submission on each of the secret test cases. This provides you with much details. For example, you can get a sense of how correct or wrong your algorithm is. If you only fail 1-2 cases, you probably just have a minor bug, but your algorithm in general is probably correct. You can also see if your algorithm is fast enough, since you will be told the execution time of your program on the test cases. Whenever you make a change to your code which you think affect correctness or speed – submit it again! This gives you a sense of your progress, and also works as a good regression test. If your change introduced more problems, you will know.

Whenever your solution should pass a subtask, submit it. These subtask results will help you catch bugs earlier when you have less code to debug.

17.1.2 Getting Better

The IOI usually tend to have pretty hard problems. Some areas get rather little attention. For example, there are basically no pure implementation tasks and very little geometry.

First and foremost, make sure you are familiar with all the content in the IOI syllabus[1]. This is an official document which details what areas are allowed in IOI tasks. This book deals with most, if not all of the topics in the IOI syllabus.

In the Swedish IOI team, most of the top performers tend to also be good mathematical problem solvers (also getting IMO medals). Combinatorial problems from mathematical competitions tend to be somewhat similar to the algorithmic frame of mind, and can be good practice for the difficult IOI problems.

When selecting problems to practice on, there are a large number of national olympiads with great problems. The Croatian Open Competition in Informatics[2] is a good source. Their competitions are generally a bit easier than solving IOI with full marks, but are good practice. Additionally, they have a final round (the Croatian Olympiad in Informatics) which are of high quality and difficulty. COCI publishes solutions for all of their contests. These solutions help a lot in training.

One step up in difficulty from COCI is the Polish Olympiad in Informatics[3]. This is one of the most difficult European national olympiad published in English, but unfortunately they do not publish solutions in English for their competitions.

There are also many regional olympiads, such as the Baltic, Balkan, Central European, Asia-Pacific Olympiads in Informatics. Their difficulty is often higher than that of national olympiads, and of the same format as an IOI contest (3 problems, 5 hours). These, and old IOI problems, are probably the best sources of practice.

[1] `https://people.ksp.sk/~misof/ioi-syllabus/`

[2] `http://hsin.hr/coci/`

[3] `http://main.edu.pl/en/archive/oi`

17.2 ICPC

In ICPC, you compete in teams of three to solve about 10-12 problems during 5 hours. A twist in in the ICPC-style competitions is that the team shares a single computer. This makes it a bit harder to prioritize tasks in ICPC competitions than in IOI competitions. You will often have multiple problems ready to be coded, and wait for the computer. In ICPC, you see the progress of every other team as well, which gives you some suggestions on what to solve. As a beginner or medium-level team, this means you will generally have a good idea on what to solve next, since many better teams will have prioritized tasks correctly for you.

ICPC scoring is based on two factors. First, teams are ranked by the number of solved problems. As a tie breaker, the penalty time of the teams are used. The penalty time of a single problem is the number of minutes into the contest when your first successful attempt was submitted, plus a 20 minute penalty for any rejected attempts. Your total penalty time is the sum of penalties for every problem.

17.2.1 Strategy

In general, teams will be subject to the penalty tie-breaking. In the 2016 ICPC World Finals, both the winners and the team in second place solved 11 problems. Their penalty time differed by a mere 7 minutes! While such a small penalty difference in the very top is rather unusual, it shows the importance of taking your penalty into account.

Minimizing penalties generally comes down to a few basic strategic points:

- Solving the problems in the right order.
- Solving each problem quickly.
- Minimizing the number of rejected attempts.

In the very beginning of an ICPC contest, the first few problems will be solved quickly. In 2016, the first accepted submissions to five of the problems came in after 11, 15, 18, 32, 44 minutes. On the other hand, after 44 minutes no team had solved all of those problems. Why does not every team solve the problems in the same order? Teams are of different skill in different areas, make different judgment calls regarding difficulty or (especially early in the contest) simply read the problem in a different order. The better you get, the harder it is to distinguish between the “easy” problems of a contest – they are all “trivial” and will take less than 10-15 minutes to solve and code.

