Class Notes for CSCI 104: Data Structures and Object-Oriented Design

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Preface

These lecture notes grew out of class notes provided for the students in CSCI 104 ("Data Structures and Object-Oriented Design") at the University of Southern California in Fall of 2013. The class is typically taken in the second semester of freshman year or the first semester of sophomore year. Students are expected to be familiar with structural programming in the C++ programming language, the basics of dynamic memory management, and recursion. Brief refreshers on these two specific topics are included at the beginning of the notes, and typically covered for about one lecture each, but a student not already familiar with these concepts is likely to struggle in the class.

These notes represent the specific way in which we like to present the material, by motivating object-oriented design primarily from the point of view of implementing data structures. There is perhaps somewhat more focus on analysis and allusions to advanced topics than in a typical programming-heavy data structures course for undergraduates. The notes are, at least at present, not intended to replace an actual detailed textbook on data structures. We currently use the book "Data Abstraction and Problem Solving" by Carrano and Henry.

The notes are based on lecture notes taken by the CSCI 104 sherpas in Fall 2013: Chandler Baker, Douglass Chen, Nakul Joshi, April Luo, Peter Zhang, Jennie Zhou. Douglass was the main notetaker, in charge of about half of the notes himself, and coordinating the others' notes as well. The notes were subsequently expanded significantly by David Kempe, and then expanded further and reorganized again for the Spring 2014 and Fall 2015 semesters, when they took essentially their current form.

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Chapter 1

Overview: Why Data Structures and Object-Oriented Thinking

[Note: This chapter covers material of about 0.75 lectures.]

As a result of our introductory CS classes (CSCI 103, or CSCI 101 for earlier generations), most students are probably somewhat proficient in basic programming, including the following basic features:

Data types `int`, `String`, `float/double`, `struct`, arrays, ...

Arithmetic

Loops `for`, `while` and `do-while`

Tests `if`, `else` and `switch`

Pointers

Functions and some recursion

Other I/O and other useful functions

OOP Some students have probably already learned a bit about object-oriented programming, but for now, we will not rely on this.

In principle, these features are enough to solve any programming problem. In fact, in principle, it is enough to have nothing except `while` loops, `if` tests, integers, and arithmetic. Everything that we learn beyond those basics is "just" there to help us write better, faster, or more easily maintained or understood code. Writing "better" code comes in two flavors:

1. Learning problem-solving and conceptual ideas that let us solve problems which we didn't know how to solve (even though we had the tools in principle), or didn't know how to solve fast enough.
2. Learning new language features and programming concepts helps us write code that "feels good", in the sense that it is easy to read, debug, and extend.

The way most students are probably thinking about programming at this point is that there is some input data (maybe as a few data items, or an array), and the program executes commands to get an output from this. Thus, the sequence of instructions — the algorithm — is at the center of our thinking.

As one becomes a better programmer, it's often helpful to put the data themselves at the center of one's thinking, and think about how data get transformed or changed throughout the execution of the program. Of course, in the end, the program will still mostly do the same, but this view often leads to much better (more maintainable, easier to understand, and sometimes also more efficient) code. Along the way, we'll see how thinking about the organization of our data can be really important for determining how fast our code executes.

Example 1.1 In class, we did the following example. Two students each got a list of the names and e-mails of all students in the class. One student got the list sorted alphabetically, while the other's version contained the names in random order. Both students were asked to look up the e-mail of one particular student by name. Not too surprisingly, the student with the sorted list was much faster.

What this example showed us is that the way we organize our data can have a profound impact on how fast (or slowly) we can solve a computational task. *The basic question of how to organize data to support the operations we need is the centerpiece of what you will learn in this class.*

What do we mean by "support the operations we need"? Let's go back to the example of looking up e-mails of students by name. Here, the key operation is clearly the "lookup" operation, at least from the standpoint of the volunteer doing the looking up. But when we look at the bigger picture, those data items (pairs of a student and an e-mail) had to be added into that form somehow. And sometimes, we may want to delete them. So really, the three operations we are interested in are:

- Insert a pair of a name and e-mail into the list.
- Remove a name from the list.
- Look up the e-mail for a given name.

Purely from the perspective of speeding up the lookup operation, the sorted list was much better than the unsorted one. But in terms of inserting items, it's clearly better to keep things unsorted, as we can just append them at the end of the list, and not have to worried about putting the item in the right place. For removal, well, we'll learn about that a little more later.

It's easy to imagine scenarios where keeping the list sorted is not worth it. For instance, if we need to add data items all the time, but very rarely look them up (say, some kind of backup mechanism for disasters), then it's not worth it. Or maybe, the list is so short that even scanning through all the items is fast enough.

The main take-away message is that the answer to "What is the best way to organize my data?" is almost always "It depends". You will need to consider how you will be interacting with your data, and design an appropriate structure *in the context of its purpose.* Will you be searching through it often? Will data be added in frequent, short chunks, or in occasional huge blocks? Will you ever have to consolidate multiple versions of your structures? What kinds of queries will you need to ask of your data?

There is another interesting observation we can see from the previous example. We said that we wanted our data structure to support operations `add`, `remove`, and `lookup`. Let's be a little more general than just a list of students.

- The `add (key, value)` operation gets a *key* and a *value*. (In our case, they were both strings, but in general, they don't have to be.) It creates an association between the key and value.
- The `remove (key)` operation gets a key, and removes the corresponding pair.
- The `lookup (key)` operation gets a key, and returns the corresponding value, assuming the key is in the structure.

This type of data structure is typically called a *map*, or (in our textbook) a *dictionary*.

So is a sorted list a map? Not exactly. After all, an unsorted list would also be a map. There seems to be a difference. The main difference is that the word "map" describes the *functionality* that we want: *what* the data structure is supposed to do. On the other hand, a sorted list (or an unsorted list) is a *specific way* of getting this functionality: it says *how* we do it.

This distinction is very important. When you start to program, usually, you just go straight ahead and plan out all of your code. As you take on bigger projects, work in larger teams, and generally learn to think more like a computer scientist, you get used to the notion of *abstraction*: separating the "what" from the "how". You can work on a project with a friend, and tell your friend which functions you need from him/her, without having to think through how they will be implemented. That's your friend's job. So long as your friend's implementation works (fast enough) and meets the specification that you prescribed (say, in terms of which order the parameters are in), you can just use it as is.

So the way we would think about a map or dictionary is mostly in terms of the functions it provides: `add`, `remove`, and `lookup`. Of course, it must store data internally in order to be able to provide these functions correctly, but how it does that is secondary — that's part of the implementation. This combination of data and code, with a well-specified interface of functions to call, is called an *abstract data type*.

Once we start realizing the important role that data organization (such as using abstract data types) plays in good code design, we may change the way we think about code interacting with data. When starting to program, as we mentioned above, most students think about code that gets passed some data (arrays, structs, etc.) and processes them. Instead, we now think of the data structure itself as having functions that help with processing the data in it. In this way of thinking, an array in which you can only add things at the end is different from one in which you are allowed to overwrite everywhere, even though the actual way of storing data is the same.

This leads us naturally to *object-oriented design* of programs. An *object* consists of data and code; it is basically a `struct` with functions inside in addition to the data fields. This opens up a lot of ideas for developing more legible, maintainable, and "intuitive" code. Once we think about objects, they often become almost like little people in our mind. They serve different functions, and interact with each other in particular ways.

One of the main things that thinking in terms of object-oriented design (and abstract data types) does for us is to help achieve *encapsulation*: shielding as much of the inside of an object as possible from the outside, so that it can be changed without negatively affecting the code around it. The textbook refers to this as "walls" around data. Encapsulation helps us achieve modularity, i.e., ensuring that different pieces of code can be analyzed and tested in isolation more easily.

To summarize, the learning goals of this class are:

1. Learn the basic and advanced techniques for actually implementing data structures to provide efficient functionality. Some of these techniques will require strong fundamentals, and their analysis will enter into more mathematical territory, which is why we will be drawing on material you will be learning simultaneously in CSCI 170.

2. Learn how to think about code more abstractly, separating the "what" from the "how" in your code design and utilizing abstract data types to specify functionality.

3. Learn about good programming practice with object-oriented design, in particular as it relates to implementing datatypes.

Chapter 2

Memory and Its Allocation

[Note: this chapter covers material of about 1 lecture.]

At the physical level, computer memory consists of a large number of flip flops. Each flip flop consists of a few transistors, and is capable of storing one bit. Individual flip flops are addressable by a unique identifier, so we can read and overwrite them. Thus, conceptually, we can think of all of our computer's memory as just one giant array of bits that we can read and write.

Since as humans, we are not that good at doing all of our thinking and arithmetic in bits, we group them into larger groups, which together can be used to represent numbers. 8 bits are called 1 byte; beyond bytes, there are words (which are sometimes 16, sometimes 32 bits). Thus, more often, we conceptually regard our computer's memory as one large (size 2^{32} or so) array of bytes. A lot of things are stored in this memory.

1. All variables and other data used by all programs.

2. But also the programs' code, including the operating system's.

The compiler and the operating system work together to take care of most memory management for you, but it is instructive to see what is going on under the hood.

When you compile your code, the compiler can examine primitive data types and calculate how much memory they will need ahead of time. The required amount is then allocated to the program in the *stack*[1] space. For example, consider the following declarations:

```
int n;
int x[10];
double m;
```

The compiler can immediately see that the code requires $4 + 4 \times 10 + 8 = 52$ bytes[2].

It will insert code that will interact with the operating system to request the necessary number of bytes on the stack for your variables to be stored. In the example above, the compiler knows that the memory will look as follows:

It knows the exact memory address of each variable; in fact, whenever we write `n`, this gets translated into something like "memory address 4127963" internally.

Notice that if we attempted to access $x[10]$ here, we would access the data associated with m, and may end up reading (or overwriting) some of its bits. This would almost certainly have very undesired consequences for the rest of the program.

When functions call other functions, each function gets its own chunk of stack at the moment it is called; it keeps all its local variables there, but also a program counter that remembers where in its execution it

[1] This space is called the stack space because as functions get called, their memory gets added on top of existing memory. As they terminate, they are removed in a LIFO (last in, first out) order.

[2] That's with the current sizes for integers and doubles. About 20 years ago, `int` were typically 2 bytes, and `double` 4 bytes. Your code should never have to depend on what is at this moment the size of the basic data types.

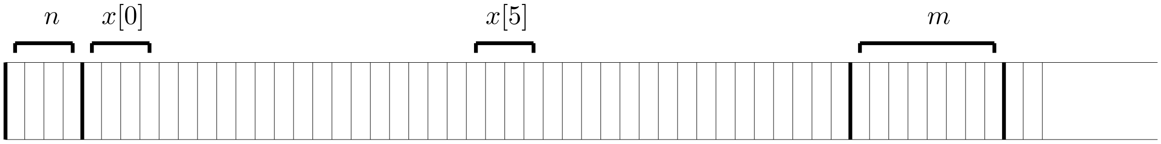


Figure 2.1: The layout of memory on the stack for the declaration above.

was. When the function finishes, its memory block is made available for other purposes again. Again, for statically allocated variables, the compiler can take care of all of this.

2.1 Scoping of Variables

While we are talking about local variables and the stack, we should briefly talk about the scope of a variable. Global variables are, of course, accessible to any function or any block of code in your program. Local variables in function or code blocks only exist while the execution is in the function or the code block. It is typically stored on the stack. As soon as the function or block terminates, the variable is deallocated.

When the execution of a function is temporarily suspended, for instance because another function got called inside this one, the variables are stored on the stack, but not active, so they cannot be accessed. Consider the following example:

```
void foo (int x)
{
  int y;
  // do some stuff
}

void bar (int n)
{
  int m;
  foo (n+m);
  // do more stuff
}
```

Here, when `bar` calls `foo`, the function `foo` cannot access the variables `n` or `m`. As soon as `foo` finishes, the variables `x` and `y` are deallocated, and permanently lost. `bar` now resumes and has access to `n` and `m`, but not to `x` or `y`.

You will sometimes have multiple variables (in different parts of your code) sharing the same name. For instance, you may have both a global variable `n` and a local variable in a function called `n`. Or you could have something like the following:

```
void foo (int n)
{
  int m = 10;
  // do something
  for (int i = 0; i < m; i ++)
    {
      int n = 3, m = 5;
      // do something
      cout << n << m;
    }
}
```

Here, the `cout << n << m` statement would output the innermost versions, so the values 3 and 5. As a general rule, when there are multiple variables with the same name, any reference is to the one in the smallest code block enclosing the statement that contains that variable.

2.2 Dynamic allocation

Unfortunately, things aren't quite as easy as statically allocated arrays when we don't know at compile time how much memory a variable will need. Suppose we want to do something like the following:

```
int n;
cin>>n;
// create an array a of n integers
```

Here, at compile time, the compiler does not know how much memory the array will need. It can therefore not allocate room for a variable on the stack[3]. Instead, our program needs to explicitly ask the operating system for the right amount of space at run-time. This memory is assigned from the *heap*[4] space.

The difference between static and dynamic memory allocation is summarized in the following table. To fully understand how dynamic memory allocation works, we need to spend some time on pointers.

Static allocation	**Dynamic allocation**
Size must be known at compile time	Size may be unknown at compile time
Performed at compile time	Performed at run time
Assigned to the stack	Assigned to the heap
First in last out	No particular order of assignment

Table 2.1: Differences between statically and dynamically allocated memory.

2.3 Pointers

A pointer is an "integer" that points to a location in memory — specifically, it is an address of a byte[5].

In C/C++, pointer types are declared by placing a star '*' behind a regular type name. Thus, `int *p; char *q; int **b; void *v;` all declare pointers. In principle, all these are just addresses of some memory location, and C/C++ does not care what we store there. Declaring them with a type (such as `int`) is mostly for the programmer's benefit: it may prevent us from messing up the use of the data stored in the location. It also affects the way some arithmetic on memory locations is done, which we explain below.

Two of the ways in which "regular" variables and pointers often interact are the following:

1. We want to find out where in memory a variable resides, i.e., get the pointer to that variable's location.

2. We want to treat the location a pointer points to as a variable, i.e., access the data at that location, by reading it or overwriting it.

The following piece of code illustrates some of these, as well as pitfalls we might run into.

[3] Technically, this is not quite true. Some modern compilers let you define arrays even of dynamic sizes, but we advise against using this functionality, and instead do things as we write in these notes.

[4] This is called the heap space since it can be selected from any portion of the space that has not been allocated already. While the stack remains nicely organized, memory in the heap tends to be more messy and all over the place. Hence the name.

[5] This means that all pointers are of the same size, and that the size of pointer used by a computer places a limit on the size of memory it can address. For example, a computer using typical 32-bit pointers can only use up to 2^{32} bytes or 4 gigabytes of memory. The modern shift to 64-bit architectures turns this to 2^{64} bytes, which will be enough for a while.

```
int* p, *q; //Pointers to two integers
int i, j;
i = 5; j = 10;
p = &i;   //Obtain the address of i and save it to p
cout << p;  //Prints the value of p (address of i)
cout << *p; //Prints the value of the integer that p points to (which is the value of i)
*p = j;   // Overwrites the value of the location that p points to (so, i) with the value of j
*q = *p;  // Overwrites the value of the location that q points to with the one that p points to
q = p;    // Overwrites the pointer p with q, so they now point to the same location
```

A few things are worth noting here.

1. The last two commands both result in `*p` being equal to `*q`, but in different ways. In the first case, we copy the *value* from one location to the other, while in the second, we make both point to the same place.

2. The second-to-last command is very risky, and will likely cause a run-time error. We have not initialized `q`, so it points to an arbitrary memory location, quite possibly location 0. We are trying to overwrite it, which most likely the program is not allowed to do. The location may belong to the operating system or some other program[6].

3. `NULL` is a special pointer we use for an uninitialized pointer variable, or to express that a pointer is not pointing anywhere. If we try to write `*p` when `p == NULL`, we get a runtime error. In a sense, `NULL` is really just another way of saying 0; we said above that pointers are just numbers, and the `NULL` pointer points to memory location 0. In C++11, there is a new keyword for this, namely `nullptr`. If you set the compiler flags to compile C++11, you can/should use `nullptr` instead of `NULL`.

4. In fact, the earlier observation about the perils of uninitialized pointers suggests that whenever you have a pointer variable, you always assign it `NULL` right away as you declare it. So in our example, we should have written `int *p = NULL, *q = NULL;` That way, if we later forget to assign it before dereferencing, at least, it will cause a crash of our program, rather than possibly processing some garbage that it reads from the location. This is good coding practice to reduce your debug time.

5. `&` and `*` are *inverses* of each other. Thus, `&*p` and `*&p` are the same as `p`. (The exception is that `&*p` throws a runtime error when applied to `p==NULL`, instead of being equal to `p`.)

In general, it is quite easy to mess up with pointers. A few rules of thumb (which we discussed in class) will weed out common mistakes, but generally speaking, it is easy to forget to assign a pointer correctly, resulting in run-time errors.

We discussed before that pointers are basically just integers. They differ in that arithmetic is somewhat different. When you have a pointer `p` to an `int`, and you write `p+1`, the compiler assumes that what you want is the address where the next *integer* will start, which is 4 bytes later. Thus, the actual address referenced by writing `p+1` is actually 4 bytes after the address of `p`.

This is where the type of pointer matters, as we hinted at above. When you have a `void*`, then addition really does refer to adding individual bytes. For all others, when you write `p+k` for a pointer `p` and integer `k`, this references memory location `p+k*size(<type>)`, where `<type>` is the type of the pointer `p`.

2.4 Dynamic Memory Allocation

In order to dynamically allocate and deallocate memory, there are two pairs of functions, one in C style and one in C++ style. In C, the function for allocating memory is `malloc`, and for deallocation `free`. In C++, the functions are `new` and `delete`. We will first discuss the C style, as it is a little closer to the actual low-level implementation; we'll then see the C++ style, which shields us from some of the low-level details.

[6] Fortunately, nowadays, all that happens is that your program throws a run-time error. In the past, the OS would often allow you to do such an overwrite, in which case often some complete system crashes would happen.

2.4.1 C Style

The function void* malloc (unsigned int size) requests size bytes of memory from the operating system, and returns the pointer to that location as a result. If for some reason, the OS failed to allocate the memory (e.g., there was not enough memory available), NULL is returned instead. The function void free (void* pointer) releases the memory located at pointer for reusing. A solution to our earlier problem of a dynamically sized array could look as follows:

```
int n;
int* b;
cin >> n;
b = (int*) malloc(n*sizeof(int));
for (int i=0; i<n; i++)
    cin >> b[i];
```

In order to request space for n integers, we need to figure out how many bytes that is. That's why we multiply with sizeof(int). Using sizeof(int) is much better than hard-coding the constant 4, which may not be right on some hardware now or in the future.

Because malloc returns a void* (it does not know what we want to use the memory for), and we want to use it as an array of integers, we need to cast it to an int*.

For good coding practice, we should probably also check whether b==NULL before dereferencing it, but this example is supposed to remain short.

Another thing to observe here is that we can reference b just like an array, and we write b[i]. The compiler treats this exactly as *(b+i), and, as you probably remember from the part about pointer arithmetic, this points to the i^{th} entry of the array. In fact, that's exactly how C/C++ internally treats all arrays anyway; basically, they are just pointers.

If we wanted to write b[i] in a complicated way by doing all the pointer arithmetic by hand, we could write instead *((int*) ((void*) b + i*sizeof(int))). Obviously, this is not what we like to type (or have to understand), but if you understand everything that happens here, you are probably set with your knowledge of pointer arithmetic and casting.

To return the memory to the OS after we're done using it, we use the function free, as follows:

```
free(b);
b = NULL;
```

Note that free does nothing to the pointer b itself; it only deallocates the memory that b pointed to, telling the operating system that it is available for reuse. Thus, it is recommended that you immediately set the pointer to NULL so that your code does not attempt to tamper with invalid memory. If you reference b somewhere, you'll just get a runtime error. If you don't set b=NULL, the OS may give the memory to another variable, and you accidentally reference/overwrite that one. That kind of mistake can be much harder to detect, and is easily avoided by setting the pointer to NULL immediately after deallocating it.

2.4.2 C++ Style

C++ provides the new() and delete() functions that provide some syntactic sugar to C's malloc() and free(). Basically, they relieve you from the calculations of the number of bytes needed, the casting of pointers, and provide a more "array-like" syntax. Our example now looks as follows:

```
int n;
int *b;
cin >> n;
b = new int[n];
```

Notice that there are no parentheses, but instead, we have brackets for the number of items. new figures out by itself how much memory is needed, and returns the correct type of pointer.

If we wanted space for just one integer, we could write int *p = new int; While this is not really very useful for a single integer, it will become very central to allocating objects later, where we often allocate one at a time dynamically.

To release memory, the equivalent of free is the delete operator, used as follows:

```
delete [] b;
delete p;
```

The first example deallocates an array, while the second deallocates a single instance of a variable (a single int in our example). This deallocates the memory pointed to by the pointers. As with free, it still leaves the pointers themselves pointing to the same memory location, so it is good style to write b = NULL or p = NULL after the delete commands.

2.5 Memory Leaks

Let us look a little more at the things that can go wrong with dynamic memory allocation.

```
double *x;
...
x = (double*) malloc(100*sizeof(double));
...
x = (double*) malloc(200*sizeof(double)); // We need a bigger array now!
...
free(x);
```

This code will compile just fine, and most likely will not crash, at least not right away. We correctly allocate an array of 100 double, use it for some computation, and then allocate an array of 200 double when we realize that we need more memory.

But notice what happens here. The moment we do the second allocation, x gets overwritten with a pointer to the newly allocated memory block. At that point, we have no more recollection of the pointer to the previous memory block. That means we cannot read it, write it, or free it. When at the end of the code snippet, the program calls free(x), it successfully frees up the second allocated block, but we are unable to tell the operating system that we don't need the first block any more. Thus, those 800 bytes will never become available again (until our program terminates — but for all we know, it may run for several years as a backend server somewhere).

This kind of situation is called a *memory leak*: available memory is slowly leaking out of the system. If it goes on long enough, our program may run out of memory and crash for that reason. It could be quite hard to diagnose why the crash happened if it does after a long time of running.

It is good practice to keep close track of the memory blocks you reserve, and make sure to free (or delete) memory pointed to by a pointer before reassigning it[7]. A better version of the code above would be the following:

```
double *x;
...
x = (double*) malloc(100*sizeof(double));
...
free(x);
x = NULL;
```

[7] There are tools for checking your code for memory leaks, and we recommend familiarizing yourself with them. The most well-known one, for which the course web page contains some links, is called valgrind.

```
x = (double*) malloc(200*sizeof(double));
...
free(x);
x = NULL;
```

That way, the memory gets released while we still have a pointer to it. You will recall that it is always good practice to immediately set pointers to NULL after deallocating their memory. In the middle of the code, that may seem very redundant: after all, we immediately overwrite x with another value. In fact, it is completely redundant. However, we still recommend that you add the line; for example, you may later insert some code between free(x) and the new assignment to x, and that could cause problems otherwise. And if you are worried about your program wasting time with unnecessary assignments, don't — the compiler will almost certainly optimize that assignment away anyway, and the final code will look exactly the same.

One question you may be wondering about is if we could just free the memory by setting x = NULL; without calling free(x) first. That would only overwrite the pointer, but it would not tell the operating system that it can have the memory back. In other words, it would exactly *create* a memory leak. Whenever you want to return memory to the system, you must do so explicitly[8].

As a side not, if you look up some of this information online or in other sources, keep in mind that the pool of memory where you allocate variables with new or malloc is called the *memory heap*. This is different from a data structure known as the *heap* which we will learn about later, in Chapter 22. Unfortunately, people (including us ...) are not quite consistent in naming these.

[8] There are other programming languages that do much more of the garbage collection and memory handling for you, but C/C++ is not one of them.

Chapter 3

Strings and Streams: A Brief Review

[Note: This chapter covers material of about 0.25 lectures.]

In this class, you will frequently need to read and process strings, and input and output in C++ are typically handled using streams. While you should have learned these in your introductory programing class, we will give a brief review here.

3.1 Strings

In basic C, string are implemented just as arrays of characters. There is no separate string type. This means that you need to allocate enough space for your character array to hold any input string that you might receive. It also means that you need a special way of marking how much of that array you are *actually* using: just because you allocated, say, 80 characters in your string doesn't mean you'll always use all 80. The way C does this is by having a special role for the character `\0`. (That's the character number 0, not the actual character '0'.) It marks the end of the used part of the string.

The `string` class in C++ is a little easier to use: in particular, it hides some of the memory management for you, so that you don't have to worry about allocating enough space. It also implements some operators that you will frequently use, such as `=` (assignment), `==` (comparison) and `+` (appending strings). The `string` class also contains a number of other very useful functions. Since you'll be doing a lot of processing of data you are reading in from files in this class, you can probably save yourself a lot of work by reviewing the `string` class and its features.

One string function which is really useful in C, but to our knowledge does not have an equivalent in C++ in standard implementations, is `strtok`. It allows you to tokenize a string, i.e., break it into smaller chunks using any set of characters as separators. Check it out!

3.2 Streams

Streams are the C++ ways of interacting with files, keyboard, screen, and also strings. They typically divide into streams you read (keyboard, files, strings) and streams you write (screen, files, strings). In all cases, they are basically a sequence of characters that you are extracting from (read) or inserting into (write). They are a fairly clean abstraction of reading and writing "items" one by one.

The standard streams you'll be interacting with are the following. They require you to `#include` different header files, also listed here.

The difference between `cout` and `cerr` is twofold: First, `cout` buffers its output instead of printing it immediately, whereas `cerr` prints immediately. This makes `cerr` very useful to output debug information, whereas you'll probably write your "real" output to `cout`. They are also two different logical streams. This means that if you redirect your output to a file (which we will do when grading you), the default is that only `cout` gets redirected. So if you print debug information to `cerr`, it still appears on the screen, and doesn't

Stream	Target	Header File
cin	Keyboard	iostream
cout, cerr	Screen	iostream
ifstream	File to read	fstream
ofstream	File to write	fstream
stringstream	String	sstream

"pollute" your output. Finally, cerr often gets displayed in a different color. All this is to say: it may be good to get into the habit to print all your "real" output to cout, and all the debug output to cerr.

To extract items from an input stream, you use the >> operator, and to insert items into an output stream, you use <<.

A few things that are worth remembering about reading from an input stream. (These frequently trip students up.)

- When reading from a stream (say, cin, or a ifstream myinput), you can use cin.fail() (or myinput.fail()) to check whether the read succeeded. When one read fails (and the fail flag is set), it will remain set until you explicitly reset it with cin.clear() or myinput.clear(). Until then, all further reads will fail, since C++ assumes that until you've fixed the source of the problem, all incoming data will be unreliable now.
- Remember that >> reads until the next white space, which includes spaces, tabs, and newlines.

  Be careful here when entering things manually. If at the first prompt, you enter multiple items separated by space, they will "supply" the next few extractions. That is, if you write code like

  ```
  cout << "Please enter n:"
  cin >> n;
  cout << "Please enter m:"
  cin >> m;
  ```

  and enter "5 3" at the first prompt, it will read 5 into n and 3 into m.
- If you want to also read spaces, then instead of using >>, you should use getline, such as cin.getline() or myinput.getline(). It lets you specify a string to read into, a maximum number of characters to read, and character to stop at (default is newline), and will then read into the string. That string can later be further processed.

  Notice that you need to be a bit careful about getline at the end of a file, and reading the correct flags to avoid reading the last line multiple times.
- If you want to "clear" off the remaining characters in a stream so they don't cause issues later, you can use the ignore() function, which will ignore the next n characters (which you can specify — default is 1).

File Streams and String Streams

File streams are the typical C++ way of reading data from files. They two types are ifstream (for files you read) and ofstream (for files you write). A file stream needs to be opened before you can read/write from it. Once you have opened it, it can basically be used like cin and cout.

Notice that in file streams, when you read *over* the end of the file, you will get a fail condition. That happens after you *reach* the end of the file, which is often cause for confusion when using getline.

The other thing to keep in mind about file streams is that after you're done, you should call close() on them.

Since strings are sequences of characters, just like files, it's natural to treat them as streams as well. This is what the `stringstream` type is for. This is particularly useful when you've read an entire string and want to break it into smaller pieces, e.g., separated by spaces. You can treat the string as a `stringstream`, and then use extraction operations on it to get the different items. It's also a convenient way to convert strings to integers.

As a piece of advice, avoid using the same `stringstream` object multiple times — or if you do, at least make sure to reset it.

Chapter 4

Recursion

[Note: this chapter covers material of about 1.5 lectures.]

The adjective *recursive* means “defined in terms of itself”. (If you Google “recursion”, you get the answer: “Did you mean recursion?”) As computer scientists, we frequently run into recursion in the form of recursive functions, which are functions that call themselves (directly, or indirectly through another function). However, as we see below, another very important application is recursive definitions of objects. We will explore recursion through several examples.

4.1 Computing Factorials

The first one is to compute the factorial of n, which is defined as $n! = n \cdot (n-1) \cdot (n-2) \cdots 2 \cdot 1 = \prod_{i=1}^{n} i$. Of course, we could use iteration (a simple `for` loop) to compute $n!$.

```
int factorial(int n) {
    int p=1;
    for (int i=1; i<=n; i++)
        p*= i;
    return p;
}
```

This is a perfectly valid, and probably even the best, way to compute the factorial of a number. But instead, we would like to use this very easy example to illustrate how recursion works.

Looking at the definition, we observe that $0! = 1$ (by definition), and $n! = n \cdot (n-1)!$. This suggests a recursive solution:

```
int factorial (int n) {
    if (n==0) return 1;
    else return n*factorial(n-1);
}
```

Notice that the function `factorial` calls itself; this is what makes this a recursive implementation. Students often have trouble thinking about recursion initially. Our instinct is often to make a complete plan for the computation: first multiply n with $n-1$, then with $n-2$, and so on, all the way to 1. In a recursive solution, we instead treat most of the work as a “black box”: we don’t really worry *how* the call with parameter $n-1$ will obtain the correct results, and just trust *that* it does. (Of course, that only works if the function is actually correct.)

In class, we illustrated this with acting out recursion with a group of students. Each student was in charge of computing $n!$ only for one particular number n. The student in charge of computing 5! relied on another student to compute 4!, then used that other student’s result and multiplied it with 5. The important insight was that the student who computed 5! did *not* need to know how 4! was computed; so long as the 4! student got the right result, it could just be plugged in.

Again, to recap this once more, in a recursive solution, we don't have to think of every step, nor do we have to keep track of various intermediate results, as those are returned as values by the other function calls. Students getting started on recursion often try as hard as possible to have recursion emulate loops, by passing around "global variables" (or pointers to variables, which amounts to the same thing) that are altered and store intermediate results.

This type of thinking can take a while to get used to, but once you firmly grasp it, a lot of things — induction in CSCI 170 and dynamic programming in CSCI 270 — will come to you much more easily.

Two things that pretty much all correct recursive functions share are the following:

- A recursive function needs one or more base case: at some point, the function must hit a point where it will no longer call itself (like the `n==0` case for the factorial). Otherwise, the function will keep calling itself forever, and eventually run out of stack memory.

- Recursive calls must have "smaller" inputs than the main input. In the case of the `factorial` function, the recursive call within `factorial(n)` was for `factorial(n-1)`. In this case, it is clear that $n-1$ is "smaller" than n. In other cases, "smaller" refers to the remaining size of an array, or even a number that is closer to an upper bound. (For instance, the base case could be `i==n`, and the call with input i could be to $i+1$.)

Let us look quickly at two examples violating these conditions, and see what happens.

```
int UCLAfact (int n) // apologies to our neighboring school
{
   if (n == 0) return 1;
   else return UCLAfact (n); // error: input not getting smaller!
}

int NDfact (int n)
{
   return n*NDfact (n-1); // ...this doesn't stop!
}
```

Neither of these functions will terminate. In the first example, we do have a base case, but the recursive call has the same size. It is of course correct that $n! = n!$ (which is what the functions uses), but it doesn't help us compute it. In the second example, we do have a smaller input in the recursive call, but no base case, so the function will continue calling itself with different values forever (or until it runs out of stack space and crashes).

4.2 Binary Search

(Note: We did not cover this one in Spring of 2014. But it's a useful example to know anyway, and we'll return to it.)

Admittedly, computing factorials is not a very strong example to show why recursion is useful, since the iterative solution is short and elegant. However, we were able to illustrate some of the important properties of recursion with an easy enough general setup. Next, let us look at a somewhat more challenging task: Given a (pre-sorted) array of integers in increasing order, find the location of a target element, or return -1 if it is not in the array.

This is accomplished using the *Binary Search* algorithm: Check the middle of the remaining array. If the element is there, we are done. If the desired element is smaller, continue searching to the left of the middle element; otherwise, continue searching to the right. A corresponding iterative solution looks as follows:

```
int binarySearch (int n, int* b, int len)
{
   int lo = 0, hi = len, mid;
   while(lo <= hi) {
       mid = (hi+lo)/2;
       if (b[mid]==n) return mid;
       else if(n < b[mid])
                 hi = mid-1;
            else lo = mid+1;
    }
    return -1;
}
```

A recursive solution would look as follows instead:

```
int recSearch(int n, int* b, int lo, int hi) {
    if (hi < lo) return -1;  // not in the array
    else
      {
        int mid = (hi+lo)/2;    // the midpoint of the array
        if (n == b[mid]) return mid;    // we found it
        else if (n < b[mid])
             return recSearch(n, b, lo, mid-1);  // element to the left of the midpoint
        else return recSearch(n, b, mid+1, hi);  // element to the right of the midpoint
      }
}
```

We then call the function as `recSearch(n, b, 0, len)`. Whether you like the iterative or the recursive solution better here may be a matter of taste, but notice that there is a certain elegance to the recursive solution. When we have decided where the element must be (to the left or the right), rather than updating a variable and repeating, we simply ask the function to find it for us in that (correct) subarray, and return its return value unchanged.

Notice that both implementations will work whether the array has an even or odd number of elements. If we hadn't written `mid-1` and `mid+1` for the recursive calls, we might have needed another base case when `lo == hi`.

Let us check that we satisfy the two conditions above for a recursive solution to have a shot:

- If the array is empty (which is the case `hi < lo`), the function returns directly, reporting that the element was not found.

- If `n` is less than the midpoint, the function recurses on the left half of the array; otherwise, on the right half. In either case, because we eliminate at least the midpoint, the remaining array size is strictly smaller than before.

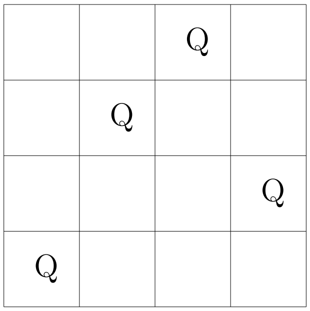
One of the things that can be confusing about recursion is that there seem to be many "active" versions of the function at once. What is "the" value of variables like `n`, `lo`, `hi`, or `mid`? After all, different invocations of the function will have different values for them. To solve this "conundrum", remember from our overview of memory that local variables are stored on the stack, and translated into memory locations by the compiler and OS. Thus, when the function `recSearch(12,b,0,10)` calls `recSearch(12,b,0,4)`, their variables `lo`, `hi` translate to completely different memory locations. When the call `recSearch(12,b,0,4)` executes, the values are `lo=0, hi=4`, and `mid=2` will be computed. In the call `recSearch(12,b,0,4)`, we instead have `lo=0, hi=10, mid=5`. The computer has no problem with the same variable name, as only one meaning of the variable is in scope at a time.

4.3 The n-Queens problem

The first two examples we saw of recursion in class were pretty easily coded with a simple loop, as you saw. In general, if you have a recursive function that uses just one recursive call to itself, it is often easily replaced by a loop. Recursion becomes much more powerful (as in: it lets you write short and elegant code for problems that would be much more messy to solve without recursion) when the function calls itself multiple times.

We will see several examples of that later in class with some clever recursive sorting algorithms and others. Another very common application is via a technique called *Backtracking* for solving complicated problems via exhaustive search. In this class, we saw the classic n-queens problem as an example for this technique.

In the n-queens problem, you want to place n queens on an $n \times n$ chessboard (square grid). Each queen occupies one square on a grid and no two queens share the same square. Two queens are *attacking* each other if one of them can travel horizontally, vertically, or diagonally and hit the square the other queen is on. The problem is to place the queens such that no two queens are attacking each other. For instance, what you see in Figure 4.1 is not a legal solution: the queens in rows 1 and 2 attack each other diagonally. (All other pairs of queens are safe, though.)



		Q	
	Q		
			Q
Q			

Figure 4.1: Illustration of the 4-queens problem

Before we try to solve the problem, we make some observations. Because queens attack each other when they are in the same row or column of the chessboard, we can phrase the problem equivalently as follows: place exactly one queen per row of the board such that no two queens are in the same column or attack each other diagonally.

We can solve this by having n variables $q[i]$, one per queen. Each variable loops from 0 to $n-1$, trying all n places in which the queen could be theoretically placed. Of all those at most n^n ways of placing the queen, we check if they are legal, and output them if so. Of course, it will be more efficient if we abort a search as soon as there is an attack between queens, since placing more queens can never fix that.

So we will have an array $q[0 \ldots (n-1)]$ that contains the positions within the rows for each of the n queens. Those will be a global variable. Also, we'll have a global variable for the size n of the grid:

```
int *q; // positions of the queens
int n;  // size of the grid
```

Then, the main search function will be of the following form:

```
void search (int row)
{
   if (row == n) printSolution (); // that function shows the layout
   else
      {
        for (q[row] = 0; q[row] < n; q[row]++)
```

```
           {
               search (row+1);
           }
      }
}
```

That's the general outline of most Backtracking solutions. At each point where a decision must be made, have a loop run over all options. Then recursively call the function for the remaining choices.

Of course, so far, we don't check anywhere to make sure that the solution is legal, i.e., no pair of queens attack each other. To do that, we want to add an array that keeps track of which squares are safe vs. attacked by a previously placed queen. We capture it in an array *t* (for "threatened"), which we can make a global variable. (It's a two-dimensional array, which translates to a pointer to a pointer.)

```
int **t;
```

Now, we need to check whether the place we're trying to place a queen at is actually legal, and update the available positions when we do. Instead of just keeping track *whether* a square is attacked by any queen, we should actually keep track of *how many* queens attack it. Otherwise, if we just set a flag to `true`, and two queens attack a square, when we move one of them, it will be hard to know whether the square is safe. The more complete version of the function now looks as follows:

```
void search (int row)
{
   if (row == n) printSolution (); // that function shows the layout
   else
      {
        for (q[row] = 0; q[row] < n; q[row]++)
           if (t[row][q[row]] == 0)
           {
               addToThreats (row, q[row], 1);
               search (row+1);
               addToThreats (row, q[row], -1);
           }
      }
}
```

We still have to write the function `addToThreats`, which increases the number of threats for the correct squares. The function should mark all places on the same column, and on the two diagonals below the current square. For the latter, we need to make sure not to leave the actual grid. Looking at it a little carefully, you'll see that the following function does that:

```
void addToThreats (int row, int column, int change)
{
   for (int j = row+1; j < n; j++)
      {
         t[j][column] += change;
         if (column+(j-row) < n) t[j][column+(j-row)] += change;
         if (column-(j-row) >= 0) t[j][column-(j-row)] += change;
      }
}
```

Finally, we need to write our `main` function that reads the size, creates the dynamic arrays, initializes them, and starts the search.

```
int main (void)
{
   cin >> n;
   q = new int [n];
   t = new int* [n];
   for (int i = 0; i < n; i++)
      {
        t[i] = new int [n];
        for (int j = 0; j < n; j ++)
            t[i][j] = 0;
      }
   search (0);
   delete [] q;
   for (int i = 0; i < n; i ++) delete [] t[i];
   delete [] t;
   return 0;
}
```

If you do not yet fully understand how the above solution works, try tracing its execution by hand on a 5 × 5 board, by simulating all the $q[i]$ variables by hand. That will probably give you a good idea of backtracking.

4.4 Some General Comments on Recursive Functions

At a high level, there are two types of recursion: *direct* and *indirect*. Direct recursion happens when a function f calls itself. That's what we have seen so far. Not quite as frequent, but still quite common, is *indirect* recursion: you have two functions f, g, and f calls g, and g calls f. There is nothing particularly deep about this distinction: we're mentioning it here mostly so that you are familiar with the terms. If you find yourself using indirect recursion and running into compiler errors, the problem could be that one of the two function definitions has to be first, and when you define that function, the compiler does not know about the other function yet. The way around that is as follows (in the examples, we assume that our functions are from `int` to `int`, but there's nothing special about that):

```
int f (int n); // just a declaration of the signature (this will often go in the .h file)

int g (int n)
{
  // insert code for g here, including calls to f
}

int f (int n)
{
  // insert code for f here, including calls to g
}
```

This way, when the compiler gets to the definition of `g`, it already knows that there is a function `f`; when it gets to `f`, you have already defined `g`.

Among direct recursion, if the function calls itself just once, there are also two common terms: *head* recursion, and *tail* recursion. These refer to when the recursive call happens. If it happens at the end of a function, this is called tail recursion. Tail recursion is particularly easily replaced by a loop. When the recursive call happens earlier than the end (e.g., at the beginning), this is called head recursion. Head recursion turns out to be able to easily do some surprising things, such as print strings or linked lists in reverse order. The distinction isn't really a huge deal, but it's probably good to have heard the terms.

Another thing to keep in mind is that there are some programming languages (called *functional languages*) in which typically all problems are solved using recursion. Several of them do not even have loops. Some examples of such languages are ML (or its variant OCAML), Lisp, Scheme, Haskell, Gofer. There are others. Some of these (in particular, ML) are actually used in industry, and Lisp is used in the Emacs editor.

Functional languages make functions much more central than procedural ones. It is very typical to write a function that takes another function as an argument. For instance, you may think of a function g that operates on an array or list, and gets passed another function f as an argument, and what it does is apply f to each element of the array/list. (For instance, you could have a function that turns each entry of an array into a string.) This operation is called *map*. Another common thing is to have a function h that applies some other function to compute a single output from an entire array/list. An example would be to sum up all elements of an array/list, or to compute the maximum. This operation is called *reduce*.

Programs that are written by applying only these two types of operations can often be very easily parallelized over large computation clusters, which is why the *Map-Reduce* framework has become quite popular lately (e.g., in Google's *Hadoop*). It has led to a resurgence in interest in some aspects of functional programming.

From a practical perspective, when you write functional programs, it often takes longer to get the program to compile, because many logical mistakes that lead to weird behavior in C++ can't even be properly implemented in a functional language. Once a functional program compiles correctly, it is much more often bug-free than a procedural program (assuming both are written by fairly experienced programmers).

4.5 Recursive Definitions

So far, we have talked about recursion as a programming technique. An almost equally important application of recursion is as a way of specifying objects concisely, by virtue of recursive definitions. These will come in very handy later on when defining lists, stacks, heaps, trees, and others. To be ready for that when we need it, we'll practice here with a few easier recursive definitions. The first of these are examples that you can define pretty easily without recursion (just like our earlier examples of using recursion as a programming technique), while the later ones may be more involved (and would be very hard to define non-recursively).

1. A string of (lower-case) letters is either: (1) the empty string (often written as ϵ or λ), or (2) a letter 'a'–'z', followed by a string of letters.

   The recursion happens in case (2), and case (1) is the base case. Of course, for this one, we could just have said that a string is a sequence of 0 or more lower-case letters, which would have been just fine. But we're practicing recursion on easy examples here.

2. A non-negative integer is either: (1) the number 0, or (2) $n + 1$, where n is a non-negative integer.

   Here, defining *what exactly* integers are without referring to integers in the first place may be a little puzzling. Recursion helps with that. It says that there is a first one (the number 0), and a way to get from one to the next one. In this sense, 4 is really just shorthand for $0 + 1 + 1 + 1 + 1$.

3. A palindrome is either: (1) the empty string ϵ, or (2) a single letter 'a'–'z', or (3) a string xPx, where x is a single letter 'a'–'z', and P is a palindrome itself.

   Here, we needed two base cases; case (3) is the recursion. Notice that the other definition of a palindrome, "a string that reads the same forward as backward", is correct, but much more procedural: it tells us how to test whether something is a palindrome ("Is it the same forward as backward?"), but it doesn't tell us how to *describe* all of them.

4. A simple algebraic expression consists of numbers, variables, parentheses, and + and *. (We leave out - and / to keep this a little shorter.) We'll use abundant parentheses and forget about the precedence

order here. We now want to express that something like "(5*(3+x))" is legal, while "x (5 * * +)" is not. We can recursively say that the following are legal expressions:

- Any number. (This is a base case, and we could use our definitions of numbers above.)
- Any variable. (This is another base case; we could use our definition of strings.)
- $(\langle A\rangle + \langle B\rangle)$, where both $\langle A\rangle$ and $\langle B\rangle$ are legal expressions themselves.
- $(\langle A\rangle * \langle B\rangle)$, where both $\langle A\rangle$ and $\langle B\rangle$ are legal expressions themselves.

For this example, you'd probably be very hard-pressed to come up with a non-recursive definition. What we have written down here is called a "context-free grammar" (or CFG). There are tools (a program called *bison*, which is the newer version of one called *yacc*) which, given such a recursive definition, will automatically generate C code for parsing inputs that conform to the definition. They are quite useful if you are trying to define your own input format or programming language.

5. In fact, following up on the previous discussion, you can write down a complete recursive definition of the C or C++ programming language. In fact, that is how programming languages are specified. It would be pretty hopeless to try this without recursion.

Chapter 5

Linked Lists

[Note: this chapter covers material of about 1 lecture.]

Arrays are nice, simple ways to store blocks of data, but we don't always know the necessary array size right off the bat. How many spaces should we reserve/allocate? Allocating up to an arbitrary size (say, 1000) is not a good idea because it may be too much or too little memory for particular cases.

Dynamically sized arrays, which we saw in the previous lectures, give us a partial solution to the problem: at least, we don't need to know the array size at *compile time*. But we do still need to know how large to make the array at *run time* when we declare it. How large do you think that Facebook should have made its user array when it started? If you have more and more customers arriving over time, it will be very hard to guess the "right" size.

In this class, we will be looking at many data structures that don't need to know the required number of elements beforehand; rather, their size can dynamically change over time. Perhaps the easiest such data structure is called the *linked list*; it nicely illustrates many of the techniques we'll see reappear many times later.

Consider how an array (dynamically or statically allocated) stores data. Whenever new users arrive, a really convenient way of dealing with it would be to just ask the operating system to expand our block of memory to the required size. However, there is no way to do this, and with good reason: the memory right after our array may be in use for some other data, so expanding our array may overwrite existing memory just after our array's memory block. A way to "expand" our array may be instead to just get a second block of memory somewhere else, and put a pointer at the end of our first block to indicate where the other half is. This loses many of the advantages of arrays, such as being able to do simple arithmetic to look up elements. But at least, it would solve the problem in principle. Once we think about it that way, we could go to the extreme and make *every* element of our "array" point to the next element, removing all semblance of an array. This is what a linked list is: a series of nodes where each one points to the next one in memory, and each node contains a piece of data. We often depict linked lists as follows:

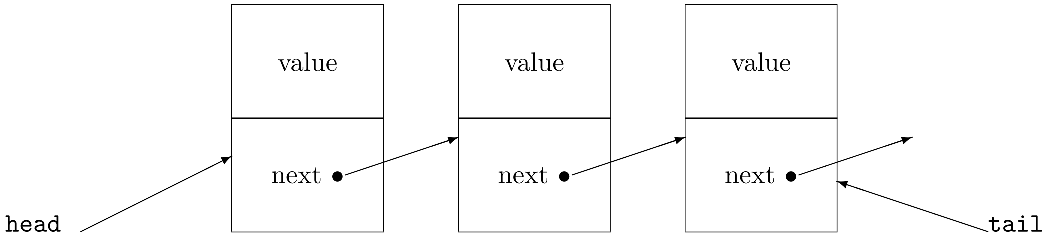


Figure 5.1: Basic illustration of a linked list

Linked lists can be made as long as we want without declaring an initial size first. All we have to do is attach a node after the last one, and ensure that the previously last element of the list now points to the new one.