Unless you are a very good team or have very significant variations in skill among different areas (e.g., you are graph theory experts but do not know how to compute the area of a triangle), you should probably follow the order the other teams choose in solving the problems. In this case, you will generally always be a few problems behind the top teams.

The better you get, the harder it is to exploit the scoreboard. You will more often be tied in the top with teams who have solved the exact same problems. The problems which teams above you have solved but you have not may only be solved by 1-2 teams, which is not a particularly significant indicator in terms of difficulty. Teams who are very strong at math might prioritize a hard maths problem before an easier (on average for most teams) dynamic programming problem. This can risk confusing you into solving the wrong problems for the particular situation of your team.

The amount of cooperation during a contest is difficult to decide upon. The optimal amount varies a lot between different teams. In general, the amount of cooperation should increase within a single contest from the start to the end. In the beginning, you should work in parallel as much as possible, to quickly read all the problems, pick out the easy-medium problems and start solving them. Once you have competed in a few contests, you will generally know the approximate difficulty of the simplest tasks, so you can skim the problem set for problems of this difficulty. Sometimes, you find an even easier problem in the beginning than the one the team decided to start coding.

If you run out of problems to code, you waste computer time. Generally, this should not happen. If it does, you need to become faster at solving problems.

Towards the end of the contest, it is a common mistake to parallelize on several of the hard problems at the same time. This carries a risk of not solving any of the problems in the end, due to none of the problems getting sufficient attention. Just as with subtasks in IOI, this is the hardest part of prioritizing tasks. During the last hour of an ICPC contest, the previously public scoreboard becomes frozen. You can still see the number of attempts other teams make, but not whether they were successful. Hence, you can not really know how many problems you have to solve to get the position that you want. Learning your own limits and practicing a lot as a team – especially on difficult contests – will help you get a feeling for how likely you are to get in all of your problems if you parallelize.

Read all the problems! You do not want to be in a situation where you run out of time during a competition, just to discover there was some easy problem you knew how to solve but never read the statement of. ICPC contests are made more complex by the fact that you are three different persons, with different skills and knowledge. Just because you can not solve a problem does not mean your team mates will not find the problem trivial, have seen something similar before or are just better at solving this kind of problem.

The scoreboard also displays failed attempts. If you see a problem where many teams require extra attempts, be more careful in your coding. Maybe you can perform some extra tests before submitting, or make a final read-through of the problem and solution to make sure you did not miss any details.

If you get Wrong Answer, you may want to spend a few minutes to code up your own test case generators. Prefer generators which create cases where you already know the answers. Learning e.g. Python for this helps, since it usually takes under a minute to code a reasonable complex input generator.

If you get Time Limit Exceeded, or even suspect time might be an issue – code a test case generator. Losing a minute on testing your program on the worst case, versus a risk of losing 20 minutes to penalty is be a trade-off worth considering on some problems.

You are allowed to ask questions to the judges about ambiguities in the problems. Do this the moment you think something is ambiguous (judges generally take a few valuable minutes in answering). Most of the time they give you a "No comment" response, in which case the perceived ambiguity probably was not one.

If neither you nor your team mates can find a bug in a rejected solution, consider coding it again from scratch. Often, this can be done rather quickly when you have already coded a solution.