It may be instructive to compare vectors and linked lists. Of course, part of why we learn about these things here is that we want to *understand* here how something like vectors works under the surface. Someone programmed vectors as an abstract data type, by using the types of primitives we are learning about in this class.

But also, there is a fundamental difference: What a vector really does is allocate a dynamic array and keep track of its size. When the size is not sufficient any more, an array with larger size will be allocated. (Typically, implementations will double the size, but this can often be changed by passing parameters into the `vector` at creation.) Next, all data will be copied from the old array to the new one. This copying could slow down the use of the data structures.

More importantly, vectors provide a functionality that we may or may not need: namely, accessing elements by an index. Linked lists don't really allow that. On the other hand, linked lists are tailored towards appending elements cheaply, and traversing all elements. Like with practically any question about "Which data structure should I use?", the answer is "It depends". Namely, it depends on what types of operations you will frequently need to use.

Finally, the main "real" reason to study linked lists is that understanding them thoroughly practices dynamic memory and recursion, and prepares you for some of the more complex data structures we will see later in the class; they rely on many of the same principles as a linked list, but are more complex. It's usually a good idea to practice with easier examples first.

Some analogies to keep in mind for linked lists are the following:

- A treasure hunt for children. The parents provide a clue for the first treasure. When the children figure out the clue, they go there, and find a treasure, along with a note that has the next clue. Following that clue, they get to the second treasure, where they find another note with a clue to the next treasure, and so on. The clues play the role of pointers.

- The game of "Assassin," in which each participant gets the name of another participant to "kill" in a an agreed-upon way (shooting with a nerf gun, touching with a plastic spoon, etc.). When one participant is "killed," his killer inherits his next assignment, and the winner is the last survivor. Again, the assignments can be thought of to form a linked list (except the tail points back at the head).

- There are several other analogies of sequential events, like dominoes, train cars, and others. What's nice about the two examples example is the explicit nature of the "pointers".

5.1 Implementing Linked Lists

Each node/element in the linked lists contains data (such as an `int`, `string`, etc.) as well as a pointer to the next node/element of the same type. Here, we will build a linked list of integers — it will be pretty obvious how to alter this for other types. In order to keep track of these two elements, we create a struct which we call `Item`.

```
struct Item {
        int value;
        Item *next;

        Item (int val, Item *n)
        { value = val; next = n; }
}
```

Every `Item` has an `int` — a piece of data in the linked list — and a pointer `next` to another node. The first node will have a pointer to the second node, and so on. For the last node, we need a way to make sure to remember that there's no node after it. The most common way is to have its next pointer go to NULL, but some people also have it link back to itself instead.

The function Item we declare inside the struct is used to make initialization easy. This way, we can just write something like `Item* p = new Item (5, NULL);` instead of `Item *p = new Item; p->value = 5; p->next = NULL;` It is basically the same as a constructor of a class, which we will learn about in roughly a week.

Note that, in order to access the first element of the list at all, we need a head pointer to the first Item. (If we lose track of this, the rest of the list can no longer be accessed.)

5.1.1 Linked list operations

At a minimum, we want to be able to add elements to our list, remove them, and traverse the entire list. Here is how to implement those.

Traversal: Unlike arrays, linked lists do not supply functionality to directly access the i^{th} element. Instead, we start from the first node and then visit the next node repeatedly. To do so, we declare a variable Item *p that will keep track of the current node we are looking at. p starts out as the pointer to the head element. Then in each iteration of a for loop, we update it to its next pointer. So the code looks like this:

```
void traverse (Item *head)
{
   for (Item *p = head; p != NULL; p = p->next)
     { // Do something with p, such as print or read its value
     }
}
```

We can also traverse a list recursively, as follows:

```
void traverse (Item *head)
{
  // Do something with head, such as print or read its value
  traverse (head->next);
}
```

The nice thing about the recursive implementation (besides its extreme simplicity) is that it is very easy to make it traverse the list in *reverse* order, even if the list is singly linked. You simply change the order of the two statements, calling traverse (head->next) *before* doing the processing (such as the printing). Notice that the task of printing a linked list in reverse order is a very popular job/internship interview question, because it tests knowledge of linked lists and recursion.

Addition: We take our input data item and create a new Item from it. This element will typically be appended to the end of the list, so its next pointer will be set to NULL. (We could also add it at the beginning of the list, which would change the implementation below.) In order to append it at the end of the list, we first need to find the last element tail, then set its next pointer to our new element.

We need a special case for a previously empty list, as then, we also have to set the head pointer which was previously NULL. In summary, the code for adding a new element looks as follows:

```
void append (Item *&head, int n)
{
  Item *newElement = new Item (n, NULL);
  if (head == NULL) head = newElement;
  else {
        Item *p = head;
        while (p->next != NULL) p = p->next;
        p->next = newElement;
       }
}
```

Notice the somewhat strange construction of the `Item *&head`. We want to pass the head of the list, which is an `Item *`. But we may also need to change it (when it was `NULL`), so we need to pass the pointer by reference.

A somewhat shorter implementation can be obtained by using recursion:

```
void append (Item *&head, int n)
{
  if (head == NULL) head = new Item (n, NULL);
  else append (head->next, n);
}
```

Notice that both the recursive and the iterative implementation have to traverse the entire list to find the last element. This seems rather inefficient, and unnecessarily so. This is why typically, it is a good idea to not only maintain a `head` pointer, but also a `tail` pointer to the last element of the list. That way, we don't have to traverse the entire list every time we want to add something.

Removal: If we are given a pointer `Item *toRemove` to an element of the list we'd like to remove, we'll eventually have the command `delete toRemove;` But before that, we also need to make sure that the link structure of the list stays intact. To do so, we need a pointer `prev` to the element right before `toRemove` in the list, so that we may set `prev->next = toRemove->next;`

One way to get this pointer (if it exists — otherwise, `toRemove` itself must be the `head` of the list) is to start from the beginning of the list and scan through until we find the node `p` with `p->next == toRemove`. But that would take a long time and be cumbersome.

The better solution is to store in each `Item` not only a pointer to the next element in the list, but also to the previous element. The result is called a *doubly linked list*, and unless you have a strong reason to prefer a singly linked list (such as a job interview or homework assignment specifying it), you should normally make your linked list doubly linked. In the definition of `Item`, we add the line `Item *prev;` In the function for adding an element, we set `newElement->prev = NULL` in the first case, and `newElement->prev = p` in the second case.

For removing an element, we can now write something like:

```
void remove (Item *&head, Item *toRemove)
{
  toRemove->prev->next = toRemove->next;
  toRemove->next->prev = toRemove->prev;
  delete toRemove;
}
```

This sets the `next` pointer of the preceding element to the `next` pointer of the element to be deleted, effectively unlinking it. Similarly for the second line with the `prev` pointers. While this looks good at first sight, we have to be more careful when the element we want to remove is the head or tail of the list (or both, for a list of a single element). Then, `toRemove->prev` or `toRemove->next` could be `NULL`, which means we can't change their pointers. However, in those cases, we don't need to update the corresponding pointers, so the actual implementation looks as follows:

```
void remove (Item *&head, Item *toRemove)
{
  if (toRemove != head)
     toRemove->prev->next = toRemove->next;
  else head = toRemove->next;
  if (toRemove->next != NULL)
     toRemove->next->prev = toRemove->prev;
  delete toRemove;
}
```

As we saw, the real reason for having doubly linked lists is that they make deletions much easier and cleaner. (For your own amusement, you should perhaps also implement deletion in a singly-linked list, and measure how much slower it is.) A side benefit is that a doubly linked list can be easily traversed back to front. Sometimes, that's listed as a reason for having a double linked list, but I think that that's a red herring: first, traversing a linked list back to front is not hard even for a singly-linked list, if you use recursion. And second, it's not a functionality that is often needed.

Once we really wrap our heads around the idea of having a pointer (or two) to other elements in our `Item`, we may ask ourselves why not have more pointers to different elements. In fact, that is exactly what we will be doing when we get to more complex data structures such as trees and heaps later on.

5.2 Recursive Definition of Linked Lists

While we know intuitively what a linked list is based on our discussion so far, we haven't defined it formally. In other words, we haven't yet said exactly how to distinguish a "Linked List" from a "Not Linked List". In trying to come up with a definition, our intuition tells us that it is a bunch of items, where each item has associated data and points to another item. But first of all, one of the items doesn't point to anything. And second, this would include a lot of nodes, all of which point to *one* other node. That's not what we want. We may try something like "a bunch of item each of which points to 1 other node, and is pointed to by 1 other node, except for one node that points to no other node and 1 node which is not pointer to by any other." This would be correct, but getting a little cumbersome.

To keep the definition short yet clear, we can draw on recursive definitions which we saw a few lectures ago, and define Linked Lists as follows:

- The empty list is a linked list.
- A node that points to a "shorter" linked list is a linked list.

We need the adjective "shorter" to exclude, for example, a one-node list where the node points to itself; in that case, it would be pointing to a linked list of the same length. (Remember that for recursive functions and definitions, we should only reference "smaller" objects, which we do so explicitly here.)

Chapter 6

Abstract Data Types

[Note: this chapter covers material of about 0.5 lectures.]

If we take a step back from what we have been doing with Linked Lists, we can think about the functionality they enable. Let's say we look at the version we just analyzed, which allows us to do three things:

1. Add an integer n to the list.
2. Remove an item from the list.
3. Print all the items in the list, in the order they were added.

If all we care about is being able to perform these three operations, it doesn't matter so much whether we implement them using linked lists, or perhaps arrays, or vectors, or some other method. What we really want is some data structure that stores data internally, and allows us to use these three operations. In other words, we focus on *what* we want to do, not *how* exactly it is done. Linked lists were one answer to *how*.

Being precise about the *what*, i.e., the operations we want to see implemented, or are implementing, is what is specified as an *Abstract Data Type (ADT)*. An ADT is defined entirely by the operations it supports, such as the ones above. In this class, we will spend a lot of time focusing on the following three ADTs.

List: A list data type is defined by supporting the following key operations (where `T` denotes any type, such as `int`, `string`, or something else):

1. `insert (int position, T value)`: inserts the value right before the given position, moving all the later elements one position to the right.
2. `remove (int position)`: removes the value at the given position, moving all later elements one position to the left.
3. `set (int position, T value)`: overwrites the given position with the given value.
4. `T get (int position)`: returns the value at the given position.

Thus, the `List` data type is a lot like an array in its functionality, but it allows inserting and removing elements while shifting all others.

Notice that this definition is not quite complete. For instance, it does not tell us what values of `position` are legal, or what happens when they are out of range. For instance, if we are trying to insert something right before position 4 of a 2-element list, what should happen? Should an error be signaled? Should the list be filled up with dummy elements to make it possible? Similarly, we haven't said what the legal ranges are of the `position` variable for the other operations. Here, we intend that `position` needs to be between 0 and `size-1` (where `size` is the number of elements in the list) for all operations except `insert`, where it needs to be between 0 and `size`.

Of course, we could add other functions that should be supported, such as `size()` or `isEmpty`. The textbook lists several others, but the four we have given are really the key functions that most define a `List`.

You are probably already familiar with the C++ `vector` and `deque` data types, which are two natural implementation of the `List` data type (and provide a few other functions). But they are not the only ones, and we will look into this a bit more soon.

Bag (set): A `set` (called `Bag` in the textbook) supports the following operations:

1. `add (T item)`: Adds the item into the set.
2. `remove (T item)`: Removes the item from the set.
3. `bool contains (T item)`: Returns whether the set contains the given item.

This is a rudimentary implementation of a mathematical set (see CSCI 170). Again, our specification isn't complete. For instance, we do not say what should happen if an item is added multiple times: are multiple copies added, or only one, and is an error signaled? If multiple copies are added, then what does `remove` do? Does it remove just one of them or multiple?

Typically, in a `set`, we only allow one copy. If we want to allow multiple copies of the same item, we call it a *multiset*.

Dictionary (map): A `map` (or `Dictionary`, as it is called in the textbook) is a data structure for creating and querying associations between *keys* and *values*. Both keys and values can be arbitrary data types `keyType` and `valueType` themselves. The supported operations are:

1. `add (keyType key, valueType value)`: Adds a mapping from `key` to `value`.
2. `remove (keyType key)`: Removes the mapping for `key`.
3. `valueType get (keyType key)`: Returns the value that `key` maps to.

Again, this is a bit underspecified. What happens if the given `key` is not in the map? What should `remove` and `get` do now? Will they signal an error? Also, if another mapping is added for the same `key`, what will happen? Can two mappings co-exist? Will an error be signaled? Does the new one overwrite the old one?

Typically, one would not allow co-existences of mappings for the same keys. The data type implements basically a (partial) function from keys to values, and you can't have a key mapping to multiple values in a function.

Let's look a bit at commonalities and differences between these abstract data types. First, all of them support storing data and accessing them; after all, they are abstract data types.

The big difference between `List` and the others is that a list really cares about the order. A list in which the number 2 is in position 0 and the number 5 in position 1 is different from a list in which the two numbers are in opposite order. On the other hand, neither a `set` nor a `map` care about order. An element is either in a set or not, but there isn't even any meaning to such a thing as an index in a set. Similarly, elements map to others under a `map`, but there is no sense in which the elements are ordered or in a designated position.

Let's illustrate this in terms of some applications for these data structures. A `List` may be a good thing for such a thing as a music playlist, the lines in a computer program, or the pages of a book. For all of them, the order of the items is important, as is the ability to access specific items by index (page, or place in a playlist). On the other hand, a `map` is a natural fit for any kind of directory (student records or e-mail address, phone book, dictionary of words, web page lookup by search query). Here, it doesn't matter in what order the items are stored, so long as it is easy, given the key, to find the corresponding record.

While a `List` is thus fundamentally different from a `map`, a `set` is actually quite similar to a `map`. The main difference is that for a `map`, we store additional information for each item that we store, whereas for the `set`, we only remember the presence (or absence) of items. In other words, `set` is a special case of `map`, where the value associated with each key is some kind of dummy that is never used. For that reason, we will not really look much at implementing `set`. Instead, we will put a lot of emphasis on implementing `map`, and `set` then falls out for free.

Of course, just because a `List` by itself is a very different object from a `map` does not mean we cannot use one to implement the other. In fact, a pretty natural (though not very efficient) way of implementing maps is to use lists as the place to store the data. It is important to notice, though that this is now a "how" question: just because we can use one technology to solve a different problem does not mean that the two are the same.

Learning which ADT most naturally fits the requirements of what you are trying to do is an important skill. That way, you separate out the implementation of whatever uses the ADT from the implementation of the ADT itself, and structure your code much better.

Chapter 7

Classes and Objects

[Note: this chapter covers material of about 0.5 lectures.]

Last time, we learned about Abstract Data Types. The notion of an Abstract Data Type goes hand in hand with Object-Oriented Design. In Object-Oriented Design of programs, we group together data items with the operations that work on them into *classes*; classes are data types, and we can then generate instances of these classes called *objects*. The objects have both the data inside them and the functions that operate on the data.

When specifying a class, we usually take good care to keep two things separate: (1) the *specification* of the functions that other classes can call. This is like the specification of an abstract data type, and usually given in a header (`.h`) file. (2) the *implementation* of how the functions are actually doing their job, and how data items are stored internally. This is in a `.cpp` file, and hidden from other classes. Hiding it allows us to change the implementation without needing to change the implementation of other pieces of code that use our classes. We will see way more about classes and object-oriented design in the next few lectures.

A *class* maps almost exactly to an Abstract Data Type; you can think of it as essentially a `struct` with functions in it. An *object* is one data item whose type matches a class; think of a class as the abstract notion of a car and the operations it supports (accelerate, slow down, honk the horn, switch on/off the lights, ...), while an object is a particular car that implements these properties. So while there is only one "car" class, there can be many objects of type "car".

Remember how we implemented Linked Lists recently? Inside our `main` function, we had a variable for the head of the list, and we provided functions for appending and removing items from the list, as well as for printing (or processing) items. In a sense, the data storage and the functions belong together. The `append` or `remove` function is useless without the data to operate on, and the data do not help us without those functions to operate on them. Classes are exactly the way to group them together.

Once you get more experienced with object-oriented design ideas, you will start thinking of your objects not just as pieces of code, but real entities which sometimes interact with each other in complex ways, notifying each other of things going on, helping each other out, and so on. One sign of a more experienced programmer in an object-oriented language (such as C++ or Java) is to be able to think of code not just as many lines in a row, but as almost an eco-system of different objects, each fulfilling its own little well-defined role, and interacting with each other in interesting and productive ways.

7.1 Header Files and Declarations

As a first cut, our class declaration for a linked list of integers may look as follows:

```
class IntLinkedList {
  void append (int n);
  void remove (Item *toRemove);
  void printlist ();
  Item *head;
}
```

Notice that the class includes both functions and data (`head`). Also notice that because the class contains the pointer `head` itself, we do not need to pass the head of the list to the function any more, as we did earlier.

Of course, we still need to implement the functions. But before going there, we notice that this is what the rest of the world really needs to know about our class: they need to know the functions to invoke and (maybe) about the variables we use. Thus, these parts should go into a *header file* (with extension `.h`), while the actual implementation will go into a `.cpp` file.

The header file should make copious use of comments to describe what *exactly* the functions do. For instance, what happens if the `toRemove` is not actually an element of the list? What format is used for printing the list?

A moment ago, we said that the header file also contains the variables `head` inside the class. While this is true, to keep our code as modular as possible, other pieces of code should not really be allowed to directly access those variables[1]. For instance, if a week later, we decide to use a `vector` implementation to achieve the same functionality, we don't want any code out there to rely on the existence of a variable named `head`. We want to hide as much about the class as possible.

The way to do this is to declare the variables `private:` this means that only functions in the class are allowed to access those variables, but not any other code. (We can also declare functions to be `private`, something we mostly do for internal helper functions.) The opposite of `private` variables/functions are `public` ones: these can be used by all other parts of the program. (There is also a `protected` modifier, which we will learn about later, when we learn about inheritance.) `private, public`, and `protected` are called *access modifiers*, since they modify who can access the corresponding elements of the class. Our new version of the class declaration will look as follows:

```
class IntLinkedList {
  public:
    void append (int n);
    void remove (Item *toRemove);
    void printlist ();

  private:
    Item *head;
}
```

In this context, it is also important to know about `get` and `set` functions. Often, you will declare a class for which you really kind of do want to be able to overwrite the elements. For instance, think about `Item`, which we previously declared as a `struct`. Instead, we could declare it as a `class`, as follows:

```
class Item {
  public:
    int value;
    Item *prev, *next;
}
```

In order to emulate the functionality of a `struct` when using a `class`, it is necessary to make all elements `public`. But making all elements `public` is very bad style: it allows other code to see the internals of a class, which could mean that changing things in the future is harder. But if we make the fields `private`, how can we read and change the `value` field? The answer is to add two functions `getValue` and `setValue`, which will read/write the `value` variable. Often, these functions can be as easy as `return value;` or `value`

[1] One downside of this example is that our `remove` function actually works with a pointer to an element. So in this sense, the implementation is not really hidden. We should overlook this issue for now, for the sake of continuing with this example.

= n;. The reason to have them is that you may later change your mind about something. For instance, you may decide that value is a bad name for the variable, and you want to call it storedNumber instead. But if you do that, then all code that referenced value will break. If you have a getValue and setValue function, then you just have to change their implementation.

More importantly, the get and set functions allow you to filter out illegal values, or perform other transformations. For instance, if you decide that only positive numbers are supposed to be stored, then you can create an error (or do something else) whenever the given value is negative. This kind of filtering can be very useful in implementing something like a Date class for storing a day of the year, or others where there is a natural desire to restrict values that can be stored.

7.2 Implementation of Member Functions

Now that we have sorted out the header file, we can think about the implementation, which we would do in a file called IntLinkedList.cpp. At the top, we would include the header file:

```
//IntLinkedList.cpp

#include "IntLinkedList.h"
```

Then, we can start associating functions with our IntLinkedList. The syntax for implementing class functions is of the following form:

```
void IntLinkedList::append (int n) {
  // implementation...
}
```

That is, the function name is really the class name, followed by two colons, and then the name of the function. This tells the compiler that this code belongs to the class. If we did not include IntLinkedList:: in the method signature, append would just be a simple global function. The compiler has no way to know that we intend our function to be part of a class, unless we either put it inside class IntLinkedList { ... } (which is bad style), or put the class name in the signature, as we just did.

For the actual implementation of the functions, we can just basically copy over the code from our previous linked list implementation — the only difference is that now, the functions are member functions of a class, rather than global functions, and the variable head is a (private) member variable of the class rather than having to be passed as a function parameter. So we won't repeat all the code here. Inside the class, you can treat all variables (even the private ones) like global variables: all member functions know about all of the class's members.

However, before moving on, let us briefly revisit our nice recursive traverse() function, which we could use, for instance, to print the entire list, or print it in reverse order. Let's look at the reverse order print version, and call it printreverse().

```
void printreverse (Item *head)
{
  printreverse (head->next);
  cout << head->value;
}
```

Here, the head pointer wasn't always pointing to the actual head of the list, but rather, we had it point to different members of the list during different function calls. On the other hand, the overall public signature for the function should probably be

```
...
  public:
    void printreverse ();
...
```

So how can we implement the recursive function? The answer is that we declare a private helper function. Something like

```
...
  private:
    void _printreversehelper (Item *p);
...
```

Then, the implementation of `printreverse` is just

```
void LinkedList::printreverse ()
{ _printreversehelper (head); }
```

7.3 Constructors and Destructors

We could now use our implementation to create an object of type `IntLinkedList` and append/remove elements from it:

```
// main.cpp
int main (void)
{
  IntLinkedList *myList = new IntLinkedList;
  for (int i = 1; i < 10; i ++) myList->append (i);
  myList->printlist ();
  return 0;
}
```

But one concern at this point is: where does the `head` variable get initialized? Earlier, we said that we express an empty linked list by having `head=NULL`. How can we be assured that when we create a new object of type `IntLinkedList`, the pointer is actually `NULL`? Because we made the variables private, we cannot add the line `head=NULL;` before the loop. So perhaps, we should create a member function `initialize` in the class `IntLinkedList`. Then, we just have to remember to call it right after generating the object.

Fortunately, C++ has a mechanism called *constructor* to do just that. We can define functions with a special name which get automatically called when we create a new object of that class. That's the right place to put initialization code. The name of a constructor is always the name of the class, and a constructor does not return anything. The constructor will be run as soon as an object is created. It looks as follows:

```
IntLinkedList::IntLinkedList() {
  head = NULL;
}
```

Notice (again) that there is no return type. You can have multiple constructors; for instance, we may add a constructor that initializes the list to contain one element with a given number already:

```
IntLinkedList::IntLinkedList(int n) {
  head = NULL;
  append (n);
}
```

If we define two constructors, when we create the object, we can write things like

```
IntLinkedList *p = new IntLinkedList (), *q = new IntLinkedList (3);
```

The first case calls the first constructor (and creates an empty list), while the second calls the second constructor (and creates a list with one item, containing the number 3). This is often useful for copying the data from one object to another, or reading an entire object from a file or a string. (We will learn more about those so-called copy constructors soon.) So long as their signatures (number or types of arguments) are different, we can create as many constructors as we want. Of course, they should all be declared in the header file, and implemented in the `.cpp` file.

Similar to the initialization, we may also want to destroy data objects we created when deleting an object. Per default, when we call `delete myList;` in the code above, it will free up the space used for storing the pointer `head`, but it will not free up any of the memory for the elements of the linked list. That is a good thing — after all, other code may still need them. So if we do want them deleted, we need to create a function that does the "opposite" of the initialization.

Such a function is called a *destructor*, and the destructor is automatically called when the object is deleted. Just as for constructors, there is a naming convention for destructors: they always have the same name as the class, with a preceding tilde: `IntLinkedList::~IntLinkedList()`. Our implementation of the destructor will look something like the following:

```
IntLinkedList::~IntLinkedList ()
{
  Item *p = head, q;
  while (p != NULL)
       {
          q = p->next;
          delete p;
          p = q;
       }
}
```

7.4 The `this` pointer

Sometimes, in implementing a member function, you will run into scoping issues, such as: a function has a local variable with the same name as a member variable. For instance, imagine that we write a `setValue` function for the class `Item`, and it looks as follows:

```
void setValue (int value)
{ // code here
}
```

We now want to somehow set the `value` field of the class to the variable value, but writing `value=value` clearly isn't going to work, since — whichever variable `value` actually refers to (the answer is the function's parameter) — both mentions of `value` will refer to the same variable. To make explicit that an assignment or other operation is talking about a member of the particular object to which the function belongs, there is the keyword `this`.

`this` is always a pointer to the object to which the method belongs. So we can write `this->value` to refer to the data of the object itself, and write the above code as:

```
void setValue (int value)
{ this->value = value; }
```

There are other, more important, uses of the `this` pointer that you will learn about, partly in this class, and more importantly as you move on. One of the most important ones arises when you have one object A generating another object B, and B is supposed to know A's identity. For instance, A could be the main part of an application, and B a part of the user interface that is being created on the fly. Now, A might want B to call some function in A when the user presses a certain button. But for that, B needs to be told the “identity” of A. The way one normally does this is that when B is created, it gets passed the `this` pointer of A, and thus knows about A.

Chapter 8

Analysis of Running Time

[Note: this chapter covers material of about 1 lecture.]

A recurring theme throughout the semester will be the following: when we design and implement data structures, we need to understand how efficiently they support different operations; this will let us decide which data structure is right for the particular task we have to perform. This means understanding what is good *and bad* about a particular data structure.

When analyzing the running time of certain operations, there are a lot of factors at play: How fast is the machine? What other processes are running? For that reason, just measurements alone don't tell us the whole story. While measuring running time empirically for a bunch of inputs is important, it must be complemented by a theoretical analysis.

8.1 Which running time?

What exactly do we mean when we talk about the running of an algorithm? Even if we resolve such issues as what exactly we are counting, on what machines, etc., there is the much more fundamental issue of: which input? Clearly, if you have an algorithm that runs on arrays, its running time will depend on what's in the arrays, or at least on how big they are. So what's really going on is that we have a function T that maps inputs I to the time it takes the algorithm, which we denote by $T(I)$. A complete description of the algorithm's running time would simply list $T(I)$ for all inputs. The problem? There are infinitely many such I (or at least a very large finite number), and unless there's a nice pattern, this will be neither feasible nor helpful. So we'd like to summarize all this information more concisely.

Usually, the standard way is to group inputs together by size. Most inputs have a natural measure of size, such as the number of bytes in a file, or the number of entries in an array. We can then write $\mathcal{I}_n$ for the set of all inputs of size n. We would now like to define $T(n)$ as somehow a summary of $T(I)$ for all inputs $I \in \mathcal{I}_n$. Then, we could figure out how the running time will grow as the size of the input gets larger, which tells us how well our solution will scale to larger scenarios.

So how should we combine the running times into one $T(n)$? There are probably three natural candidates: worst case, best case, and average case.

The best case would be defined as $T_{\text{best}}(n) = \min_{I \in \mathcal{I}_n} T(I)$. Best case clearly does not make sense; imagine promising a prospective customer that if only he feeds your program the one input it was optimized for, it will run fast enough. Not a good selling point. Forget that the notion of "best case" exists![1]

Average case is more meaningful. It would be defined as $T_{\text{avg}}(n) = \frac{1}{|\mathcal{I}_n|} \sum_{I \in \mathcal{I}_n} T(I)$. Average case also has downsides. Imagine that you are writing the software for a self-driving car, which needs to react to a car in front of yours breaking. Suppose that 99% of the time, the software reacts in 0.01s, and 1% of the time, it takes 30s. On average, it takes much less than half a second. But I'm not sure you'd like your car to crash

[1] The only reason to consider a "best case" is the following: If you can show that even in the best case, a proposed idea is very slow, then you can clearly discard it without further consideration.

1% of the time when someone breaks in front of you. What's really going on is that when you analyze an average case, what you assume is that each input is equally likely, and that the average is the right measure for you. Those assumptions are sometimes true, but if you want to make them, you should be absolutely sure that they are right. There are cases when average case analysis is the right thing, and you might see it in CS270 or more advanced algorithms classes. There is another reason against average case analysis: it's usually more technically difficult to carry out, though it can be a lot of fun if you like mathematical puzzles.

For now, the thing we care about is "worst case". The worst-case running time is defined as $T_{\text{worst}}(n) = \max_{I \in \mathcal{I}_n} T(I)$. Because it is the only one we really care about here, we'll usually just write $T(n)$ for brevity, leaving out the "worst" subscript. If you do a worst-case analysis, you can confidently promise your customers (or collaborators) that your code *never* takes more than a certain amount of time. That's the kind of useful guarantee you want.

8.2 The Value of Big-O Notation

Next, we need to think about how exactly to report those worst-case running times. Which machine? Clearly, that can make a difference, as some computers are (much) faster than others. But in the end, it's not a property of our algorithm or data structure, so maybe we shouldn't measure performance in seconds. How about we count operations that are performed? That sounds better, but it raises the question what an "operation" is. Different processors differ in whether they have a few simple operations (this is called RISC) from which you build up complex ones, or implement many complex operations. For instance, is `a[i] ++` one operation? Technically, we first have to read the value of `i`, then use it to read the value of `a[i]`, then increment it, and then write it back to its memory position. So four operations? More, depending on memory hierarchies? Quite a difficult decision.

This kind of fine-grained analysis is quite cumbersome, and also does not tell us much about whether a data structure is actually good. In order not to waste time on unimportant details, almost all theoretical analyses of running times of data structures and algorithms are carried out using big-O notation. Notice that big-O notation is not tied to running time of algorithms — you can apply it to many other functions as well. It's just that this is the area where computer scientists need it most frequently. Here is a refresher on what you should have learned by now in CSCI170 about big-O notation:

- When we say that a function (call it $T(n)$) is $O(f(n))$, we mean that $T(n) \leq c \cdot f(n)$ for all n. So T is never bigger than f times a constant.

- When we say that T is $\Omega(g(n))$, we mean that $T(n) \geq c' \cdot g(n)$ for all n. So T is never less than g times a constant $c' > 0$.

- Finally we say that T is $\Theta(f(n))$ if it is both $O(f(n))$ and $\Omega(f(n))$. That means that up to constant factors, T and f are the same function.

(Some textbooks and sources only require that the inequalities hold for all $n \geq n_0$, for some n_0. The two definitions are the same whenever $T(n)$ is guaranteed to always be positive. The subtle distinction only matters if we consider functions that could be 0, which we'll not do here.)

Big-O allows us to be sloppy in a precise sense. We know exactly what we are ignoring (constant factors, and thus also lower-order terms) and what we are keeping: the growth of T as a function of n. The latter is the important part: we want to know how well our data structure or algorithm performs as the size (e.g., number of items stored in a data structure) grows large. That's exactly what big-O notation is there for. Whenever you analyze any kind of algorithm or data structure, we recommend that you don't say that something takes "n steps", and instead say "$\Theta(n)$ steps" (or "$O(n)$ steps"). This makes clear that you understand that "steps" is an amorphous concept, and are focusing on the big picture.

8.3 Obtaining Upper and Lower Bounds

Say that you have an algorithm, and you want to figure out a form of $T(n)$ that you can actually understand, and that helps you choose the best algorithm. What is it that you need to do and prove? Here, we will look at this question a bit in the abstract, and in the next section, we will see how to do it in practice. But first, let's ask ourselves why we care about lower bounds, and not just upper bounds, on running time.

Suppose that we had two algorithms for the same problem. For one of the algorithms, we have shown that $n \leq T_1(n) \leq n^4$, and for the other, we have shown that $n^2 \leq T_2(n) \leq n^3$? (In reality, we would probably have shown that $T_1(n) = O(n^4)$ and $T_1(n) = \Omega(n)$, and $T_2(n) = O(n^3)$ and $T_2(n) = \Omega(n^2)$.) Now which algorithm is better? The answer is that we don't know. For both implementations, there's just way too wide a range of possibilities, which include scenarios in which the first is better, and ones where the second one is better. So ideally, we would like our upper and lower bounds to match, making a comparison possible. That's the case where we get that $T(n) = \Theta(f(n))$ for some function f that we can understand.

Is it always possible to get matching bounds? Yes, in principle. For each function (and thus also for $T(n)$, the worst-case running time of our algorithm), there is a correct answer: some f such that the running time is $\Theta(f(n))$. Sometimes, determining this f can be quite complex, which is why sometimes, we have upper and lower bounds that do not match. In this class, typically, it will not be too hard.

Our first hope for determining $T(n)$ would be the following: for each n just figure out the worst-case input I of that size, and then count (in big-O notation) the number of steps on input I. That would give us the running time. The problem with that approach is that figuring out the actual worst case can be very difficult or even impossible, since it may depend on a lot of things. Instead, we usually analyze upper and lower bounds using different approaches.

1. To get an upper bound of $O(f(n))$, we have to show that for *every* input $I \in \mathcal{I}_n$, the running time is at most $O(f(n))$. The way we do this is is to take an arbitrary input I, and going through our code, counting (or upper-bounding) the number of operations. Along the way, to keep things simple enough on ourselves, we drop constant factors and terms that grow less fast than the dominant term. That way, you arrive at an *upper bound* in big-O notation for the worst-case running time.

2. Students generally seem to be more mystified about using big-Ω notation with worst-case running time. After all, big-Ω gives a *lower bound*, so the natural (but wrong!) assumption is that this must involve proving that the running time is *always at least* some function $g(n)$. The mistake here is in the word "always". If we write "always", we are implicitly talking about the best-case running time. Or rather, the confusion probably arises because we substituted "running time" for "worst-case running time", i.e., we are trying to prove upper and lower bounds on the "running time". As a slightly different illustration, suppose that instead of running time, we looked at students' heights, and "worst-case" means "tallest". Then, to prove that the worst case is large, we'd just have to find at least one student who is very tall, not prove that all students are.

   So when we try to prove a lower bound on the *worst-case running time*, it is enough to show that there is *one case* of size n (for each n) on which the algorithm takes $\Omega(g(n))$ steps. We recommend that you re-read the previous paragraph a few times, to make sure it sinks in correctly.

   The input on which we get a lower bound of $T(n) = \Omega(g(n))$ could be the worst case, which would be a good choice. But since we don't necessarily know the actual worst case, it's enough to have a "pretty bad" input, which takes almost as much time as the worst case. Often, finding a "pretty bad" input is much easier to do than finding an actual worst case.

So when we have a data structure, we want to get upper and lower bounds. If we succeed in showing that $T(n) = O(f(n))$ and $T(n) = \Omega(f(n))$ (for the same function f), we have shown that $T(n) = \Theta(f(n))$; at that point, we know essentially everything there is to know about the time for the algorithm or data structure: except for ignoring constant factors, we know that on the worst-case input of size n, the function will take a constant times $f(n)$ steps.

If we know that $T(n) = O(f(n))$ and $T(n) = \Omega(g(n))$, but f and g are not the same, there are multiple alternatives:

- Our big-O analysis was not careful enough, and the task is actually performed in $O(g(n))$ steps. In that case, the algorithm may be better than we first thought.

- Our big-Ω analysis was not careful enough, and there are inputs on which it does take $\Omega(f(n))$ steps. Then, the algorithm may be worse than we first thought.

- Something in between: maybe both our upper and lower bound are wrong, and the correct answer was something between, like $\Theta(\sqrt{f(n)g(n)})$.

To summarize once more: when you say that an algorithm's worst-case running time is $O(f(n))$, you say that it can never take more than $c \cdot f(n)$ steps. When you say that it is $\Omega(g(n))$, you say that there are some cases when it is as bad as $c' \cdot g(n)$ steps.

Here's a little question about these concepts. Could it be possible that the big-Ω bound is larger than the big-O bound? For instance, could an algorithm have a running time of $O(n^2)$ and $\Omega(n^3)$? The answer is "No", as this would mean that it takes at most n^2 and at least n^3 steps in some cases, which is impossible.

8.4 Computing Upper Bounds in Practice

Hopefully, you now understand in the abstract what you need to do. If not, reread the previous section. This is something that it typically takes students a while to understand, but once you do, you will have crossed a barrier.

But the previous section doesn't tell you how to actually carry out the process of upper-bounding the running time in practice. At a very basic level, what you are trying to do is count the number of steps, while simplifying. This motivates the following rules for deriving big-O bounds:

1. If you have an elementary statement (like `a[i] ++;` or `if (x==0) return -1; else return x*x;`), those take just some constant number of steps, which we write as $O(1)$ or $\Theta(1)$. How long they take does not depend on how large your input is.

2. If you have two functions or code blocks for which you already have determined the running times to be $T_1(n)$ and $T_2(n)$, and you now have code that contains the two blocks in sequence, then you just add the times: the running time is $T(n) = T_1(n) + T_2(n)$.

3. This idea generalizes to loops. When you have a loop (say, running i from 0 to $n-1$), you execute n separate code blocks, one for $i = 0$, one for $i = 1$, and so on, up to $i = n-1$. The total time for executing them is $T(n) = \sum_{i=0}^{n-1} T_i(n)$. Notice that we added another variable i to our running time as a subscript: the time to run the block for a particular i will often (not always, though) depend on the value i.

4. Recursive functions can be a bit challenging to analyze. Typically, when the function is called with an input of size n, it performs some internal computation, which takes total time $f(n)$. And then, it calls itself once or more on smaller inputs. Suppose that those recursive calls are on inputs of sizes $n_1, n_2, \ldots, n_k$ (think of $k = 2$, meaning two recursive calls).

   How long will those recursive calls take? We don't know for real, but we have a name for it. In the worst case, they will take at most $T(n_1), T(n_2), \ldots, T(n_k)$ steps. This means that we know that $T(n) \leq f(n) + T(n_1) + T(n_2) + \ldots + T(n_k)$. This kind of relationship is called a *recurrence relation* for describing the running time of the recursion. Setting up this recurrence relation is always the first step in analyzing a recursive function. The second is *solving* the recurrence, which can sometimes be hard. But setting it up at least shows that you understood how to calculate running times, even if the actual math is difficult.

The typical way to go about it is to first set up one or more sums (if you have one or more nested loops) or to set up the recurrence relation, simplifying them as much as possible. Always do this as a first step, even if you don't know yet how to solve them.

The second step is then to determine the value of what you've set up (the sum or recurrence). Sometimes, that's pretty straightforward; other times, it can be very challenging. For dealing with sums, the following basic sums are important to remember:

- $\sum_{i=1}^{n} i = \frac{n(n+1)}{2} = \Theta(n^2)$. This is called an arithmetic series, and you *must* know it as a computer scientist. More generally, $\sum_{i=1}^{n} \Theta(i^p) = \Theta(n^{p+1})$. (The rule to remember is that sums behave roughly like integrals.)
- $\sum_{i=0}^{n} c^i = \frac{c^{n+1}-1}{c-1} = \Theta(c^n)$. This is the geometric series, and as a computer scientist, you *must* know it.
- $\sum_{i=1}^{n} 1/i = \Theta(\log n)$. This is called the Harmonic series, and is also often useful.

For dealing with recurrences, we will see a few examples and basic techniques later in the semester when we get to recursive sorting algorithms. You will learn this more in depth in CS270, where you will learn general theorems for dealing with many types of recurrences.

8.5 Some Examples

As a first example, consider the following piece of code.

```
for (int i = 0; i < n; i ++)
    for (int j = 0; j < n; j ++)
       a[i][j] = i*j;
```

The rules we saw above suggest analyzing this inside out. The line `a[i][j] = i*j` takes time $\Theta(1)$. The inner loop runs over n values of j, and $T_j(n) = \Theta(1)$ as we saw. So we get that the inner loop takes $T'_i(n) = \sum_{j=0}^{n-1} \Theta(1)$. The outer loop runs over n values of i, and takes $\sum_{i=0}^{n-1} T'_i(n) = \sum_{i=0}^{n-1} \sum_{j=0}^{n-1} \Theta(1)$. We have successfully set up the sum, and next, we need to evaluate it.

Fortunately, this one is pretty easy to evaluate: $\sum_{j=0}^{n-1} \Theta(1) = n \cdot \Theta(1) = \Theta(n)$ for the inner sum. Now, the outer sum is $\sum_{i=0}^{n-1} \Theta(n) = n \cdot \Theta(n) = \Theta(n^2)$. So the upper bound is $O(n^2)$. In fact, since there is no input, every input is worst case, and our entire analysis was in $\Theta()$ from the start. We got a running time of $\Theta(n^2)$. This example was particularly easy because the running time of the inner loop did not depend on i.

Let's do a second example, slightly more interesting:

```
for (int i = 0; i < n; i ++)
    if (a[i][0] == 0)
       for (int j = 0; j < i; j ++)
           a[i][j] = i*j;
```

There are two small changes: we added the `if` statement, and the inner loop only runs up to i. The beginning of our analysis stays the same: the innermost statement takes $\Theta(1)$. But now, when we calculate the running time of the inner loop, we get $T'_i(n) = \sum_{j=0}^{i-1} \Theta(1)$. Next, we go one level further out, to the `if` statement. What does that do? It means that there are some inputs on which the last 3 lines don't take $T'_i(n)$ steps, but only a constant number, namely, when $a[i][0] \neq 0$. So we need to convince ourselves that this part still takes $\Theta(\sum_{j=0}^{i-1} \Theta(1))$.

The upper bound $O(\sum_{j=0}^{i-1} \Theta(1))$ is clear, because we at most add a constant number of operations for the check. For the lower bound $\Omega(\sum_{j=0}^{i-1} \Theta(1))$, we want to find an input where we indeed execute the inner loop every time. That's not too hard: if we pick a bad case input on which $a[i][0] = 0$ for all i, we do call that loop. So we have convinced ourselves that the stuff inside the outer loop takes $\Theta(\sum_{j=0}^{i-1} \Theta(1))$.

So now, we can again look at the outer loop, and sum up the times for what happens inside the loop, which gives us $\sum_{i=0}^{n-1} \Theta(\sum_{j=0}^{i-1} \Theta(1))$. So we have set up the sum. Now the second step is to actually evaluate it.

The sum can be simplified a bit, by getting rid of one of the Θ, which is unnecessary, and noticing that $\sum_{j=0}^{i-1} \Theta(1) = \Theta(i)$. So now we have $\Theta(\sum_{i=0}^{n-1} i)$. That's where one of our sum formulas comes in and tells us that the result is $\Theta(n^2)$. So we again proved a tight bound of $\Theta(n^2)$.

At this point, we might start to suspect that any time we have two nested loops, the answer is $\Theta(n^2)$. Or maybe at least the product of how often they run. Unfortunately, this is not true, and it is a mistake made by many many students. Please be sure to understand this well enough to avoid. Here is an example that shows what can happen.

```
for (int i = 1; i < n; i = i*2)
    for (int j = 0; j < i; j ++)
        a[i][j] = i*j;
```

As before, the inner step takes $\Theta(1)$, so the inner loop takes time $\sum_{j=0}^{i} \Theta(1) = \Theta(i)$. But now, the outer loop is a bit more interesting. It doesn't run over all i, since instead of `i++`, we wrote `i=i*2`. So we only run over powers of 2. So the running time we get is $\Theta(1) + \Theta(2) + \Theta(4) + \Theta(8) + \ldots + \Theta(n)$. What's the value of that?

Let's first see how many terms are in this sum. Since we double i each time, there are $\log(n)$ terms (up to rounding up or down). We can write those terms as $2^0, 2^1, 2^2, \ldots, 2^{\log(n)}$. So the running time is $\sum_{k=0}^{\log(n)} \Theta(2^k)$. So we've set up our sum, and now need to evaluate it.

To evaluate, we see that we can apply the geometric series formula, which tells us that $\sum_{k=0}^{\log(n)} \Theta(2^k) = \Theta(\sum_{k=0}^{\log(n)} 2^k) = \Theta(2^{\log(n)}) = \Theta(n)$. So the running time is linear, even though we have two nested loops! Make sure you understand what happened here.

As a final example, let's look at setting up a recurrence relation. Here's a piece of code that actually does something semi-useful. (It may amuse you to find out what.)

```
int *a;

void f (int l, int r, int d)
{
  for (int i = l; i <= r; i ++)
      a[i] += d;
  if (r > l)
    {
       f(l, (l+r)/2, 0);
       f((l+r)/2+1, r, 1);
    }
}

int main ()
{
  a = new int[n];   // assume n is a power of 2
  for (int i = 0; i < n; i ++) a[i] = 0;
  f(0, n-1, 0);
  return 0;
}
```

For quick practice, let's analyze `main`. The loop takes $\Theta(n)$, the return statement $\Theta(1)$. The declaration of `a` takes $\Theta(1)$, so the total is $\Theta(n)$, plus whatever `f` takes. So we need to find that out.

Let $T(l, r, d)$ be the running time of `f` on inputs l, r, d. That's three variables, more than what we are used to. First, we notice that d doesn't really affect the running time at all, since it's just added to some values. So we can omit that. Next, we notice that `f` seems to run a loop from l to r, so the running time depends on $r - l$. Let's call that k. Then the `for` loop in the function takes time $\Theta(k)$. And the two recursive calls have regions of size $k/2$. So, because there are two recursive calls, we get the recurrence relation $T(k) = \Theta(k) + T(k/2) + T(k/2) = \Theta(k) + 2T(k/2)$.

We don't know yet how to solve this, but we will learn it in about 1.5 months. Notice that setting up the recurrence already was half the work, and showed that we understood what was going on in terms of running time.

Chapter 9

Array Lists

[Note: this chapter covers material of about 0.5 lectures.]

In Chapter 6, we introduced the List data type as one of the three central data types for this class. Remember that lists capture basically an expanding array: you can address positions by their numerical index, and get, set, insert, and remove items. As such, a List is the right data type when we need a more flexible array, which happens when we care about having data in a particular order.

We've been using our Linked List based implementation of a List as the running example for various programming tasks all semester long. An alternative implementation is based on arrays as the internal data storage. In fact, that's how C++ implements its own vector class. As a reminder, here is a C++ style definition of the core functions of the List data type. We will just define our list for integers — you will learn in Chapter 18 how to define generic template types that you can use for lists of different types of objects.

```
class List
{
   // everything assumes that pos is in bounds

   void insert (int pos, int data) = 0;
      // inserts the data immediately before position pos.
   void remove (int pos) = 0;
      // removes the data at position pos.

   int get (int pos) const = 0;
      /* returns the data stored at position pos. */
   void set (int pos, int data) = 0;
      // sets the entry at position pos to data.
}
```

Using an array to store data internally will make reading and writing individual entries nice and easy, since that's what arrays are really good at. On the other hand, arrays are not designed to delete elements from the middle or insert them in the middle. Whenever we do so, we will need to move all the items which occur to the right of that position. Also, arrays don't dynamically grow just because we want to insert more stuff. So when — as a result of our insertions — the array is not large enough any more, we need to allocate a new larger array and copy over all the data.

So internally, we will need three (private or protected) variables:

```
int *a;          // the array that contains all the data.
int length;    // the number of elements we are storing right now.
int arraysize; // the size of the array, including elements not currently in use.
```

Whatever array size we start out with, there may be a time (after enough insertions) when the array is not large enough. At that time, we will allocate a new larger array, and copy all the items over, then change a to point to the new larger array (and of course de-allocate the old array to avoid memory leaks). How much larger should that new array be? There are different approaches:

- Increase the size by 1. This way, we never "waste" space, because the array is exactly large enough to hold all its elements. But this is also inefficient, because we have to copy the whole array *every time* a new element is added. And copying is the most expensive part of the operations.

- A natural choice is to double the size of the array every time it becomes too small. That way — except for removals — the array is never more than twice as big as it really needs to be, and we are not "wasting" much space. And we will see below that we also don't waste much time on array copying this way.

- As a solution somewhere between, we could grow the array by some factor other than 2, say, by increasing the size by 10% or something like that. Or we could increase it by adding a number more than 1, say, adding 10 each time the array grows.

Implementing the get and set functions is really easy so we won't even give the code here.

For the insert function, we'll want to do something like this first:

```
void ArrayList::insert (int pos, int value) {
   length++;
   if (length > arraysize)
      //allocate new array and copy stuff over
}
```

Next, we need to make room at position pos by moving all entries from pos to length-2 one position to the right. Our first thought might be the following:

```
for (int i=pos; i < length-1; i++)
   a[i+1] = a[i];
```

However, this doesn't work because we are overwriting everything with the same initial value. By the time we get to position pos+2, we have overwritten it with the value from pos+1, which itself was previously overwritten with the value from pos. The easiest way to fix this is to move the elements in reverse order.

```
for (int i=length-2; i >= pos; i--)
    a[i+1] = a[i];
```

Notice that the starting index is length-2 because we have already incremented length earlier, so length-1 is the last element that should be in use, and we're copying to position i+1.