17.2.2 Getting Better

- Practice a lot with your team. Having a good team dynamic and learning what problems the other team members excel at can be the difference that helps you to solve an extra problem during a contest.
- Learn to debug on paper. Wasting computer time for debugging means not writing code! Whenever you submit a problem, print the code. This can save you a few minutes in getting your print-outs when judging is slow (in case your submission will need debugging). If your attempt was rejected, you can study your code on paper to find bugs. If you fail on the sample test cases and it takes more than a few minutes to fix, add a few lines of debug output and print it as well (or display it on half the computer screen).
- Learn to write code on paper while waiting for the computer. In particular, tricky subroutines and formulas are great to hammer out on paper before occupying valuable computer time.
- Focus your practice on your weak areas. If you write buggy code, learn your programming language better and code many complex solutions. If your team is bad at geometry, practice geometry problems. If you get stressed during contests, make sure you practice under time pressure. For example, Codeforceshas an excellent gym feature, where you can compete retroactively in a contest using the same amount of time as in the original contest. The scoreboard will then show the corresponding scoreboard from the original contest during any given time.

eforces.com

Appendix A

Discrete Mathematics

This appendix reviews some basic discrete mathematics. Without a good grasp on the foundations of mathematics, algorithmic problem solving is basically impossible. When we analyze the efficiency of algorithms, we use sums, recurrence relations and a bit of algebra. One of the most common topics of algorithms is graph theory, an area within discrete mathematics. Without some basic topics, such as set theory, some of the proofs – and even problems – in this book will be hard to understand.

This mathematical preliminary touches lightly upon these topics and is meant to complement a high school education in mathematics in preparation for the remaining text. While you can probably get by with the mathematics from this chapter, we highly recommend that you (at some point) delve deeper into discrete mathematics.

We do assume that you are familiar with basic proof techniques, such as proofs by induction or contradiction, and mathematics that is part of a pre-calculus course (trigonometry, polynomials, etc). Some more mathematically advanced parts of this book will go beyond these assumptions, but this is only the case in very few places.

A.1 Logic

In mathematics, we often deal with truths and falsehoods in the form of theorems, proofs, counter-examples and so on. Logic is a very exact discipline, and a precise language has been developed to help us deal with logical statements.

For example, consider the statements

1. an integer is either odd or even,
2. programming is more fun than mathematics,
3. if there exists an odd number divisible by 6, every integer is even,
4. x is negative if and only if x^3 is negative,
5. every apple is blue,
6. there exists an integer.

The first statement uses the conjunction *or*. It connects two statements, and requires only one of them to be true in order for the whole statement to be true. Since any integer is either odd or even, the statement is true.

The second statement is not really a logical statement. While we might have a personal conviction regarding the entertainment value of such topics, it is hard to consider the statements as having a truth value.

The third statement complicates matters by introducing an *implication*. It is a two-part statement, which only makes a claim regarding the second part if the first part is true. Since no odd number divisible by 6 exists, it makes no statement about the evenness of every integer. Thus, this implication is true.

The fourth statement tells us that two statements are equivalent – one is true exactly when the other is. This is also a true statement.

The fifth statement concerns *every* object if some kind. It is a false statement, a fact that can be proved by exhibiting e.g., a green apple.

Finally, the last statement is true. It asks whether something exists, a statement we can prove by presenting an integer such as 42.

To express such statements, a language has been developed where all these logical operations such as existence, implication and so on have symbols assigned to them. This enables us to remove the ambiguity inherent in the English language, which is of utmost importance when dealing with the exactness required by logic.

The ***disjunction*** (a is true **or** b is true) is a common logical connective. It is given the symbol $\vee$, so that the above statement is written as $a \vee b$. The other common connective, the ***conjunction*** (a is true **and** b is true) is assigned the symbol $\wedge$. For example, we write that $a \wedge b$ for the statement that both a and b are true.