After we have shifted everything to the right to make room at position pos, we can write the element there using a[pos] = value.

The implementation of the remove function is quite similar. We don't need to resize the array[1], and we don't need to write a new element. But we do need to shift all elements from pos+1 all the way to length-1 one position to the left. That is done with a very similar loop. Notice that here, the loop will run from left to right (pos+1 to length-1), because the element in position i should be saved into position i-1 *before* position i is overwritten.

[1] Optionally, one could shrink the array when too much of it is unused. Again, one may want to shrink only when half or more is unused, or something in between.

9.1 Comparison of Running Times

Now that we have seen two implementations (including the Linked List one from earlier), we want to compare them and figure out which one is better. Since they have different advantages for different types of operations, we'll want to analyze the running time of the different operations in big-O notation, and see what comes out.

Let's start with the implementation based on linked lists. Here, all functions first have to find the element at a given position i, to return or change or insert or remove there. Searching for position i by iterating from the head of the list takes $\Theta(i)$ steps. After that, all of the operations take just constant time to return or overwrite the content of the node at position i, or to update a constant number of pointers. So the running time is $\Theta(i)$ for all operations, though we also want to keep in mind that it's all spent just scanning through a list and not overwriting — the amount of writing is $\Theta(1)$.

For arrays, the `get` and `set` functions take constant time $\Theta(1)$, since they know exactly what element to access. The `remove` and `insert` functions need to move all elements located to the right of the position i. There are $\Theta(n-i)$ of those elements, so we spend a total of $\Theta(n-i)$ steps moving things. So in summary, we get the following running times.

	Linked List	Array
`get (i)`	$\Theta(i)$	$\Theta(1)$
`set (i,newvalue)`	$\Theta(i)$	$\Theta(1)$
`remove(i)`	$\Theta(i)$	$\Theta(n-i)$
`insert(i,value)`	$\Theta(i)$	$\Theta(n-i)$

In the case of `insert` for an array-based implementation, we have been a little casual. We have not accounted for the cost of copying the entire array when the array needs to grow. That would take $\Theta(n)$ in addition to the $\Theta(n-i)$. If we allocate new arrays of size just one larger, this time will be incurred for each `insert`, which is quite a lot slower.

But when we always double the array size (or multiply it with a constant fraction, such as increasing by 10%), there is a nice analysis trick we can do. It is true that in the worst case, *one* `insert` operation may take a long time ($\Theta(n)$). But if we look at a sequence of many `insert` operations, then for every one that takes $\Theta(n)$, there will be n operations that will now be fast, because we know that the array has n empty locations, and won't double in size until they are full. So on average over all operations, the extra cost of $\Theta(n)$ can be averaged out over the next (or previous) n operations, so that the total average cost per operation is actually only $\Theta(n-i)$. Notice that the average here is taken over a *sequence of operations*, and not over anything random. This type of analysis, which some people consider more advanced, is called *amortized analysis*; it is quite common in analyzing more advanced data structures, and we will learn a bit more about it in Chapter 10.

The upshot of the table above is the following: if we expect to be doing mostly `get` and `set` operations, there's no debate that an array-based implementation will be much faster than one based on linked lists. If we expect to do a lot of `insert` and `remove`, then we have to trade off $\Theta(i)$ vs. $\Theta(n-i)$. There is really not much difference: linked lists do better when we access the first half of the list, while arrays do better for the second half. That doesn't really guide us, unless we have strong reason to believe that our application really will prefer one half over the other.

The one sense in which linked lists have an advantage is that most of their work only involves scanning over the list, while for arrays, much of the work is copying data around. Writing data tends to take a bit longer than reading, so we would expect the array-based implementation to be a little slower.

Chapter 10

Amortized Running Time

[Note: this chapter covers material of about 0.5 lectures.]

In Chapter 8, we stressed the importance of summing all steps that an algorithm performs, in order to accurately evaluate its running time. While sometimes, we can use shortcuts such as multiplying the number of iterations of a loop with the cost per iteration, this shortcut sometimes gives wrong answers, namely, if different iterations can have vastly different running times.

We promptly saw an example illustrating this in the analysis of array implementations of the `List` data type: if we execute `push_back`[1] repeatedly on a list, the insertion each time takes $O(1)$, but there is the risk of an expensive $\Theta(n)$ array resize happening. So the worst-case time we could guarantee per `push_back` operation was $\Theta(n)$. Yet, we also claimed that any sequence of n `push_back` operations takes only $\Theta(n)$ time in total, so the average cost per operation is $O(1)$.

Notice that this average is not taken over random *inputs*, but rather over multiple worst-case operations in sequence. We therefore call it not "average-case" running time (which is what you analyze if you assume that inputs are random), but *amortized* running time.[2] When we talk about the amortized worst-case time, we always think about a *sequence* of operations being executed, and the amortized worst-case time is then the maximum time per operation, averaged over the operations in this sequence. One then considers the worst case over all sequences.

Amortized worst-case guarantees are, theoretically speaking, somewhat weaker than absolute worst-case guarantees per operation, but in practice, we are typically quite happy if expensive operations can happen, but are rare enough not to matter in the average sense. Of course, whether this is true in a particular case depends on the application.

Later on (in particular, in Chapters 29 and 30), we will see data structures with amortized worst-case guarantees. For now, we will practice on some simple examples, in part because understanding amortized analysis will really help you grasp the fundamentals of "standard" running time analysis better.

10.1 Two Ways of Analyzing Amortized Running Time

There are two natural ways of analyzing amortized running time. One is pretty much a direct application of standard running time analysis, and will here mostly serve to illustrate standard running time analysis more carefully. It can be a bit easier when it works, but typically will be too cumbersome for sufficiently complex data structures. The other treats running time as "money," and uses credit schemes. It is a bit counter-intuitive at first, but can be very fun once well understood, and is the way you need to go when analyzing more complex data structures (such as Splay Trees, Fibonacci Heaps, etc.).

[1] We talked about the `insert` operation, but our analysis showed that if we inserted at the end of the array, the time was $O(1)$; this is what `push_back` does.

[2] *Amortization* is a concept from economics, where roughly speaking, we consider a big one-time expense against all the savings that it will cause further down the road.

For the first way, we simply consider any sequence of m operations (starting with an empty data structure), and in order to count the total time for all of the m operations, we keep track of how many of them take 1 step, 2 steps, 3 steps, etc. (up to whatever maximum M we know will never be exceeded). Then, we hope that the resulting sum $\sum_{k=1}^{M} k \cdot$ [number of operations taking k steps] is something we can calculate or at least come up with good bounds for.

For the second way, we treat time as though it were money. Instead of thinking of the computer taking one unit of time per operation, we can think of paying someone one dollar per operation. This way, clearly, the total amount of money we spend corresponds precisely to the total amount of time an algorithm takes. But one thing we can do with money that makes less sense in terms of time is to "pre-pay" for later operations. When we know that a particular step takes, say, two operations, we can pay our person four dollars instead. This puts two dollars of credit into an account, which we can use to pay for later, expensive operations. This way, at any given point in time, the total amount we have paid is no less than the total time the program has used. If there is a lot of money left over in our credit account at the end, then we have overestimated the total amount of time with our accounting scheme, but we still get a valid *upper bound* on the running time.

When we pursue the credit scheme, we sometimes just think of one big account into which all money is deposited, and from which operations are being paid for. But even more often, we think of each element of the data structure having its own little credit account, which is used to pay for operations that it is a part of.

If this idea of "pre-paying time" seems to be a little strange to you right now (after all, we can't make a later operation take shorter just by "wasting" time on the earlier operations), notice that what we are really doing here is grouping the terms of the sum describing the running time differently — we are just hiding this arithmetic under a more intuitive layer we call credits. As an example, supposed that we perform four operations, each costing 1, followed by one operation costing five. Then, the total time is $1+1+1+1+5 = 9$. We can also rewrite the 5 as $5 = 1+1+1+1+1$, and then regroup as

$$1+1+1+1+5 \;=\; 1+1+1+1+(1+1+1+1+1) \;=\; 2+2+2+2+1 \;=\; 9.$$

In the last step, we took four of the ones from the parentheses and paired them up with one of the earlier ones each, giving us 2 for each of those. This is what happens implicitly when we pretend that each of the earlier operations cost 2 instead of 1. If the expensive (5) operation had never come, then our estimate of 8 for the first four operations would have been an overestimate, but at least it would not have been wrong as an upper bound.

We will look at two simple examples (array resizing and a binary counter) in this chapter, and then see a slightly more complex example in Chapter 29, building up to the most interesting case, Splay Trees (in Chapter 30).

10.2 Revisiting Array Resizing

As our first example, let's look more carefully at the array resizing argument that we were being handwavy about in Chapter 9. Let's practice both ways of analyzing amortized running time on this simple example.

For the first approach, we notice that whenever the current array size k was a power of 2, the array gets doubled, giving us a cost of $\Theta(k)$. In all other cases, `push_back` just takes constant time $\Theta(1)$. So we can write the total running time of n operations (increasing the array size from 1 to roughly n ($2^{\lceil \log n \rceil}$, to be precise)) as follows:

$$\begin{aligned}\sum_{k=1, k \text{ is a power of 2}}^{n} \Theta(k) + \sum_{k=1, k \text{ is not a power of 2}}^{n} \Theta(1) &= \sum_{i=0}^{\lfloor \log n \rfloor} (\Theta(2^i) - \Theta(1)) + \sum_{k=1}^{n} \Theta(1) \\ &= \Theta(\sum_{i=0}^{\log n} 2^i) + \Theta(n).\end{aligned}$$

In the first step, we just rewrite the powers of 2. We also add a $\Theta(1)$ term for each power of 2 into the second sum, and subtract them back out with the $-\Theta(1)$ in the first sum. The lower-order $\Theta(1)$ terms can then be dropped from the first sum. Finally, notice that the remaining sum is a geometric series, and evaluates to $\sum_{i=0}^{\log n} 2^i = \Theta(2^{\log n}) = \Theta(n)$. So the total cost of all the `push_back` operations is $\Theta(n)$. Since there are n of them, each operation's amortized cost is $\Theta(1)$.

Let's redo the analysis with a credit scheme. Every time we push back an element into the list, we pay 3 units for it. One unit pays for the actual current operation, while the other two are put into a credit account. When the array needs to be resized, we have some number n of elements in it. At that point, we use the accumulated credits in the account to pay for the copying of the elements into the new array. So the question is: do we have enough credit to pay for all of the copying of n elements?

The most recent doubling must have happened when the array had size $n/2$. Since then, we have added $n/2$ elements, and each paid an extra 2 credits into the account when it was added. So we have n credits, which is enough to pay for constant-time operations for all of the n elements. Afterwards, of course, the credit account is empty, but that is fine, since we will have a lot of time to collect more credits before we need to double the array again.

10.3 A Binary Counter

For our second example, we analyze an n-bit binary counter. The counter has only two operations: `reset` (setting it to 0), and `advance`, which increments it by 1. It is stored internally as an array of n bits. Recall that to increment a binary number, you add 1 to its last (least significant) digit. If that digit was 1, it becomes 0 and a 1 is carried to the next higher bit, where we continue in the same way.

When the counter's current state is $0111\ldots1111$, then this sequence will result in n operations, and a final state of $1000\ldots0000$, so the worst case time for an `advance` operation is $\Theta(n)$. But such cases are very rare, and we hope that the amortized cost might be much better. For instance, whenever the current counter value is even (which is half the time), the last digit will be a '0', meaning that the cost is only $\Theta(1)$. Again, let's try to analyze the amortized worst-case time per operation using both of the techniques we discussed.

Suppose that we have incremented the counter m times. Every time the counter had '0' as its last digit (which was half the time), this cost 1 unit. When the last digits were '01' (a quarter of the time), it cost 2. When the last digits were '011' (one eighth of the time), it cost 3. More generally, a 2^{-k} fraction of the time, it cost k units. Thus, the total cost was at most (we pretend here that m is a power of 2 — if not, nothing much changes, except we have to write a few floors, and the bounds are marginally better) $\sum_{k=0}^{\log m} k \cdot m/2^k = m \cdot \sum_{k=0}^{\log m} k \cdot 2^{-k}$. We haven't learned how to evaluate the sum $\sum_{k=0}^{t} k \cdot 2^{-k}$ yet. (It wasn't among the three that every computer scientist has to have memorized.) There are a few ways to deal with sums you don't know, none if which is guaranteed to always work.

- You can approximate them with an integral, which is often a bit easier to work out. (In this case, it would require integration by parts.)
- You can learn about the finite calculus.
- You have a few regular tricks that you try (the most important of which is changing the order of summation), and hope one of them works.
- You ask Mathematica or Alpha for help, and then just prove the result by induction (which is often easier than guessing the result in the first place).

Here, for those of you interested in seeing this, is one way to evaluate this sum; this method can be easily adapted to powers other than $\frac{1}{2}$. (There are several other ways of evaluating this sum, too.)

$$\begin{aligned}
\sum_{k=0}^{t} k \cdot 2^{-k} &= \sum_{k=0}^{t} 2^{-k} \cdot \sum_{i=0}^{k-1} 1 \;=\; \sum_{k,i:0\leq i<k\leq t} \sum_{i=0}^{k-1} 2^{-k} \;=\; \sum_{i=0}^{t-1} \sum_{k=i+1}^{t} 2^{-k} \\
&\overset{\text{geometric series}}{=} \sum_{i=0}^{t-1} 2 \cdot ((1 - 2^{-(t+1)}) - (1 - 2^{-i})) \;=\; \sum_{i=0}^{t-1} (2 \cdot 2^{-i} - \tfrac{1}{2^t}) \\
&\overset{\text{geometric series}}{=} 2 - \tfrac{2}{2^t} - \tfrac{t}{2^t} \;=\; 2 - \tfrac{2+t}{2^t}.
\end{aligned}$$

So we see that the total cost for the m operations is at most $2m$, which gives us an amortized worst-case cost per operation of $O(1)$.

Let's again try to redo this with a credit scheme. This time, whenever we perform an increment, we create a digit of 1, which is added to the least significant digit. When we create a digit, we pay 2: one unit for the creation of the digit and the final write operation of this step, and one to give to this specific 1 as a credit. We will maintain the invariant that each 1 in the counter has a credit of one dollar at each time step. Initially, when the counter is all 0, there are no ones, so the invariant holds trivially. Now, when we increment a counter, consider a digit of 1 that must be added somewhere. If the digit currently in that other position is a 0, then the addition takes constant time, and the computation is done. This constant time was paid for with the first credit. If the digit in the position was a 1, then we overwrite it with 0, and create a new 1 which is carried to the next higher digit. At this point, notice that both the current 1 digit and the 1 that is already in the position that we are adding to had a credit each. With their combined 2 credits, we use one to write the digit of 0 into the location, and the other to give to the new carried digit of 1 to take along with it. This way, we ensure that the invariant is maintained at all times.

This is another way to show that the amortized cost per `advance` operation is $O(1)$.

Chapter 11

Stacks and Queues

[Note: this chapter covers material of about 0.75 lectures.]

11.1 A quick overview

Both stacks and queues are quite basic data structures, and their functionality can be implemented to run quite fast. They often serve key (if simple) roles in algorithms and inside computer systems. And it's surprising how much actually interesting behavior can be obtained from just such simple structures.

A *queue* is the natural analogue of a line at a store[1]: elements arrive one by one, get in the queue, and are removed from the queue in the order in which they arrived. This makes the order of a queue FIFO (first in, first out). Specifically, the functionality of a queue is the following:

- add an element.
- look at the oldest element.
- remove the oldest element.

We can visualize a queue like a conveyor belt on which we place the elements. One of the main uses of queues (outside of something like simulating a store) is to manage access to shared resources (such as a printer or processor). In fact, printers traditionally have a queue implemented on a server: when users try to print documents, those are added to the queue, and processed in the order they were received when the printer finishes the previous job.

A *stack* is the natural analogue of piling papers, boxes, or other important things on top of each other. At any time, we can only access the most recently added item, which sits on top. To get at the others, we first need to take care of and remove the more recent ones. This makes a stack LIFO (last in, first out). The functionality of a stack is the following:

- add an element.
- look at the most recently added element.
- remove the most recently added element.

A stack is often drawn in analogy with a physical stack of boxes/papers. Much of a program's variables (everything we don't put on the heap) is kept on the program stack. When one function in a program calls another (or itself), all its variables (and state) are saved on the stack, and then the next function starts. We

[1] In fact, in British English, the word "queue" means "line"; people there "queue up" in grocery stores instead of "lining up".

always have to finish the execution of the current function (and remove its variables) before we can access the variables of the other functions (those that called this function). Thus, by explicitly implementing a stack, we can get rid of recursion (which is what really happens in compiling a program).

Stacks are particularly useful when parsing programs or other types of recursively defined expressions. In fact, we will see an easy example momentarily. Another real-world example is the hiring/firing practices at LAUSD: when teachers need to be laid off due to budget shortages, the current rule is that the most recently hired teachers are laid off first. One may argue whether this is a reasonable rule, but it does implement a stack.

11.2 Stacks

As we said before, stacks are used internally by the compiler for implementing recursion; generally, they are useful for computations that proceed "inside out", as we will see below.

Let's assume that our stack stores elements of some type `T`. The functionality that a stack offers us more formally is the following.

- Adding an element: `void push (const T & data)`
- Look at the top (most recently-added) element: `T top ()` (also sometimes, for instance in the textbook, called `T peek ()`).
- Remove the top (most recently-added) element: `void pop()`.

Notice that the only element that we can look at or remove is the one on top of the stack. Also, in practice, to make the stack easier to use, you would probably add a function `bool isEmpty()` which returns whether there are any elements on the stack. But the above three are really what makes a stack a stack.

As with other data structures we have seen so far, we'd like to define formally what is and isn't a stack. As before, a recursive definition is perhaps clearest and simplest: A stack is either

1. the empty stack, or
2. of the form `S.push(data)`, where `S` is a stack, and `data` is a data item.

This tells us what is and isn't a stack, but it doesn't tell us the semantics of the stack functions, i.e., what exactly they do. The nice thing about stacks is that they are simple enough that we can completely specify the meaning of their functions using formulas. Some people would call these formulas the *stack axioms*:

1. For all stacks S: s.push(data).top() = data.
2. For all stacks S: s.push(data).pop() = S.

This says that if you read the top element after pushing something on a stack, you get that element back. And if you remove the top element after pushing something on the stack, you get the original stack back. The definition does not say what happens when you call `pop` or `top` on an empty stack. (In other words, we don't define `pop` or `top` for the base case of our recursive stack definition.) This is intentional: there is no real "correct" meaning that we could assign those operations. When you implement a stack, of course you will have to choose what happens, and you should document your choice. But behavior for cases that really shouldn't happen isn't really something that needs to go in a high-level definition of an abstract data type, and someone who plans to use a stack to solve a problem to solve some bigger algorithmic problems shouldn't rely on specific behavior for faulty inputs.

A second thing to reiterate is that it is really quite amazing that the stack functionality can be completely specified with two lines of math, and two simple lines at that. When we get to queues later, this will not be possible. At an intuitive level, for a stack, adding and removing come in pairs that are right next to each other, while for queues, there can be arbitrarily many elements between adding an element and seeing it again. This means that to specify the semantics of queue operations, one has to use much more advanced mathematical specifications.

At an even more philosophical level, this difference is why many mathematically inclined people prefer functional programming. Recursion by nature resembles stacks: the behavior of a function can be summarized, and then substituted where it occurs. Analyzing `for` loops, on the other hand, requires something called fixed point operators, which is much less intuitive. As a result, carefully thought through recursive solutions are often much more robust.

11.2.1 Example

As an example of something that is really easy to do with stacks, and wouldn't at all be obvious without stacks or recursion, let us look at the following task: You are given a string of characters: lowercase letters and opening and closing parentheses, brackets, and braces "([{ }])". The goal is to test if all of the parentheses/square brackets/braces match. To illustrate the task, here are some examples:

1. "([ab{c}]de())" is correct: all opening/closing braces match.
2. "([ab]]" is incorrect: the closing square bracket does not match the opening parenthesis.
3. "ab}" is incorrect: there is no opening brace matching the closing one.

We now outline an algorithm (using a stack) to recognize whether the string has matching parentheses and brackets and braces.

1. The stack starts out empty.
2. The string is scanned character by character, left to right.
   - Each time an opening brace/bracket/parenthesis is encountered, push it onto the stack.
   - When a letter is encountered, ignore it.
   - When there is a closing brace/bracket/parenthesis, check if it matches what is on top of the stack.
     - If it does, then pop the matching brace/bracket/parenthesis off the stack.
     - If it doesn't, then signal that this is bad input (mismatch).
     - If the stack was empty, then signal a bad input (missing opening parenthesis).
3. If the stack is not empty at the end, there was an unmatched opening parenthesis/bracket/brace, so signal an error.

In a sense, we can regard the above algorithm as a very rudimentary parser. It's easy to imagine putting numbers to add or multiply in there, or putting C++ code inside the braces. Indeed, most implementations of parsers for languages (programming languages, logic formulas, arithmetic expressions, ...) use stacks either explicitly or at least implicitly (through recursion).

When you use the above techniques to write a parser for formulas (e.g., a simple calculator, or a parser for a programming language, or for Boolean formulas), you would go one step further: whenever you encounter a closing parenthesis, you know that you reached the end of an expression that you are now ready to evaluate. Typically, you would now pop stuff off the stack until you have the entire internal expression, and instead push its value back on the stack. That way, you evaluate the formula inside out.

Looking ahead a little bit to proving correctness of algorithms formally, we would like to argue that the algorithm does the right thing. Of course, it is our intuition that it does — otherwise, we wouldn't have come up with this algorithm. But sometimes, we make mistakes, not just in our implementation, but also in our logic.

There are techniques for mathematically proving that a program/algorithm is correct. These are based on phrasing axioms about what exactly certain programming constructs do, such as our axioms about the stack functions above. Whenever a program contains recursion or loops, such proofs are invariably based on using induction. For loops, a key element of a correctness proof by induction is what's called a *loop invariant*: a property that will be true after each iteration of the loop, such that it's trivial that is true at the beginning (base case), and if we can prove that it holds at the end, our program has done the correct thing. Then, proving that the invariant holds from one loop to the next is exactly the induction step of a proof by induction.

While we won't do a full correctness proof by induction for this algorithm, for the curious student, the following should be pointed out: the algorithm runs a loop over all characters of the input string. The important part of the loop invariant is that at any time, the top of the stack is the most recent unmatched opening parenthesis/bracket/brace. If one were to really attempt the proof, this isn't enough to make the induction step work. The actual hypothesis needed is the following: at any stage of the processing, the stack contains all currently unmatched parentheses, in right-to-left order (top-to-bottom in the stack).

11.2.2 Implementation of a general-purpose stack

A stack can be naturally (and quite easily) implemented using either a linked list or array (so long as we dynamically resize it, the way we suggested for implementing a `List`).

For an implementation based on linked lists, we could insert and delete either at the head or tail. Both are roughly equally easy to implement, though inserting and deleting at the head may be even easier, because even a single-linked list will do:

- To push an item create a new element, link it to the old head, and make it the new head.
- To read the top, return the head's data item.
- To pop off the stack, remove the head from the list, and set its next element as the new head.

Notice that for none of these operations do we ever need to access any element's previous element. We could also perform similar operations on the tail of a linked list, but in order to pop the last element, we need to know its predecessor, which will be the new tail; so we would need a doubly linked list, or to scan through the entire list to find the new tail. The latter would of course be inefficient.

An implementation using arrays is not much more difficult: we have an array `a` and store the size of the stack in some variable, say, called `size`.

- To push an item, we write it into `a[size]` and increment `size`. If we now exceed the allocated array size, we expand the array by allocating a new larger array and copying the data over, much like we did for the `List` datatype.
- To read the top, we simply return `a[size-1]`.
- To pop an element off the stack, we decrement the size.