An ***implication*** is a statement of the form "if a is true, then b must also be true". This is a statement on its own, which is true whenever a is false (meaning it does not say anything of b), or when a is true and b is true. We use the symbol $\rightarrow$ for this, writing the statement as $a \rightarrow b$. The third statement would hence be written as

$$(\exists p : p \text{ is prime} \wedge p \text{ is divisible by } 6) \rightarrow \forall \text{ prime } p : p \text{ is even}$$

The next statement introduced the ***equivalence***, a statement of the form "a is true if, and only if, b is true". This is the same as $a \rightarrow b$ (the only if part) and $b \rightarrow a$ (the if part). We use the symbol $\leftrightarrow$, which follows naturally for this reason. The statement would then be written as

$$x < 0 \leftrightarrow x^3 < 0$$

Logical also contains ***quantifiers***. The fifth statement, that every apple is blue, actually makes a large number of statements – one for each apple. This concept is captured using the ***universal quantifier*** $\forall$, read as "for every". For example, we could write the statement as

$$\forall \text{ apple } a : a \text{ is blue}$$

In the final statement, another quantifier was used, which speaks of the existence of something; the ***existential quantifier*** $\exists$, which we read as "there exists". We would write the second statement as

$$\exists x : x \text{ is an integer}$$

The ***negation*** operator $\neg$ inverts a statement. The statement "no penguin can fly" would thus be written as

$$\neg(\exists \text{ penguin } p : p \text{ can fly})$$

or, equivalently

$$\forall \text{ penguin } p : \neg p \text{ can fly}$$

Exercise A.1

Write the following statements using the logical symbols, and determine whether they are true or false:

1) If a and b are odd integers, $a + b$ is an even integer,
2) a and b are odd integers if and only if $a + b$ is an even integer,
3) Whenever it rains, the sun does not shine,
4) ab is 0 if and only if a or b is 0

Our treatment of logic ends here. Note that much is left unsaid – it is the most rudimentary walk-through in this chapter. This section is mainly meant to give you some familiarity with the basic symbols used in logic, since they will appear later. If you wish to gain a better understanding of logic, you can follow the references in the chapter notes.

A.2 Sets and Sequences

A ***set*** is an unordered collection of **distinct** objects, such as numbers, letters, other sets, and so on. The objects contained within a set are called its ***elements***, or ***members***. Sets are written as a comma-separated list of its elements, enclosed by curly brackets:

$$A = \{2, 3, 5, 7\}$$

In this example, A contains four elements: the integers 2, 3, 5 and 7.

Because a set is unordered and only contains distinct objects, the set $\{1, 2, 2, 3\}$ is the exact same set as $\{3, 2, 1, 1\}$ and $\{1, 2, 3\}$.

If x is an element in a set S, we write that $x \in S$. For example, we have that $2 \in A$ (referring to our example A above). Conversely, we use the notation $x \notin S$ when the opposite holds. We have e.g., that $11 \notin A$.

Another way of describing the elements of a set uses the ***set builder*** notation, in which a set is constructed by explaining what properties its elements should have. The general syntax is

$$\{\text{element} \mid \text{properties that the element must have}\}$$

To construct the set of all even integers, we would use the syntax

$$\{2i \mid i \text{ is an integer}\}$$

which is read as "the set containing all numbers of the form $2i$ where i is an integer. To construct the set of all primes, we would write

$$\{p \mid p \text{ is prime}\}$$

Certain sets are used often enough to be assigned their own symbols:

- $\mathbb{Z}$ – the set of integers $\{\dots, -2, -1, 0, 1, 2, \dots\}$,
- $\mathbb{Z}_+$ – the set of *positive* integers $\{1, 2, 3, \dots\}$,
- $\mathbb{N}$ – the set of *non-negative* integers $\{0, 1, 2, \dots\}$,
- $\mathbb{Q}$ – the set of all rational numbers $\{\frac{p}{q} \mid p, q \text{ integers where } q \neq 0\}$,
- $\mathbb{R}$ – the set of all real numbers,
- $[n]$ – the set of the first n positive integers $\{1, 2, \dots, n\}$,
- $\emptyset$ – the empty set.

Exercise A.2

1) Use the set builder notation to describe the set of all odd integers.
2) Use the set builder notation to describe the set of all negative integers.
3) Compute the elements of the set $\{k \mid k \text{ is prime and } k^2 \leq 30\}$.

A set A is a ***subset*** of a set S if, for every $x \in A$, we also have $x \in S$ (i.e., every member of A is a member of S). We denote this with $A \subseteq S$. For example

$$\{2,3\} \subseteq \{2,3,5,7\}$$

and

$$\left\{\frac{2}{4}, 2, \frac{-1}{7}\right\} \subseteq \mathbb{Q}$$

For any set S, we have that $\emptyset \subseteq S$ and $S \subseteq S$. Whenever a set A is not a subset of another set B, we write that $A \not\subseteq B$. For example,

$$\{2, \pi\} \not\subseteq \mathbb{Q}$$

since π is not a rational number.

We say that sets A and B are ***equal*** whenever $x \in A$ if and only if $x \in B$. This is equivalent to $A \subseteq B$ and $B \subseteq A$. Sometimes, we will use the latter condition when proving set equality, i.e., first proving that every element of A must also be an element of B and then the other way round.

Exercise A.3

1) List all subsets of the set $\{1,2,3\}$.
2) How many subsets does a set containing n elements have?
3) Determine which of the following sets are subsets of each other:
   - $\emptyset$
   - $\mathbb{Z}$
   - $\mathbb{Z}_+$
   - $\{2k \mid k \in \mathbb{Z}\}$
   - $\{2, 16, 12\}$

Sets also have many useful operations defined on them. The ***intersection*** $A \cap B$ of two sets A and B is the set containing all the elements which are members of **both** sets, i.e.,

$$x \in A \cap B \Leftrightarrow x \in A \wedge x \in B$$

If the intersection of two sets is the empty set, we call the sets ***disjoint***. A similar concept is the ***union*** $A \cup B$ of A and B, defined as the set containing those elements which are members of **either** set.

Example A.1 Let

$$X = \{1, 2, 3, 4\}, Y = \{4, 5, 6, 7\}, Z = \{1, 2, 6, 7\}$$

Then,

$$X \cap Y = \{4\}$$

$$X \cap Y \cap Z = \emptyset$$

$$X \cup Y = \{1, 2, 3, 4, 5, 6, 7\}$$

$$X \cup Z = \{1, 2, 3, 4, 6, 7\}$$

Exercise A.4

Compute the intersection and union of:

1) $A = \{1, 4, 2\}, B = \{4, 5, 6\}$

2) $A = \{a, b, c\}, B = \{d, e, f\}$

3) $A = \{\text{apple}, \text{orange}\}, B = \{\text{pear}, \text{orange}\}$

A *sequence* is an **ordered** collection of values (predominantly numbers) such a $1, 2, 1, 3, 1, 4, \dots$. Sequences will mostly be a list of sub-scripted variables, such as $a_1, a_2, \dots, a_n$. A shorthand for this is $(a_i)_{i=1}^{n}$, denoting the sequence of variables a_i where i ranges from 1 to n. An infinite sequence is given ∞ as its upper bound: $(a_i)_{i=1}^{\infty}$

A.3 Sums and Products

The most common mathematical expressions we deal with are sums of sequences of numbers, such as $1 + 2 + \cdots + n$. Such sums often have a variable number of terms and complex summands, such as $1 \cdot 3 \cdot 5 + 3 \cdot 5 \cdot 7 + \cdots + (2n + 1)(2n + 3)(2n + 5)$. In these cases, sums given in the form of a few leading and trailing terms, with the remaining part hidden by $\dots$ is too imprecise. Instead, we use a special syntax for writing sums in a formal way – the *sum operator*:

$$\sum_{i=j}^{k} a_i$$

The symbol denotes the sum of the $j - k + 1$ terms $a_j + a_{j+1} + a_{j+2} + \cdots + a_k$, which we read as "the sum of a_i from j to k".