For both implementations, the running time of the `top` and `pop` operations is clearly $O(1)$, as we only return a directly accessible element, and update only a constant number of pointers or integer variables. For `push`, the linked list implementation is also clearly $O(1)$. For the array implementation, it is $O(1)$ except when the array size has to increase (in which case it is $\Theta(n)$). However, if we double the array size every time the array is too small (rather than, say, incrementing it only by 1), then for every operation that takes $\Omega(n)$, the next n operations will require no doubling and thus take $O(1)$. In total, those $n+1$ operations thus take $O(n)$, which means that on average, they take $O(1)$. This is another example of "amortized analysis", which was discussed in the context of the `Array List` implementation.

11.3 Queues

Recall that queues provide "First In First Out" (FIFO) access to data. When elements are added into a queue, they can be read/removed only in exactly the order in which they were added. The functionality of queues (storing elements of some type `T`) is the following:

- Adding an element: `void enqueue(const T & data)`.

- Look at the oldest element in the queue: `T peekfront()`.

- Remove the oldest element from the queue: `void dequeue()`.

As with stacks, you'd likely want to add a function `bool isEmpty()` in practice. Notice again the contrast to stacks: with a stack, you can only access (read/remove) the most recently added element, while a queue only allows you to access the oldest element.

Much like with stacks, we can define formally what is and isn't a queue. A queue is either:

1. the empty queue, or

2. of the form `Q.enqueue(data)`, where `Q` is a queue, and `data` is a data item.

As we discussed above, the precise semantics of the operations on a queue are much harder to specify, and far beyond what we can do in this class. (And unfortunately, at USC, we do not have a class on semantics of programming languages.)

11.3.1 Implementation of a queue

Just like with a stack, a queue can be implemented using a linked list or an array.

For an implementation using linked lists, we have two choices: (1) insert at the head and read/remove at the tail, or (2) insert at the tail and read/remove at the head. There's a slight advantage to the second version, because a singly linked list suffices: when we delete, we only need to set `head=head->next` (and deallocate the old `head`). In order to delete at the tail, we would need to know the tail's predecessor, which would require a doubly linked list or a linear-time search.

For an implementation using arrays, compared to stacks, we now need two integer indices: one (say, `newest`) for the position of the newest element in the array, and one (say, `oldest`) for the position of the oldest element. When enqueueing a new element, we can write it into `a[newest]` and increment `newest`. To implement `peekfront`, we can return `a[oldest]`, and to dequeue the oldest element, we can just increment `oldest` by one. As before, when enqueueing a new element and exceeding the current array size, we need to expand the array.

One downside of this implementation is that it may be quite wasteful of space. In particular if the queue is used for a long time, after a while, both `newest` and `oldest` may be large, which means that most of the array is unused. Instead, we could have the array "wrap around", by doing calculations of the index `newest` modulo the array's size. This makes better use of space, but we now have to be careful not to overwrite the older elements with newer elements. None of this is a huge obstacle, but one has to be a bit more careful in the implementation, which perhaps makes an implementation based on linked lists slightly more attractive.

The running time analysis is pretty much identical to the one for a stack. All operations are $O(1)$ because they just involve updates of a small number of variables. As before the only exception is the possible expansion of the array, which may take $\Theta(n)$, and which can again be amortized if the array size doubles (or gets *multiplied* with some number $b > 1$, rather than having something *added* to it) whenever the array is too small.

11.4 Why use restrictive data structures?

As we saw, a stack only allows access to the most recently added element, while a queue only allows access to the oldest element in the data structure. Couldn't we have a data structure that allows access to either, as we need it?

Indeed, we can. There is a data structure called `Deque`, which does exactly that: it allows adding and accessing (reading/removing) elements at both ends. If you understood how to implement a stack and a queue, implementing a `Deque` will be easy for you. So why wouldn't we use a `Deque` everywhere instead of stacks or queues?

Or, perhaps more strongly: why don't we just use the C++ `vector` class for all data structures? It combines the functionality of a stack, queue, and `List` in the sense in which we defined it in previous lectures. So it is much more powerful.

One answer to this question is pedagogical: in this class, we want to learn how these data structures work internally, and using a powerful tool without understanding it does not contribute to learning.

A second answer arises when we have to implement the data structures ourselves: if a data structure provides more functions, then it is more work to implement, and offers more places to make implementation mistakes. So if we implement them ourselves, there's something to be said for keeping our data structures simple. But of course, that argument does not apply when we use data structures provided in a programming language.

A third, and often appropriate, answer is that in order to implement more functions, the implementation of other functions may be less efficient. For instance, in order to allow access to each element in constant time, `vector` is implemented internally as an array. That may slow down the implementation of some other functions, which could be implemented faster if we didn't also need access by index.

The fourth, and real, answer lies in our goal of writing code that we and our collaborators can understand easily in the future. If you write code in which you explicitly use a variable of type `Stack`, you make it clear that all your code needs is the `Stack` functionality, which will help others (and yourself, if you return to your code weeks or months later) parse the logic of your code. If instead, you had used `Deque` or `Vector` types, others may wonder whether somewhere buried in line 1729 of your code, you actually access specific elements, or need to access both the head and tail of your `Deque`. That makes it harder to understand the logic. So in general, it is a good idea to think through your code's logic ahead of time, and only declare those data structures that you really need.

We could of course try to make this clear with our variable names, say, by writing something like `vector<int> stack`. If we do this, it might convey our intention. But of course, another interpretation would be that we had initially written `Stack<int> stack`, and then later realized that we actually needed extra functionality. But because we didn't want to rename the variable everywhere, we just changed its type to `vector<int>`, so even though the variable is called `stack`, it's not actually used as one.

So the upshot is that you should ideally declare your variables to be of the type that you actually need, not giving yourself extra functionality you don't intend to use. In particular, you may not find too many immediate uses for a `Deque`, since most of the time, you'll want either a `Stack` or `Queue`.

Chapter 12

Operator Overloading and Copy Constructors

[Note: this chapter covers material of about 1 lecture.]

In this chapter, we will first learn about overloading and operators, then see how to combine them to create easier-to-read code that utilizes operators we have come to use widely. We will also see where and how copy constructors are used, and learn about the difference between shallow and deep copying.

12.1 Overloading and Operators

Function overloading simply means having multiple functions of the same name, but with different types of parameters. For instance, when we write something like:

```
int minimum (int x, int y);
double minimum (double x, double y);
```

we have overloaded the `minimum` function. Doing this is perfectly acceptable, as the compiler can tell from the arguments which of the two function to use when you write `cout << minimum (a, b)`. It is only when you try to have two functions with the same exact signature that you run into trouble:

```
bool foo (int x);
void foo (int y);
```

Now, if you call `foo(a)` on an integer `a`, the compiler wouldn't know which of the two functions you mean, so it won't let you write this code in the first place. So overloading is nothing but having multiple functions of the same name.

Operators are symbols such as `==`, `!=`, `=` (assignment), `<=`, `+`, `-`, `++`, `*` (multiplication, and dereferencing), `[]`, `<<`, `>>`, and many others. Most operators are binary, i.e., they take two arguments, such as `x==y`, `x=y`, `a+b`, `a[i]`, but there are also some unary ones, such as `!b`, `*x`, `i++`, meaning that they only take one argument. For operators, C++ knows where the arguments go. For many operators (`=`, `==`, `<=`, `+`, `<<`), one argument goes before the operators, the other after. But for instance, for `a[i]`, one argument goes "in the middle" of the operator.

Using operators is really just shorthand for calling a function. When you write the following code:

```
    if ( a1 == a2 ) cout << "They're equal!";
```

it actually gets translated to

```
    if (operator==(a1, a2)) cout << "They're equal!";
```

If you wanted, you could directly write the second version in your code. The reason you don't do that is that it would be much harder to read. So in a sense, operator overloading is just what some people call "syntactic sugar": parts of the programming language that don't really add functionality, or even necessarily good coding practices (like code reuse), but just make your code look prettier. For instance, suppose that `x,y` are variables of some class you have written yourself. Something like

```
if (x > 0) y++;
   else if (x == 0) y = 0;
        else y --;
```

is much easier to read than

```
if (isGreater(x,0)) addOne(y);
   else if (equals(x,0)) set(y,0);
        else subtractOne(y);
```

or

```
if (x.isGreater(0)) y.addOne();
   else if (x.equals(0)) y.setEqual(0);
        else y.subtractOne();
```

The cumbersome syntax of operators does tell you how to overload operators in general: all you need to do is to overload a function whose name is the word `operator`, followed by the operator itself. For instance, if we wanted to overload the `*` operator to allow "multiplying" a number by a string (and define it to mean concatenating that many copies of the string), we could do that as follows:

```
string operator* (int n, string x)
{
  string s;
  for (int i = 0; i < n; i ++) s.append (x);
  return s;
}
```

We could now write something like `cout << 5*"Hello"` or `cout << operator*(5,"Hello")`.

12.2 The const keyword

The `const` keyword is not directly related to operator overloading or copy constructors, but this is the context where it makes a lot of sense and becomes important for the first time in this class, so we have a discussion here.

When you initially learned about passing parameters to functions by reference (with '&'), the purpose was probably always so that the function could modify the content of the variable, and the modification would be seen by whichever other function had called it. But there is another reason to pass parameters by reference: when you pass by value, a copy of your parameter is made, which involves calling the copy constructor (see Section 12.6). There are some dangers to this: if no copy constructor is implemented, the default is to make a shallow copy, and in some cases, that's not what you wanted. And if you do make a deep copy, that could be quite inefficient at times. To avoid ambiguities like this, when the types of your parameters are more complex (like `vector` or our own `ArrayList`, or later on in Chapter 18 generic/template types), it's often easiest to just pass by reference.

But if you do that, then someone using your function might suspect that you intend to alter the object that is passed in, even when that's not your intention. The solution to this is to use the `const` keyword; not only does it tell the user of your class that the function does not alter its argument, but the compiler will *ensure* that you cannot alter it. For instance, if we wanted to write a function `append` that appends the second `ArrayList` at the end of the first one, its syntax would be as follows:

```
void ArrayList::append (const ArrayList & value) {
    //code
}
```

By adding `const`, we ensure that the code inside the function can not alter the value of `value` or any of its fields. If we include code that tries to alter `value`, the compiler will return an error.[1] The main point of `const` is to make it clear to others using the function(s) about what can and cannot happen to the parameters.

Suppose that you are now implementing the `append` function above, and as part of it, you want to call some other member function on `value`. How is the compiler supposed to know that this function call will not suddenly result in changes to the member fields of `value`? This is where the second use of `const` comes in. The syntax is like in the following example:

```
ArrayList::print () const {
    //code
}
```

Here, we might be defining a function to print the `ArrayList`, which — if implemented correctly — should not alter any member fields of the object. In this case, what the `const` says is that the function `printlist` will not change *the object* on which it is called, i.e., after it executes, the object will be in the same state. This means that the function cannot alter the member variables of the object.

There is a third use of the `const` keyword. Sometimes, it is useful for a function to return its result by reference. This is typically for the same (or similar) reasons as you want to pass arguments by reference: either because you want to allow the code that calls the function to modify the returned value, or the returned value is a complex object that you don't want to call a copy constructor on. In the second case, you again want to make it clear that the returned object can/should not be altered. You do this by returning a `const` reference.

All three uses are illustrated with the following example of the `get` function of a `map` implementation:

```
const ValueType & Map::get(const KeyType & key) const;
```

Because the key could be a complicated object, you want to pass it in by reference, but the `get` function should not modify it, so we pass it by `const` reference. The `get` function should also not modify the state of the map, so the whole function is declared `const`. Finally, the value associated with the key could be a complex object, so we return it by reference, but unless we want someone to be able to modify it (and thus implicitly modify the map), we should return it by `const` reference. Notice that there are three objects around here: the key, the value, and the map. Each `const` refers to a different of those three objects that may not be altered.

Use the following as a guideline for when to mark things `const` and when to pass by reference:

- If a member function does not need to alter the object on which it runs, then mark it `const`. It cannot hurt to do so, and might help you being allowed to call this function from within a context where the object is `const`.

- If you are passing around complicated objects, unless you see a good reason to pass them by value, pass them by reference.

- If you are passing an object by reference only for the above reason, but not because the function you are writing is supposed to modify it, then pass it by `const` reference.

[1] The exact meaning of "altering" `value` is a bit subtle. To be precise, when you use the `const` keyword, you cannot make assignments to the member variables of `value`. But if `value` has a field that is a pointer (for instance, the internal array for the `ArrayList`), we *are* allowed to change what's stored at the memory locations that the pointer points to. This may at first seem unintuitive.

- If you are returning an object by reference just because it is complicated, but not because you want to be able to alter it, then return it by `const` reference.

One more thing that often confuses students about the `const` keyword: While it prevents you from changing *member* variables of the object, it of course does not prevent you from changing local variables of a function.

12.3 Operator Overloading and Classes

By far the most frequent case for operator overloading is in the context of defining new classes. For instance, if you define your own class for complex numbers (as we'll do below), you would want to overload the arithmetic operations, equality test, assignment, and a few others. And for almost any class you define, you'll likely want to overload the assignment operator, the equality test `==`, and frequently also `<<` so that you can easily print it to the screen or a file, and don't have to write separate `print()` functions to print to `cout, cerr` and files.

The syntax for operator overloading in classes is as follows. Suppose that we had declared a class `IntArray`, which stores the size of the array and an array of integers internally. We now want to add handful of operators:

```
class IntArray {
     // for binary operators
     // pattern: [RETURNTYPE] operator[OPERATOR] ([RHS DATA])
     // Example:
     bool operator== (const IntArray& otherArray) const {
        if (this->size != otherArray.size) return false;
        else (for int i = 0; i < size; i ++)
             if (this->data[i] != otherArray.data[i]) return false;
        return true;
     }

     int & operator[] (int index) {
        return data[index];
     }

     // for unary operators
     // pattern: [RETURNTYPE] operator[OPERATOR]
     // Example:
     IntArray & operator++ () {
         // increment all entries in the data field.
         for (int i = 0; i < size; i ++) data[i] ++;
         return *this;
     }

     private:
       int size;
       int *data;
}
```

We can now write things like

```
IntArray firstArray, secondArray;
// some computation to put data in the variables.
if (firstArray == secondArray) ++firstArray;
secondArray[0] = 0;
```

as shorthand for

```
IntArray firstArray, secondArray;
// some computation to put data in the variables.
if (firstArray.operator==(secondArray)) firstArray.operator++;
secondArray.operator[](0) = 0;
```

Two small notes: first, why do we have `++` return `*this`? Couldn't we make it type void? We could, but then we couldn't write things like `cout << ++a`, because the type of `++a` would be `void`. Second, why did `operator[]` return its result by reference? The reason is that we want to be able to overwrite it, as we do in the example. If we returned it by value, then overwriting would be impossible.

One type of operator we frequently overload is the assignment operator, since we routinely want to write something like `x=y` for objects of our own newly defined class. A few interesting issues come up when you define assignment operators. Let's try for our `class IntArray` above:

```
IntArray & operator= (const IntArray & otherArray) {
    this->size = otherArray.size;
    this->data = new int[this->size];
    for (int i = 0; i < this->size; i ++)
        this->data[i] = otherArray.data[i];
    return *this;
}
```

We just copied over all of the data from `otherArray`. Why did we make the assignment operator return `IntArray&` instead of `void`? The reason is the same as for the `++` operator earlier: it allows us to write a statement such as `a = b = c`, which we routinely do with other types. For that reason, when we write `b=c`, what comes out must also be of the type that can be assigned to `a`.

However, there is something else we should think about with the code above. Our class `IntArray` has dynamically allocated data (here, an internal array), so when we write `this->data = new int[this->size]`, we create a memory leak. We have to deallocate the old `data` object before making this assignment. So suppose that we added the statement `delete [] data` as the first line of our operator. Are we good now? Not quite. Think about what happens when we write the statement `a = a`. While this is not necessarily a very useful statement to write, you wouldn't want it to break someone else's code because of *your* wrong implementation of the operator. What happens now is that first, you delete all the data inside `a`, then try to copy that (deleted) stuff into `a`. So you'll just copy garbage, and likely get a segfault (if you're lucky) or really strange behavior. So what you should do is first check that you're not assigning an object to itself; once you've ensured that, it's safe to deallocate the old data in the object you're assigning to, then copy over the data from the other object. This means we should also add a first line `if (this != &otherArray)`.

12.4 Friend Access

Sticking with our integer array example, suppose that we wanted to implement an operator that multiplies all entries of the array with the same integer. We could do that as follows:

```
class IntArray {
  // other stuff
  IntArray operator* const (int multiplier)
    {
      IntArray newArray;
      newArray.size = size;
      newArray.data = new int[size];
      for (int i = 0; i < size; i ++)
          newArray.data[i] = data[i]*multiplier;
```

```
        return newArray;
     }
}
```

Now, we can write code like a*7 to multiply the entire object of type IntArray by 7. (Again, it's shorthand for a.operator*(7).) But what if we also wanted to write 7*a? That would be shorthand for 7.operator*(a), meaning that we would have to make our operator a member function of int, which we aren't allowed to do. So in this case, we will have to revert to the earlier method we saw of defining the operator not as a member function of IntArray:

```
IntArray operator* (int multiplier, const IntArray & oldArray)
  { // same implementation }
```

But now, we have another problem: our implementation accessed private data fields, and methods that are not member functions are not allowed to do that. (Let's ignore the fact that we could instead use our assignment operator and the access to individual elements using []. We're trying to learn something new here.) What can we do? We could just make the variables public, but that would defeat the idea of hiding variables that others don't need to see. What we'd really like to do is say that these variables are still private, but we'll make an exception just for this one particular function operator*. C++ has a mechanism for doing this: you do this by declaring a function a friend of a class, as follows:

```
class IntArray {
   // other stuff
   friend IntArray operator* (int multiplier, const IntArray & oldArray);
}
```

If we put this line in the definition of the class IntArray, we can then write the exact code as above outside the class, and it does get access to private variables.

Multiplying an array is nice, but you don't do it so often. The most frequent use of friend functions is for implementing the << operator for output streams. The way you do this is as follows:

```
class IntArray {
  // other stuff
  friend ostream & operator<< (ostream & o, const IntArray & a);
}

ostream & operator<< (ostream & o, const IntArray & a)
{
  for (int i = 0; i < a.size; i ++)
      o << a.data[i] << " ";
  o << "\n";
  return o;
}
```

Notice again that we wanted to access private data fields of a, so we declared << a friend function of IntArray. Also, by now you should have gotten used to the idea of why we return an ostream here: it's so that we can write cout << a << "Hello World" with multiple <<.

12.4.1 Friend Classes

The following is not directly related to operator overloading, but since we are talking about friend functions, we should also talk about friend classes. Sometimes, you want to allow not just one function, but all functions of class X to access all private members of class A. To do so, you can simply declare X a friend class of A. (Just like with friend functions, this must of course be declared in A, not in X.) The code for doing this is:

```
class A {
  public:
    friend class X;
  private:
    ...
}
```

This piece of code would ensure that any object of type X would be allowed to access all the private parts of any object of type A.

12.5 An Illustration: Complex Numbers

The following illustration was not covered in class. But it shows in more detail how to actually code with operator overloading (whereas the preceding discussion was perhaps a bit abstract).

Suppose that we want to implement a class for complex numbers. Recall that complex numbers are of the form $a + \imath b$, where a, b are real numbers, and $\imath$ is such that $\imath^2 = -1$. The addition of complex numbers is defined as expected: $(a + \imath b) + (c + \imath d) = (a + c) + \imath(b + d)$.

We can use the following definition of a very basic Complex class:

```
class Complex {
  private:
    double re, im;
  public:
    Complex (double re, double im) {
      this->re = re;
      this->im = im;
    }

    Complex (const Complex & toCopy) {
      // let's add a copy constructor while we're at it.
      // See the next section to learn about copy constructors.
      this->re = toCopy->re;
      this->im = toCopy->im;
    }

    Complex add (Complex other) const {
      double reSum = re+other.re;
      double imSum = im+other.im;
      return Complex(reSum, imSum);
    }

    string toString() const {
      return (""+re+ "+" +im+"i");
    }
}
```

Now, we could add two Complex numbers and print the sum using the following code:

```
  Complex c1 = Complex(1.5,-3.2);
  Complex c2 = Complex(1.1,1.3);
  Complex sum = c1.add(c2);
  cout << sum.toString() << endl;
```

While this works well, it is a little tedious to have to write function calls like `add()` and `toString()`. This makes comprehending the code more difficult than it needs to be. To get around this, we can use the idea of operator overloading we just saw. Instead of (or in addition to) having a function `add()`, we could overload the operator `+`, as follows:

```
  Complex operator+ (const Complex& other) const {
      return add(*this, other);
}
```

Now, we can also perform the third line of the code above using the shortcut:

```
Complex sum = c1+c2;
```

This is exactly equivalent to the previous segment, but is much easier to interpret. We can now overload a few more commonly used operators, to get a hang of it.

```
Complex operator- (const Complex & other) const {
   double reDiff = re - other.re;
   double imDiff = im - other.im;
   return Complex(reDiff, imDiff);
}

Complex operator* (const Complex & other) const {
   // look up multiplication of complex numbers if you don't remember it.
   double reProd = re*other.re - im*other.im;
   double imProd = re*other.im + im*other.re;
   return Complex(reProd, imProd);
}

bool operator==(const Complex & other) const {
   return (re==other.re && im== other.im);
}

bool operator!=(const Complex & other) const {
   return !(*this == other);
}

bool operator< (const Complex & other) const {
   double absSq = re*re+im*im;
   double otherAbsSq = other.re*other.re + other.im*other.im;
   return (absSq < otherAbsSq);
}

bool operator<= (const Complex & other) const {
   return (*this<other) || (*this==other);
}

bool operator> (const Complex & other) const {
   return !(*this<=other);
}

bool operator>=(const Complex & other) const {
   return !(*this<other);
}
```

With these definitions in place, we could now do arithmetic and comparisons on our nice `Complex` class. In order to also be able to print them, we will overload the operator `<<`. Suppose that we didn't already have the `toString()` function. Then, to stream out the complex number, we'd write code like the following simple function.

```
ostream & operator << (ostream &out, const Complex & c) {
    out << (c.re+ "+" +c.im+"i");
}
```

Since we are trying to access the private member variables, we need to make this operator a `friend` function of the class `Complex`, by putting the line

```
    friend otsream & operator<< (ostream &out, const Complex & c);
```

into the definition of `class Complex`. We can now write code including multiple `<<` in one statement, as follows:

```
  Complex c1 = Complex(1,2);
  Complex c2 = Complex(5,7);
  cout << c1 << " + " << c2 << " = " << c1+c2 << endl;
```

12.6 Copy Constructors

When we started talking about classes and objects, we also mentioned constructors briefly. It's worth mentioning explicitly now that just like any other functions, constructors can be overloaded; i.e., a single class can have many different constructors, so long as their signatures (number or types of arguments) are different.

One type of constructor that is almost always very useful is a copy constructor, which gets another object of the same type, and "copies" its contents in some way. Its signature will usually be:

```
class A {
   A (const A & otherA);
}
```

With a copy constructor, we can "copy" objects as follows:

```
    A *a1;
    // some code to put stuff in a1.
    A *a2 = new A(a1);
    // a2 now contains a copy of a1.
```

How much should a copy constructor copy? That's quite an interesting question, and depends on context. One approach is to copy exactly the data fields of your object. This is called a "shallow copy" and is what C++ produces as a default copy constructor if you don't write one. Sometimes, that's not what you want. For instance, in our example above of an integer array `IntArray`, you would copy the `size` and `data` variables. Since `data` is a pointer, you will now have two objects whose `data` pointers point to the same memory. If you make an edit in one, it will edit the other. Perhaps that's what you want, and perhaps not. If it's not what you want, then what you wanted was likely to copy all of the contents of the array to a new location as well. In that case, you'd be making what is called a "deep copy", and you have to write a copy constructor to do it correctly. Deep copies can involve a bit of work: for instance, for a linked list, you'd be making a copy of each element of the list, and linking them all up correctly as you go along. But pretty often, that's exactly what you want from a copy. So make sure you know exactly what you want to copy and why. Otherwise, you may get surprising results.