For example, we can express the sum $2 + 4 + 6 + \cdots + 12$ of the 6 first even numbers as

$$\sum_{i=1}^{6} 2i$$

Exercise A.5

Compute the sum

$$\sum_{i=-2}^{4} 2 \cdot i - 1$$

Many useful sums have closed forms – expressions in which we do not need sums of a variable number of terms.

Exercise A.6

Prove the following identities:

$$\sum_{i=1}^{n} c = cn$$

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

$$\sum_{i=1}^{n} i^2 = \frac{n(n+\frac{1}{2})(n+1)}{3}$$

$$\sum_{i=0}^{n} 2^i = 2^{n+1} - 1$$

The sum of the inverses of the first n natural numbers happen to have a very neat approximation, which we will occasionally make use of later on:

$$\sum_{i=1}^{n} \frac{1}{n} \approx \ln n$$

This is a reasonable approximation, since $\int_1^l \frac{1}{x} dx = \ln(l)$

There is an analogous notation for products, using the *product operator* $\prod$:

$$\prod_{i=j}^{k} a_i$$

denotes the product of the $j - k + 1$ terms $a_j \cdot a_{j+1} \cdot a_{j+2} \cdot \dots \cdot a_k$, which we read as "the product of a_i from j to k".

In this way, the product $1 \cdot 3 \cdot 5 \cdot \dots \cdot (2n - 1)$ of the first n odd integers can be written as

$$\prod_{i=1}^{n} 2i - 1$$

Exercise A.7

Prove that

$$(n+2)\prod_{i=1}^{n} i + \frac{n}{n+1}\prod_{i=1}^{n+2} i = \prod_{i=1}^{n+2} i$$

A.4 Graphs

Graphs are one of the most common objects of study in algorithmic problem solving. They are an abstract way of representing various types of relations, such as roads between cities, friendships, computer networks and so on. Formally, we say that a graph consists of two things – a set V of ***vertices***, and a set E of ***edges***. An edge consists of a pair of vertices $\{u, v\}$, which are called the ***endpoints*** of the edge. We say that the two endpoints of the edge are ***connected*** by the edge.

A graph lends itself naturally to a graphical representation. For example, the graph given by $V = \{1, 2, 3, 4, 5\}$ and $E = \{\{1, 2\}, \{3, 1\}, \{4, 2\}, \{4, 1\}\}$ can be drawn as in Figure A.1.

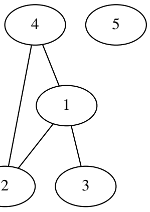

Figure A.1: The graph given by $V = \{1, 2, 3, 4, 5\}$ and $E = \{\{1, 2\}, \{3, 1\}, \{4, 2\}, \{4, 1\}\}$.

Graphs bring a large vocabulary with them. While you might find it hard to remember all of them now, you will become intimately familiar with them when studying graph theoretical algorithms later on.

A *path* is a sequence of *distinct* vertices $p_0, p_1, ..., p_{l-1}, p_l$ such that $\{p_i, p_{i+1}\} \in E$ $(i = 0, 1, ..., l - 1)$. This means any two vertices on a path must be connected by an edge. We say that this path has ***length*** l, since it consists of l edges. In Figure A.1, the sequence $3, 1, 4, 2$ is a path of length 3.

If we relax the constraint that a path must contain only distinct vertices, we instead get a ***walk***. A walk which only contain *distinct edges* is called a ***trail***. The graph in Figure A.1 contains the walk $1, 3, 1, 2$ (which is not a trail, since the edge $\{1, 3\}$ is used twice). $3, 1, 4, 2, 1$ on the other hand is a trail.

If a path additionally satisfy that $\{p_0, p_l\} \in E$, we may append this edge to make the path cyclical. This is called a *cycle* . Similarly, a walk with starts and ends at the same vertex is called a ***closed walk***. If a trail starts and ends at the same vertex, we call it a ***closed trail***.