For instance, suppose that for our `IntArray` above, we make a shallow copy, and have the following implementation:

```
class IntArray {
  // other stuff
  IntArray (const IntArray & otherArray)
    { size = otherArray.size; data = otherArray.data; }
  ~IntArray ()
    { delete [] data; data = NULL; }
}

int main (void)
{
  IntArray a1;
  IntArray a2 (a1);
  return 0;
}
```

This program will segfault. What happens is that `a2` is a shallow copy of `a1`. When the program terminates, the destructors of both objects are called, to give them a chance to clean up their affairs before going away (e.g., the objects may want to store some data on disk). Let's say that `a1` gets destroyed first. Then, its `data` gets deleted, and is deallocated. But the pointer `a2.data` still points to the location, and when `a2` gets destroyed, it tries to delete memory that has already been deallocated. Sometimes, subtle errors can show up in unexpected parts of your program, caused by the wrong type of copy constructor.

Why are copy constructors so important? To return to that question, let's return to our earlier discussion of pass-by-value vs. pass-by-reference. You recall that in this class, we have been doing much of our passing of parameters by reference, and then declaring them `const` to avoid them getting altered. So far, we've been a bit vague about "passing around big objects", and "it's not clear what happens when you pass a complicated object" into a function as a parameter by value. Actually, it *is* clear what happens. C++ generates code that initializes your local variable using a copy constructor. So when you have code:

```
int foo (A myAObject)
  { ... }
```

and you call `foo (b)`, what will happen is that `myAObject` gets initialized via copy constructor from `b`. So if your objects have a good copy constructor that does exactly what you want, passing complex objects by value is perfectly fine, and your code should execute exactly as you expected (except it may be a bit inefficient to do all this copying).

Exactly the same thing applies when your function returns by value vs. returning by reference. When you return by value, the variable that you assign to (or where things are used) gets initialized by copy constructor from the local variable or whatever expression you return. Again, it's better to return by value only things for which you are sure the correct copy constructor has been implemented. Remember: when it has not been explicitly defined, C++ will generate a default copy constructor which performs a shallow copy. In particular if you dynamically allocate anything inside your object, that's likely not what you want.

Chapter 13

C++ Standard Template Library

[Note: this chapter covers material of about 0.5 lectures.]

The ADTs we have learned about and implemented so far, and most of the ones we will learn about later, actually come pre-implemented with C++, in the Standard Template Library (STL). The STL also contains implementations of several frequently used algorithms.

While many students surely have been waiting eagerly to use STL implementations instead of having to code data types from scratch, some may wonder why one would use STL. The advantage of standard libraries is that they save us some coding, and more importantly, a lot of debugging, as they presumably have been much more carefully debugged than our own code. When our own project is big enough, we'd like to avoid having to debug the basic data structures *in addition to* the high-level logic. The contents of STL can be roughly categorized as follows:

Containers : These are data structures; the name arises because they *contain* items. They can be further divided as follows:

1. Sequence containers: These are data structures in which items are accessed by the position they are stored at, like arrays. Our example from class was called `List`.
2. Associative containers: Here, items are accessed via their "identity" or key. The user does not know which index an element is stored at — in fact, there may not be a clear notion of an index. The associative data structures we have seen are `Set` and `Map`.
3. Adapters: these are restricted interfaces that give you specific functionality, such as `Stack`, `Queue`, or `Priority Queue` (we'll learn about that one soon). They are often implemented on top of other classes, such as `List`.

Algorithms : To use pre-implemented algorithms, you should `#include<algorithm>`. The algorithms all live in the `namespace std`. They are roughly divided as follows:

1. Search and compare: these are mostly iterator-based. They allow you to run some algorithm (compare elements to a given one, count/add all elements, etc.) on all elements of a container. To use these algorithms, you need to pass in an iterator of the container. A brief introduction to iterators is given below, and we will discuss them in more detail later in the semester, and in Chapter 27.
2. Sequence modification: These will affect the entire container, such as filling an array with zeros, or performing a computation on all elements. They are also iterator-based.
3. Miscellaneous: These contain mostly sorting algorithms, and algorithms for manipulating heaps, but also computing moments of a distribution and partitioning items.

13.1 More Details on Container Classes

All containers implement at least the following functions:

```
bool empty();
unsigned int size();
operator= is overloaded
iterators
```

The `size()` function doesn't tell you how many elements are in the container, but rather how many elements it can hold (which we typically call its *capacity* in class).

For all of the container classes described next, if you want to use them, you need to `#include<container-name>`, where `container-name` is the name of the container you wish to use. You also must either use `namespace std` or precede each container name with `std::`. Remember that except in your main file, using `namespace std` is generally a bad idea, as it forces every program that includes your code to use that namespace, sometimes causing clashes in variable or class names.

Also, as the name says, these classes are "templated." This means that you can easily build stacks, queueues, maps, etc., with any kinds of data stored in them (whereas earlier, we just built them for integers). You will learn later, in Chapter 18, how to build your own template classes. (It's not difficult, but can cause compiler/linker errors if you're not careful.) For now, you need to know how to use them. That's actually not hard. When STL has declarations such as

```
template <class T>
class stack {
  ...
  void push (T item);
  ...
};

template <class keyType, class valueType>
class map {
  ...
  void erase (keyType key);
  ...
}
```

you can define your own versions as follows:

```
stack<string> myStringStack;
map<int,bool> myIntToBoolMap;
```

You can substitute any types there, including ones you have defined yourself, or other container types. (For instance, you could have a map each of whose values is a stack.) To use the functions, you can now write

```
string s = "Hello World";

myStringStack.push (s);
myIntToBoolMap.erase (5);
```

In other words, C++ will automatically make sure that the right functions exist for the types you specified.

13.1.1 Sequence Containers

As we mentioned above, sequence containers are similar to List<T> from class, in that they implement access to elements typically by index position. They allow reading, overwriting, inserting, and removing. Also, most of them implement swapping, and several other functions. There are several sequence container classes, with different tradeoffs and implementations.

vector<T> : This is basically our List<T> type, implemented using an expanding (doubling) array internally.

array<T> : This implements a fixed-size array, i.e., it does not grow and does not provide insert or remove. Its interface and functionality is basically the same as a standard array. (It is available only starting with C++11.)

The main advantage over T* a = new T[100] is that it catches array indices out of bounds and throws exceptions, instead of leading to segfaults or other bad errors.

list<T> : This is a doubly-linked list. It does not allow access by index. In C++11, there is also a singly linked list as forwardlist<T>; it saves a bit of memory. The linked list contains some additional list-specific operations such as combining and splicing lists.

deque<T> : This is *not* a deque in the sense that it combines a stack with a queue. Rather, it is a data type similar to vector<T>, but implemented with non-contiguous memory blocks. (Basically, it internally keeps a lookup table which of multiple separate memory blocks to access when a particular index is requested.)

Because it does not need to copy over all elements when the size grows, inserting elements is faster. On the other hand, some operations have more complex implementations and are a bit slower. If you anticipate that you will be spending a lot of time growing your arrays, consider using deque<T> instead of vector<T>.

13.1.2 Adapter Containers

The adapter containers are called this because they "adapt" the interface of another class, and are not implemented from scratch. They provide special and restricted functionality. The three adapters in STL are stack<T>, queue<T>, and priority-queue<T>, implementing the data types we have learned about in this class, or (in the case of priority-queue<T>) will learn about soon.

13.1.3 Associative Containers

In sequence containers, we access elements by their position in the container, so it matters *where exactly* an element is stored. In associative containers, we only know that we want to insert, remove, and look up elements, but we don't care where or how they are stored, so long as the data structure can find them for us (by their identity or key) when we want to access them.

The two associative container types we have seen so far are Set<T> and Map<T1, T2>. Recall that Set<T> provides the following functions:

```
insert(T item)
remove(T item)
bool contains(T item)
```

A *Map/Dictionary* is similar, but it creates an association between a key (such as a word) and a value (such as the definition of the word). The name used in STL and elsewhere is usually map. The functions that a map should provide are:

```
insert (keyType & key, valueType & value)
remove (keyType & key)
valueType & lookUp (keyType & key)
```

While this is how we have been thinking about sets and maps, the actual implementation and naming in STL is a little different, as described below.

Different Set/Map classes

STL provides implementations of `set` and `map`, differing in several parameters.

`set<T>` : implements a set that can contain at most one copy of each element, i.e., no two elements may have the same key.

`multiset<T>` : implements a multiset of elements, which means that it may contain multiple elements with the same key.

`map<keyType, valueType>` : implements a map from keys to values, ensuring that there is at most one copy of each key.

`multimap<keyType, valueType` : implements a map from keys to values that allows the data structure to contain more than one copy of a key.

All of these data types are implemented using balanced search trees (which we will learn about in a month or so). What this means is that you will have to provide a comparison operator (i.e., overload `<=`, `<` etc.) for your type `T` if you want to use these types, or hope that whatever default is implemented will work well enough.

There is an alternative implementation using hash tables (which we will learn about right after balanced trees). To access those implementations instead, you put the word `unordered_` in front of the type's name, e.g., `unordered_map`.

The hash table implementation is often faster, but it depends on a good implementation of a hash function, which you may have to write and provide yourself to suit your type `T`. On the other hand, the tree-based version is very fast at iterating over all entries in sorted order, since that's how they are stored internally anyway.

Functions in STL Set/Map classes

Here are the most relevant functions for set in STL:

`set::insert (T element)` : inserts the element into the set. It returns an iterator to the element, but this is usually not so relevant for you.

`void set::erase (T element)` : removes the element from the set.

`size_type set::count (T element)` : returns the number of times the element occurs in the set, which is 0 or 1 for a regular set (not multiset). Allows you to test if the set contains the element.

`iterator set::find (T element)` : returns an iterator to the element in the set. You can use this for removing the element. If the element is not in the set `s`, the iterator will be equal to `s.end()`; see the discussion of iterators below.

For maps, while we had written `add` as a function with two parameters, the way it is actually implemented in STL is with just a single parameter, which is of type `pair`; a `pair` is just a `struct` of two individual types. It is essentially defined as follows:

```
template <class S, class T>
class pair {
  public:
  S first;
  T second;
  Pair (S s, T t) { first = s; second = t; }
}
```

This type is used in a number of places, as we will see. Throughout the following list, we assume that we have a `map<keyType, valueType>`.

`map::insert (pair<keyType,valueType>)` : inserts the association between `p.first` and `p.second` into the map, and returns an iterator to that element. If the map already contained an association for the key `p.first`, `insert` does not change anything, and instead returns an iterator to the existing pair.

`void map::erase (keyType key)` : removes the association for `key` from the map. If there was no association for the key, it doesn't do anything.

`size_type map::count (keyType key)` : returns the number of associations for the given `key`, which is 0 or 1 for a regular map (not multimap). Allows you to test if the map already has an assignment for the key.

`iterator map::find (keyType key)` : returns an iterator to the pair `(key, value)` associated with `key` in the map. If the key has no association in the map `m`, the iterator will be equal to `m.end()`; see the discussion of iterators below. The iterator iterates over *pairs*, so if you want to extract the value, you get it with `m.find(key)->second` (and the key itself should be `m.find(key)->first`). Make sure to test that there was actually a mapping for your `key` before you dereference the iterator.

`valueType & map::operator[] (keyType key)` : allows you to treat your map essentially like an array, by writing things like

```
map<string, int> myMap;
myMap["Hello World"] = 101;
myMap["Hello World"] = 103;
myMap["Thanks for the fish!"] = 42;
cout << myMap["Hello World"];
```

Different from the `insert` function, this one allows you to overwrite the mapping for a given key, e.g., the code above would output `103`. When you try to read the value for a key that isn't in the map, this will *insert* the key into the map, with some dummy value assigned to it. It will then return the dummy value. So be forewarned in using this!

13.1.4 Iterators

Iterators are a systematic and unified way of traversing arrays and other data structures. You will learn much more about them (including how to write your own) in Chapter 27. For now, just a quick primer on how to use them.

When you go through an array with a loop, your code might look like the following:

```
int a[10];
int *i;

for (i = a; i < a + 10; ++ i)
   cout << (*i);
```

Notice that instead of writing `a[i]`, we basically treated the index itself as a pointer. Iterators try to resemble this code as much as possible. When you have a data structure that implements/allows iterators, it will give you two functions: `a.begin()` and `a.end()`. The former gives you an iterator pointing to the "first" element, and the latter an iterator pointing to the element just after you are done (which in the above loop is `a+10`). So you would write code like this:

```
MyDataStructure a;
iterator i;

for (i = a.begin(); i != a.end(); ++ i)
   cout << (*i);
```

Iterators typically overload `=`, `==`, `!=`, `++`, `*`, and `->` so that your code looks as similar as possible to the loop over arrays. It is convention that `a.end()` is used for "We're done".

Therefore, when `it = map::find(...)` returns an iterator, its value will equal `m.end()` if the element was not found, and otherwise, it can be treated almost like a pointer in an array. In particular, you can use `*it` to get to the *pair* that the iterators is pointing to, and `(*it).second` or `it->second` to reference its second component, which is the value you want.

You can also output all the values in a map with an iterator, as follows:

```
map<string, int> m;
// put stuff into the map here first

for (iterator it = m.begin(); it != m.end(); ++it)
   cout << "Key: " << it->first << "  Value: " << it->second << "\n";
```

Chapter 14

Inheritance and Polymorphism

[Note: this chapter covers material of about 1 lecture.]

Suppose that a friend has coded an integer (or perhaps templated) List class based on linked lists and you want to create a deluxe version of it. The deluxe class `DeluxeLinkedList` would do the same thing except that it has an `isEmpty` function and an upgraded version of your friend's `print` function. There are two natural ways of accomplishing this.

1. You could just change your friend's code everywhere. But your friend may not like this; perhaps, he/she needed the particular format of printing the list, and you just destroyed his/her code. In particular if you are working on a project together, both versions may be needed at the same time, so it's not just about choosing the "better" version.

2. You could just copy and paste your friend's code and write your own modifications into the copied version. But that also has problems:

   - There are now two versions of the original code, so changes made to one have to be carefully copied over to the other. In particular, if your friend discovers a bug in his/her code, it now has to be fixed in two places (or more, if you made different versions).
   - Copying/pasting is very inelegant as a general programming technique.

Both methods also require you to have access to your friend's complete source code in the first place, and not just the compiled object files and headers.

The solution is called *inheritance*, and it is really *the* central notion of object-oriented design/programming. Given a class A, inheritance allows you to define a new class B that 'inherits' (automatically copies) all data and functions from A. Further, it allows you to modify and add functions as necessary, and overwrite existing functions. The basic syntax is as follows:

```
class B : public A
{
  ...
}
```

What this does is basically just copy-paste everything from A into B (except what you overwrite). The difference is that as soon as something is changed in A, the changed version is also used in B, so you only need to fix things in one place, and — unless you use templates (which create some problems) — you don't even need access to the implementation of A, just the header file and compiled version.

When you do this, the class you are inheriting from (here, A) is called the *base class* or *superclass*, while the class that is doing the inheriting (here, B) is called the *subclass*.

Since, as far as our thinking is concerned, the code for A is copied into B, the same rules apply for overloading functions as are in effect when you write your own class from scratch: you may overload function names so long as the functions have different signatures (numbers or types of arguments). But, as we will see, you also get to *replace* one function in A with another function in B which has the same signature.

Now that we hopefully understand the basics of inheritance, let's build `DeluxeLinkedList` by inheriting from `LinkedList`.

In class, first, we added a new function to test whether the list was empty:

```
bool DeluxeLinkedList::isEmpty () {
  return (size() == 0);
}
```

Then, we replaced the `print` function (which had previously used recursion to print the list in reverse order) with the following:

```
void DeluxeLinkedList::print() {
  for (Item *p = head; p != NULL; p = p->next)
     cout << p->value << " ";
  cout << "\n";
}
```

In addition, we put the two function headers inside

```
class DeluxeLinkedList : public LinkedList
{
  public:
    void print ();
    bool isempty ();
}
```

When we tried to compile this, the compiler noted an error, and claimed that our `DeluxeLinkedList` did not have a variable called `head`. Didn't we inherit from `LinkedList`, which has a variable called `head`?

The problem was that `head` is declared as `private` in `LinkedList`. The keyword `private` makes the variable very restricted: not even an inheriting class gets to access the variable (though of course the data item is stored in the class). A version that resembles `private` but allows all inheriting classes to access the variable directly is `protected`. Here is a summary of who is and isn't allowed to access variables or functions of a class:

public: everyone (other classes, this class) can access the field.

private: only objects of the same class can access the field. One object of class A may access the private fields of another object of class A.

protected: only objects of the same or inheriting classes can access the field.

We replaced the word `private` with `protected` in the definition of `LinkedList`, and things worked after that.

14.1 Member Visibility, Multiple Inheritance, and calling Base Class Methods

Inheritance raises a few interesting issues, such as whether subclasses (the inheriting ones) can access methods and variables from the superclasses, how to inherit from multiple classes, and how to explicitly call a member function of the base class when you are also overwriting it in the inheriting class. We will discuss those here.

14.1.1 Inheritance and Visibility

You were probably wondering why we were writing `class B : public A`; in particular, why we needed the word `public` here. When you have a class B inheriting from A, sometimes, you want to restrict access to variables that were `public` in A, i.e., make them `private` or `protected` in B. For instance, you may want to inherit the functionality of a linked list to use it, but show the world a different set of functions to call, and keep the other ones only for internal use. Then, you'd want them to become private. To do that, you can inherit in one of three ways:

public: All elements in A have the same protection in B as they had in A, so everything stays as it was.

protected: Private elements of A remain private in B, but protected and public elements of A both become protected in B. In other words, the minimum protection level for elements of A is now `protected`.

private: All elements of A become private in B.

So by writing `class B : private A` instead, we would ensure that whatever B has inherited from A cannot be accessed from any other classes: neither those inheriting from B, nor those using objects of type B.

Of course, it is important to remember that even when you inherit privately, all variables and functions that were part of A are still there in B — they are just not accessible to the outside world. But you may have some functions in B that use variables of A that are now private, so it's still possible to access those now-private members indirectly, just not directly.

14.1.2 Multiple inheritance

C++ allows a single class to inherit from multiple classes. We strongly advise you to not use this feature, as quite a few things can go wrong. For instance, if the two classes you are inheriting from have variables or functions of the same name, you get clashes. For some discussion, look up "C++ Diamond of Dread". If you find yourself inheriting from more than one class, it is often a sign that you should rethink your program's class structure.

The most frequent "legitimate" use of multiple inheritance is when you want to genuinely inherit the functionality of one class, and add functions to meet all the specs of a pure abstract class. (We'll talk about pure abstract classes momentarily.) So from the second class, you really don't "inherit" per se, but you just implement the functions that that class wants. Unfortunately, in C++, the only way to do that is multiple inheritance.

In other more naturally object-oriented languages (such as Java), purely abstract classes which specify functions you'd like to see in your class are distinguished from actual classes; in Java, they are called *Interface.* Then, you can say that your class *inherits* one class, and *implements* another interface. Unfortunately, C++ does not have a mechanism for this, so sometimes, you are stuck with multiple inheritance.

14.1.3 Calling Base Class Methods

We overwrote the `print` function in our implementation of the `DeluxeLinkedList` class. What happens if someone actually wanted to call the `LinkedList` version of `print`? For instance, suppose that instead of printing the elements in correct order, we still wanted to stick with the reverse order of `LinkedList`, but we wanted to print a message before and after. C++ allows you to do that, by explicitly putting the name of the class in front of a call. Generally, to call a function belonging to class A, you would write

```
A::functionName(parameters);
```

So specifically for the `print` function implementation, we would write

```
DeluxeLinkedList::print () {
  cout << "This is the deluxe version of print\n";
  cout << "***********************************\n";
  LinkedList::print ();
  cout << "***********************************\n";
}
```

Notice that the `print()` function does not recursively call itself, as it called the other version. Of course, if we did not add a function of the same name (as we did with `print` here), we can leave out the `A::` part, and just call it as `functionName(parameter)`, since the function is inherited, and part of our new class B.

14.2 Class Relationships

When you build a large project, you will often have objects of dozens, or even hundreds, of different classes interacting in different ways. While at first, this may seem overwhelming, if you define your class hierarchies and relationships carefully, it actually helps you organize and understand the way your code works, compared to just writing thousands of lines of code without much structure. Forming high-level conceptual ideas about how your project is organized can be really helpful.

The following three are very standard relationships between classes. However, there is way more along these lines: a topic called "design patterns" explores many different standard patterns in which classes interact. We will see a couple of simple examples later in this class, including Iterators and some QT concepts.

Is-A: We say that B *is a(n)* A if B is a more specific version of A; B has all the functionality of A and then some more. For instance, every cat *is a* mammal: it has all the abilities of a generic mammal, plus many cat-specific ones.

When you write code, *is a* relationships are typically implemented by using public inheritance: you want all the functionality of A to remain available, while possibly adding more functions or data to B.

As-A: B *as a(n)* A refers to implementing a class B using the functionality of A. B will typically look like something completely different to the outside world, but internally, it is implemented by using just A's functionality. For instance, when you sleep on someone's couch, you are implementing the functionality of "bed" using a "couch". (You implement "bed" *as a* "couch" — even though that's the opposite as you would refer to it with the verb "use".) If instead, you sit on the couch, you may be implementing the functionality of "chair" using a "couch".

When you write code, *as a* relationships are typically implemented by using protected or private inheritance: you do not want other classes to see the underlying functionality, only the new stuff you implement using it.

Has-A B *has a(n)* A if one of the fields of B is of type A. For instance, your car probably *has a* radio. That does not mean that your car itself has a function "switch station", but that it contains an object which itself has that function.

Has a relationships require no inheritance; they simply involve creating a member variable of type A in B.

The boundaries between *has a* and *as a* can be pretty fluid, and sometimes, it makes sense to think about solving a particular design issue in either way. For instance, are we implementing a `Map` *as a* `List`, or does a Map *contain* a List? In your homework, you implemented the second version, but mostly because you hadn't learned about inheritance yet. One could argue that really, one should implement a Map as a List. This distinction tends to give students a bit of trouble, so make sure you understand it.

14.3 Static vs. Dynamic Binding

We saw that when one class `B` inherits from another `A`, it can overwrite/replace some of the functions that already existed in `A`. For instance, our `DeluxLinkedList` inherited from the more basic `LinkedList`, and we changed the `print` function from one to the other.

One of the nice things that inheritance does for us is that when `B` inherits from `A`, it must have all the functionality of an object of type `A`. Therefore, we can assign objects of type `B` into variables of type `A`. In other words, for our example of `DeluxeLinkedList` inheriting from `LinkedList`, the following would be perfectly valid code:

```
    LinkedList *p;
    DeluxeLinkedList *q = new DeluxeLinkedList ();
    p = q;
    p->print();
```

Figure 14.1: Which version of `print` is called?

Because by our inheritance, every `DeluxeLinkedList` is-a `LinkedList`, we can assign objects of type `DeluxeLinkedList` into variables of type `LinkedList`. And because objects of type `LinkedList` have a `print` function, we can call it.

Notice that this assignment only works in this direction: assigning a more specific object to a less specific variable. This way, we can be sure that the actual object has all of the required functionality. It does not work the other way 'round. Think about a real-world example: we have one class "human" and one class "student", which inherits from "human". Every student has all the abilities of a generic human, plus some extra ones. When you need a human for a particular task (e.g., "donate blood"), you can just substitute a student. But when you need a student (e.g., for "take exam"), you cannot substitute just any human, since they may not be of the right type to know how to execute the necessary functions.

Also notice that this works only for *public* inheritance. If a class inherits from another privately or protectedly, it does not have the same methods and variables visible, so you may not be able to use it. For instance, if you were planning to use your "couch" for sitting on it, and you implemented "bed" as-a "couch", then the bed is not helpful: by hiding the "couch" functionality, it cannot be used as a couch any more.

Now that we know that we can use a `DeluxeLinkedList` anywhere that a `LinkedList` has been called for, the following question arises: since `DeluxeLinkedList` and `LinkedList` both implement different versions of a `print` function, which one is called in the last line? We could try out two arguments:

1. The compiler knows that `p` points to an object of type `LinkedList`. It cannot really figure out by code analysis that it so happens that this time (not even always), `p` points to an object that's actually of type `DeluxeLinkedList`. So the call must be to the version of `print` defined in `LinkedList`.