A graph where any pair of vertices have a path between then is called a ***connected*** graph. The (maximal) subsets of a graph which *are* connected form the ***connected components*** of the graph. In Figure A.1, the graph consists of two components, $\{1, 2, 3, 4\}$ and $\{5\}$.

A ***tree*** is a special kind of graph – a **connected** graph which does not contain any cycle. The graph in Figure A.1 is not a tree, since it contains the cycle $1, 2, 4, 1$. The graph in Figure A.2 on the other hand, contains no cycle.

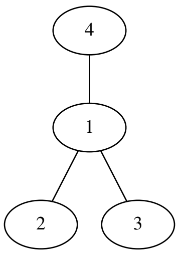

Figure A.2: The tree given by $V = \{1,2,3,4\}$ and $E = \{\{1,2\},\{3,1\},\{4,1\}\}$.

Exercise A.8

Prove that a tree of n vertices have exactly $n-1$ edges.

So far, we have only considered the ***undirected*** graphs, in which an edge simply connects two vertices. Often, we want to use graphs to model asymmetric relations, in which an edge should be given a direction – it should go *from* a vertex *to* another vertex. This is called a ***directed*** graph. In this case, we will write edges as ordered pairs of vertices (u,v), where the edge goes from u to v. When representing directed graphs graphically, edges will be arrows, with the arrowhead pointing from u to v (Figure A.3).

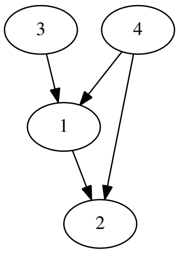

Figure A.3: The graph given by $V = \{1,2,3,4\}$ and $E = \{(1,2),(3,1),(4,2),(4,1)\}$.

Terms such as cycles, paths, trails and walks translate to directed graphs in a natural way, except we must follow edges in their direction. Thus, a path is a sequence of edges $(p_0,p_1),(p_1,p_2),...,(p_{l-1},p_l)$. In the graph in Figure A.3, you may notice that there is no directed cycle. We call such a graph a ***directed acyclic graph*** (DAG). This type of graph will be a recurring topic, so it is a term important to be well acquainted with.

Another augmentation of a graph is the ***weighted graph***. In a weighted graph, each edge $e \in E$ is assigned a weight $w(e)$. This will often represent a length or a cost of the edge. For example, when using a graph to model a network of roads, we may associate each road $\{u, v\}$ between two locations u and v with the length of the road $w(\{u, v\})$.

So far, we have only allowed E to be a set. Additionally, an edge has always connected to different vertices (in contrast to a self-loop, an edge from a vertex to itself). Such a graph is sometimes called a ***simple*** graph. Generally, our examples of graphs will be simple graphs (even though most of our algorithms can handle duplicate edges and self-loops). A graph where E may be a multiset, or contain self-loops is called a *multigraph*.

A.5 Chapter Notes

If you need a refresher on some more basic mathematics, such as single-variable calculus, *Calculus* [22] by Michael Spivak is a solid textbook. It is not the easiest book, but one the best undergraduate text on single-variable calculus if you take the time to work it through.

Logic in computer science [11] is an introduction to formal logic, with many interesting computational applications. The first chapter on propositional logic is sufficient for most algorithmic problem solving, but the remaining chapters shows many non-obvious applications that makes logic relevant to computer science.

For a gentle introduction to discrete mathematics, *Discrete and Combinatorial Mathematics: An Applied Introduction* [9] by Ralph Grimaldi is a nice book with a lot of breadth.

One of the best works on discrete mathematics ever produced for the aspiring algorithmic problem solver is *Concrete Mathematics* [7], co-authored by famous computer scientist Donald Knuth. It is rather heavy-weight, and probably serves better as a more in-depth study of the foundations of discrete mathematics rather than an introductory text.

Graph Theory [6] by Reinhard Diestel is widely acknowledged as the go-to book on more advanced graph theory concepts. The author is freely available for viewing at the book's home page[1].

[1] `http://diestel-graph-theory.com/`

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