2. While the compiler does not know at compile time what exactly `p` points to, when it comes time to actually *call* a function (during execution), it must know the precise object that's pointed to by `p`, and it so happens to be of type `DeluxeLinkedList`. Therefore, the call will be to the version of `print` defined in `DeluxeLinkedList`.

It turns out that both are by themselves valid arguments. The first version is the default. If we do not put any additional instructions in the code, C++ will call the version of the function corresponding to the declared type of the variable we are using. This is called *static binding.*

But sometimes, we would really like the second option to happen — we will see some examples in a moment. We can tell the compiler to do this, by declaring the `print` function to be *virtual.* We do this by just adding the word `virtual` in the definition of the function (both in the parent and child class), as follows:

```
class LinkedList {
   ...
   virtual void print ();
   ...
}
```

The keyword `virtual` tells the compiler to not try to figure out at compile time which version of the function to call, but leave that decision until runtime, when it knows precisely the type of the object. This process — figuring out which version of the function to call at runtime — is called *dynamic binding*, as opposed to *static binding*, which is when the compiler figures out at compile time which version to call.

14.4 Pure virtual functions and abstract classes

Sometimes, we want to declare a function in a class, but not implement it at all; we will see in a moment why. Such a function is called a *pure virtual function.* The declaration lives entirely in the base classes' header files, and we do not need to care about it at all from the implementation files. The syntax is

```
class A {
  public:
  virtual void print() = 0;
}
```

The `= 0` part tells the compiler that the class does not implement this function. Of course, if a class has one or more pure virtual functions in it, the class cannot be instantiated. Such a class is called an *abstract class.* No object can be created from an abstract class. After all, if we could create objects, then what would code like the following do?

```
A *obj = new A;
obj->print();
```

What code should be executed when we get to `obj->print()`? There is no function to call.

14.4.1 Why and how to use virtual functions

The main reason to create pure virtual functions is to force inheriting classes to implement a function. For instance, in our example above, if we later implement classes `B` and `C` which inherit from `A`, we have forced them to provide a `print()` function. So we can safely call the `print()` function on them.

This kind of stuff is very useful in structuring one's classes, and in avoiding code (and error) duplication. For a standard example, imagine that you are developing a graphics program that lets you draw basic shapes. Since all graphics objects (rectangles, circles, polygons, etc.) share some properties (such as perhaps color, line width, line style, and a few others) and maybe also some functionality, you may want to define a general class `GraphicsObject` which captures those. You also want each of these objects to provide some functions, such as perhaps `draw` (drawing itself), `resize`, or others. But absent a specific definition of an object type (e.g., circle), you don't know how to implement the functions yet. Yet, you want to force all `GraphicsObject` objects you later define to provide these functions, so that you can put them all in one big array and process them the same way. In other words, you would like to do something like the following:

```
  List<GraphicsObject> allMyObjects;
  // code that loads a bunch of different objects into the list.
  for (int i = 0; i < allMyObject.size(); i ++)
     List[i].draw();
```

Even though `allMyObjects` may contain many different types of graphics objects, so long as all of them inherit from `GraphicsObject`, and thus have to implement a `draw()` function, the above code will work perfectly fine.

The way to get there is to declare pure virtual functions draw(), resize(), and whatever other functions you want. Now, all classes you define later (like Circle, Rectangle, Polygon, etc.) that inherit from GraphicsObject must implement this function in order to have objects generated from them.

This type of thing is also very useful to specify an abstract data type, and separate its functionality from its implementation. After all, we have said before that an abstract data type is characterized by the functions it supports, and there may be many ways to implement them. For instance, a while back, we specified the ADT Set, which looks as follows when written as an abstract class. (Let's say we're interested in sets of integers.)

```
class Set {
  public :
     virtual void add (int item) = 0;
     virtual void remove (int item) = 0;
     virtual bool contains (int item) const = 0;
}
```

This only says that any class that wants to implement a Set must provide these functions. Another programmer can then create, say, a LinkedListSet, an ArraySet, a VectorSet, etc. All these classes would inherit from Set and implement the functions, though they could do so in very different ways. By inheriting from the abstract class Set, these other classes have made sure to be very easily interchanged, as follows:

```
   Set * p;
   p = new LinkedListSet();
   ... // some time later
   delete p;
   p = new ArraySet();
```

Using dynamic binding here (indicated by the virtual keyword), the code has no problem calling the right version of each function, and we can use different implementations interchangeably.

What would happen if we try to define something like a non-virtual unimplemented function?

```
  void add (int n) = 0;
```

This results in an error. There is no point in having a non-virtual non-defined function. If it's not defined, it cannot be called. And if it is not virtual, then when we overwrite it later, the compiler cannot figure out to call the overwriting version, unless the object is already of type B, in which case there is no need for inheriting.

Another classic reason for using virtual functions is that we can often avoid rewriting very similar code. For instance, imagine that we are implementing an abstract data type (say, List), and focus on variants of the insert function. In addition to the basic insert version, we want to provide a bunch of special functions, like pushback (which inserts at the end), pushfront (which inserts at the beginning), and maye also others.

Since the functions like pushback can be described in terms of insert, and what pushback does looks the same regardless of the implementation of insert, we could write code like the following:

```
class IncompleteList {
    public:
       void pushback (int item);
       void pushfront (int item);
       void insert (int n, int item) = 0;
}
```

We could now implement the pushback and pushfront functions once and for all, and reuse the code in this way. Something like this:

```
IncompleteList::pushback (int item) {
  insert (size(), item);
}

IncompleteList::pushfront (int item) {
  insert (0, item);
}
```

Then, our `LinkedList` and `ArrayList` and `VectorList` wouldn't have to implement each of the functions `pushback`, `pushfront`, from scratch, but just to provide the missing piece `insert`. Because the `insert` function is virtual, whenever in the course of executing `pushfront`, the program runs into `insert`, it determines at runtime which version of `insert` to call.

This concept — determining which version of a class member function to call at runtime — is called *polymorphism*, which literally means "many forms": the object stored in a variable could be one of many forms, and the execution will do "the right thing" for the current object.

14.5 Constructors and Destructors with Inheritance

Suppose that you have a class B which is inheriting from A. What happens when you write something like the following?

```
B *myB = new B ();
```

First, appropriate space is reserved on the heap for the object of type B. But then, a constructor needs to be called. You will clearly want to call a cosntructor for B, in our case the default constructor. But if A has some private variables (which B inherits), how will they get initialized? The answer is that *before* the constructor of class B is called, C++ calls a constructor for class A. If you don't explicitly specify which constructor for A to call, C++ will substitute the default constructor. If you want to call another constructor, you have to say so explicitly.

Here's how you do this. Suppose that A has a constructor that passes a `string` as a parameter. For B, you want to implement a constructor that gets a `string` and an `int`, and uses A's constructor with a string. Here's what the code would look like:

```
class B : public A {
  public:
    B (string s, int n) : A (s)
     { rest of the code here }
}
```

So after the name of the constructor, you put a colon and then the constructor you want to call from the superclass. Again: it is important to remember that C++ always calls constructors for all superclasses before the constructor for the class itself.

How about destructors? The same argument suggests that in addition to the destructor for B, we will also need to call the destructor for A at some point. After all, A may have dynamically allocated memory for a private variable, and the only way to safely deallocate it is to have A's destructor take care of it.

Calls to destructors happen in the reverse order of constructors. That is, first the destructor of B is called, and then the destructor of A. This makes sense, since B's stuff is built "on top of" A: so we need to cleanly remove B's stuff first before it is safe to remove the stuff from A.

For destructors, since classes only have one (with no parameters), you don't have to worry about explicitly calling one or the other. C++ takes care of the destructor call chain for you; all you need to do is be aware of it, and not destroy in the destructor of B any data that you will then again attempt to destroy in A.

However, something that you should *always* do whenever you have classes that are inheriting or being inherited from is making the destructors `virtual`. This is very important for the following reason. Look back at our example in Figure 14.1. When we call `delete p`, which destructor is supposed to be called? Clearly, since we have an object of type `DeluxeLinkedList`, it may have extra data, so it would be important to call its destructor. But if the destructor is not virtual, then C++ can only go by the "official" type of `p`, which is `LinkedList`. It would call the wrong destructor, which may result in a memory leak or worse. For that reason, any class that has any chance of being inherited from, and any class that inherits from another, should make the destructor virtual.

As a general rule for both constructors and destructors, the constructor and destructor of inheriting classes should take care of the additional issues for their own class, but leave the other parts to the superclass.

Also notice that if you have an abstract class, you do not need to implement any constructors or destructors for it — in particular, for a pure abstract class, it makes no sense to build constructors or destructors.

Chapter 15

Error Handling and Exceptions

[Note: this chapter covers material of about 0.5 lectures.]

15.1 Handling errors

In previous lectures, we implemented a linked list. Suppose that we had added a function `int get (int position)` which returns the element at the given position. Now someone else who got hold of our code writes the following:

```
LinkedList *LL = new LinkedList;
for (int i = 0; i < 10; i ++) LL->append (i);
cout << s->get(15) << endl;
```

When `get(15)` is called, the List does not have 15 elements yet. What should be returned? If we ran a loop of 15 steps through the list, the result here will likely be an attempt at dereferencing a `NULL` pointer, triggering a segfault. The program will quit, and the person using our Linked List will not really know what went wrong (except after some debugging). Also, simply ending the program may not be the right thing to do here. What's the right way to deal with this problem?

- The simplest way is to claim that this is not your problem, and hold the user responsible for correct usage of your code. This falls into the broader paradigm "garbage in, garbage out". This is not a completely unreasonable position to hold; the person wanting to use your class should make sure to test whether the stack is empty before accessing it. But as we all know, "should" does not mean "will", and your goal when writing code is not necessarily to help others develop good habits, but to develop good code yourself.
- A second idea would be to return a 'magic' value like -1. This might work when the list is known to only contain positive values; the programmer could then use the unexpected return to debug their code. However, if the list can contain any integers, there is no "safe" magic value. And for a more general list (of a templated type), this solution is untenable, as we wouldn't even know what to return. Further, the programmer might simply choose to ignore bad returns, which would cause errors to trickle up.
- A third, and somewhat better, approach is to use the `assert` statement. In general, `assert` statements are good debugging technique. For instance, we could insert the statement `assert (position < this->size())` as a first line of `get()`. (To use `assert` statements, you need to `#include<cassert>`.)

  An `assert` statement simply causes the program to crash when the asserted condition fails to hold. While this is still a crash, at least, it gives more useful information, namely, printing in which line the crash happened, and what condition failed. This helps significantly in debugging. However, the program still crashes, which means that it does not have the option of dealing with the error themselves.

These solutions all still involve crashes, which may not be the best way to handle mistakes, e.g., if you're running the backend database for a major website, or the control software for a rocket or a nuclear power plant. Instead, it would be better to actually signal to the caller of our function that something went wrong (and what), and give it a chance to handle the mistake.

15.2 Setting Flags

The way errors are traditionally signaled in C is by making the function return a `bool` instead of the actual value we're interested in, and passing the actual value by reference in another variable. The following example illustrates this:

```
bool LinkedList::get (int position, int & val)
{
   if (position < this->size()) {
      Item *p = head;
      for (int i = 0; i < position; i ++)
        p = p->next;
      val = p->value;
      return true;
    } else return false;
}
```

This is a significant improvement. A slight downside is that the calling function may still ignore the `bool` value, and simply use the undefined value in `val`.

15.3 Exceptions

The C++ solution is to use exceptions. Exceptions allow us to provide feedback about the success of an operation, in such a way that a caller *must* deal with the failure condition explicitly. The basic use of an exception is as follows:

1. Upon failure, the method notifies the calling code by "throwing" an exception.

2. This exception propagates "up" through the program stack until it reaches a piece of code designed to handle it; it continues there.

3. If no such code is found, the program terminates.

As an illustration, a revised version of our `get()` function may look as follows:

```
int LinkedList::get(int position) {
    if (position >= this->size()) throw logic_error ("position was too large!");
    else {
      Item *p = head;
      for (int i = 0; i < position; i ++)
        p = p->next;
      return p->value;
    }
}
```

Whenever you want to write code that throws/handles exception, you should `#include<exception>`. In principle, any kind of object (even an integer, or an `Item`) can be "thrown" and treated as an exception. However, typically, you would like to only use objects that inherit from the class `exception`, since they contain some standard methods that tell you about what caused the exception. C++ also provides a few standard "types" of exceptions pre-implemented in `#include<stdexcept>`; for instance, the class `logic_error` we used above is included in that header file. Throwing a type of exception whose name (and content) reflect the type of error that happened helps in understanding what error occurred.

At the point at which an exception can be reasonably handled, we use the `try-catch` construct to deal with it. `try` is used for a block that may throw an exception; `catch` provides code to execute in case an exception actually does happen. If a piece of code would not know what to do with an exception, it should *not* catch it, and instead let it percolate up to a higher level, where it may be reasonably handled. In our earlier list example, the `main` function may now look as follows:

```
//main
try {
       cout << s->get(15) << endl;
       cout << "Printed successfully!" << endl;
    } catch (logic_error &e) {
       cout << "A logic error occurred!" << endl;
       cout << e.what();
    }
```

Here, if/when an exception occurs, the execution of the `try` block terminates (so we never get to the second line about printing successfully); instead, the program jumps to the first `catch` block that matches the exception. In our case, because a `logic_error` is thrown, the `catch` block matches, so the program prints the message. It then also prints the string we had passed into the constructor (i.e., "head pointer was null!"), since that's what it returned by the `what()` function in the class `exception`. The existence of the `what()` function is one of the reasons to use classes derived from `exception`. If you write your own exception class, you should inherit from `exception` and overload the virtual `what()` function to report what your exception is about.[1]

Notice in the above example that `e` is an exception object, which is passed by reference. It has some data in it. For example, we just put a message string in it, but we could also have put in the description of the variables that caused the exception. We could write our own exception object to throw as well; for instance, we may decide that we want a specific exception type to signal if the index is out of bounds.

```
class OutOfBoundsException : public exception {
    public:
       int pos;
       OutOfBoundsException (int d) {
              pos = d;
       }
}
```

Then, we would throw specifically an `OutOfBoundsException` rather than a `logic_error`.

A `try` block can have multiple `catch` blocks associated with it, to deal with different types of exceptions. In this case, the program will execute the *first* `catch` block that matches the exception that is thrown. This means that the more specific types of exceptions should precede the more general ones.

```
LinkedList *L = new LinkedList ();

try {
      cout << L->get(3);
    }
catch (OutOfBoundsException &e)
      { cout << "Array Index was out of Bounds" << endl;
```

[1] We will learn about inheritance and virtual functions soon.

```
        // specific treatment when index is out of bounds
      }
catch (exception &e)
      { cout << "General Type of exception" << endl; }
```

Here, the first block may have some treatment for specifically the case when the array index was out of bounds, while the second block may have a less specific treatment (such as just an error message) when some other, less specific, error occurred. If we had put the two `catch` blocks in the opposite order, the special treatment for `OutOfBoundsException` would never kick in, as all those exceptions would already be caught in the more general block.

Chapter 16

Searching Lists and Keeping them Sorted

[Note: this chapter covers material of about 0.5 lectures.]

16.1 Searching in a list

Returning to the beginning of the semester, let's think in a bit more detail about the problem of finding one particular element in a list. Suppose that the list is stored in an object of our datatype `List`. We wish to find whether a particular item is in the list, and if so, where. Let's say that the `List` is implemented such that access to any element just takes time $\Theta(1)$.

The first approach is simply a linear search with a `for` loop. Start from the beginning of the list, run until the end (or until you find the element), and try every index in the list. The time for this is $O(n)$ for a list of length n, as we have to do at most a constant amount of work for each element. It is also $\Omega(n)$ in the worst case, as we may actually have to go through all of the elements to realize the element is not in the list. Even if the element we are looking for is just in the second half, we still have to go through half of the list, which still gives us $\Omega(n)$. So in total, this algorithm is $\Theta(n)$.

That doesn't look particularly good, but if the items are unordered in the list, there is not much else we can do. However, if the items in the list (say, integers, or perhaps strings) are sorted, then we can do much better with Binary Search. The pseudo-code, which most students have probably seen before, is as follows:

```
BinarySearch (Element x) {
   Check the median of remaining elements.
   If it equals x, we found it and are done.
   Otherwise:
        If x is smaller than the median element,
           Binary search in the left half.
        Else
           Binary search in the right half.
}
```

Next, we want to analyze the running time of binary search somewhat carefully. How many steps does it take? Every time we check at the median, the remaining array is at most half as big as the current array. (Sometimes, we may get lucky and find the element right away, but we're looking for an upper bound on the *worst* case here.) If we're already quite experienced in analyzing running times of algorithms, we can identify the fact that we have one recursive call on an array half the size as a clear sign that the running time will be $O(\log n)$.

However, most of us are not that experienced yet, so we will try to derive the exact formula more carefully. Let $T(n)$ be the worst-case running time of binary search on an array of size n. Then, we can use what we learned a few weeks ago to express the following recurrence relation for the running time of Binary Search: $T(n) \leq 1 + T(n/2), T(1) = 1$. The explanation is that we always spend one step (or a constant number of steps) for looking at the median element, and unless we are lucky and found the element, we recursively have to check another array whose size is at most $n/2$. That takes $T(n/2)$, by definition of T.

(To be more precise, we should really replace $T(n/2)$ by $\lceil T((n-1)/2) \rceil$ to make sure that all numbers are integers. However, experience with running time analysis tells us that rounding up or down virtually never is the crucial part of a running time analysis, and if leaving out ceilings or floors makes the calculations easier, it's usually worth it.)

At this point, we may wonder whether we could perhaps be better off by not checking the middle, but, say, the 3/4 point. If we did that and lucked out into the case where the element is on the smaller side, we would do better. But on the other hand, if the element we look for is in the larger part, we would spend more remaining time, namely $T(3n/4)$. As computer scientists, we are trained to be pessimistic about this kind of thing, so we need to analyze the worst case under the assumption that we will make the recursive call on an array of size $3n/4$.

The inequality $T(n) \leq 1 + T(n/2), T(1) = 1$ captures the running time of Binary Search quite precisely, but it does not actually give us a formula that we can easily use to "get a feel" for the running time. So we would like a closed-form solution, i.e., one without recursion or sums.

To arrive there, let's unroll the recursion a few steps: $T(n) \leq 1 + T(n/2) \leq 1 + (1 + T(n/4)) \leq 1 + (1 + (1 + T(n/8)))$. In doing the unrolling, we notice that we accrue a 1 for every time we halve the array size. After k steps of this (which means adding k times the number 1), the remaining array size is $\frac{n}{2^k}$. The recursion stops when the array size is (at most) 1, which means that we stop unrolling when $\frac{n}{2^k} \leq 1$. Solving this for k gives us that we are guaranteed to stop as soon as $k > \log_2(n)$. (In fact, in this class, unless otherwise specified, all logarithms are base 2, so we will leave out the base from now on.) Since each iteration does a constant amount of work, we come up with our guess that $T(n) = \Theta(\log n)$.

A guess is nice, in particular if corroborated by good reasoning. But let's actually prove this formally. Any time you prove anything about an algorithm that involves either (1) recursion, or (2) a loop (`for` or `while`), it is a good bet that somewhere in your proof, you will want to use induction. This case is no exception: we will use induction on n, the array size.

First, to make the proof of this guess work, we need to be a little more careful: for instance, for $n = 1$, the result would be $\Theta(0)$, which says that it takes no time. So we amend our guess to $T(n) \leq \log(n) + 1$.

Our base case is $n = 1$: Here, $T(1)$ is constant (since our array has size 1), which we'll just treat as 1. The right-hand side is $\log(1) + 1 = 0 + 1 = 1$. So the base case works.

For the induction step, we normally do induction from n to $n+1$. But notice that here, we are expressing $T(n)$ in terms of $T(\frac{n-1}{2})$, rather than in terms of $T(n-1)$. So our "regular" induction approach doesn't work. The simplest way around it is to use strong induction instead.[1]

The strong Induction Hypothesis states that for all $m < n : T(m) \leq 1 + \log(m)$. We have to prove that $T(n) \leq 1 + \log(n)$, and get to use the strong induction hypothesis for any numbers $m < n$. What do we know about $T(n)$? The one thing we know is the recurrence relation $T(n) \leq 1 + T(\lceil \frac{n-1}{2} \rceil)$. We can check that regardless of whether n is even or odd, $\lceil \frac{n-1}{2} \rceil < n$. Therefore, we are actually allowed to apply the induction hypothesis to $\lceil \frac{n-1}{2} \rceil$, which gives us that $T(\lceil \frac{n-1}{2} \rceil) \leq 1 + \log(\lceil \frac{n-1}{2} \rceil)$. Using rules for logarithms, we can rewrite the right-hand side as $\log(2 \cdot \lceil \frac{n-1}{2} \rceil) \leq \log(n)$. Plugging that in gives us that $T(n) \leq 1 + \log(n)$, as we wanted. This finishes the induction step and thus the proof.

We could also use induction to prove that Binary Search is actually correct, in particular, that it always finds any element that is actually in the list. We didn't get to it in class because of time constraints, but the interested student is encouraged to work through it anyway.

[1] For students sufficiently well-versed in induction proofs, it is worth noting that the "clean" way to do induction here would be to do induction on $\lfloor \log(n) \rfloor$ instead of n. We could write $k = \lfloor \log(n) \rfloor$. Then, our induction step would actually be from k to $k + 1$, and regular induction would suffice. But if we don't want to perform this variable substitution, strong induction is another correct way to do what we want, though perhaps a slightly bigger hammer.

16.2 Interpolation Search

If we go back to our initial example for searching in a phone book, we might notice that as humans, we don't exactly perform Binary Search. For instance, if we are looking for a Mr. or Ms. Algorithm, we will probably not start in the middle of the phone book. Rather, we know the range of entries to expect, and that suggests that the entry is likely close to the beginning, so we look immediately close to the start. If we don't find it on the page — for instance because we found Mr. Boole instead, we will probably go about 1/3 of the way from the beginning to the current page.

The algorithm we'd be executing is called *Interpolation Search*. The way it works is as follows: we need to assume that there is some sense in which the entries can be translated into integers, so we can do basic arithmetic on them. Suppose that we are left with an array $a[\ell \dots r]$ with left and right endpoints ℓ, r; and we are looking for an entry x. The range of entries is $a[\ell] \dots a[r]$, so if things were evenly spaced, we would expect x to be about a fraction $\frac{x-a[\ell]}{a[r]-a[\ell]}$ into the array. Therefore, we would next search at position $m = \ell + (r-\ell) \cdot \frac{x-a[\ell]}{a[r]-a[\ell]}$. Then, we'd recurse just like for Binary Search. In fact, Interpolation Search is exactly the same code as Binary Search, with the exception of computing a different m instead of the median.

In a sense, Interpolation Search zooms in much faster on the part of the array where x is likely located. In fact, one can prove that if the elements of the array are "roughly evenly spread" (in a precise mathematical sense which is beyond this lecture, though not particularly difficult), then Interpolation Search finds x in $O(\log(\log n))$ steps, which is much faster. But notice that this only works when the elements are evenly spread. It is not very difficult to construct somewhat weird inputs in which Interpolation Search does no better than Linear Search, in that it will scan the array from left to right. Those instances contain clusters of lots of people whose names start with the same letters. We won't include it here, but it may amuse you to work out an input like that by hand.

16.3 Keeping a List sorted

In order to reap all those nice benefits of a sorted `List` (Binary Search, and maybe even Interpolation Search), we have to make sure that it remains sorted all the time. Previously, our `List` type had functions

```
void set (int pos, int data);
int get (int pos) const;
void insert (int pos, int data);
void remove (int pos);
```

Nothing needs to change for `get`, of course. And for `remove`, it also makes sense to just remove the item at position `pos` — that will not cause the List to become unsorted.

The function `set` really does not make sense to have. If we choose to overwrite an element, then how do we guarantee that the result is sorted? We should just not be allowed to overwrite.

Similarly, it doesn't really make sense for us to be allowed to insert an element at a position of our choice. Instead, we should have a function `insert-sorted (int data)`, which will find the right place to insert the element by itself.

Next, we want to see how long it takes to perform the sorted insertions and subsequent lookups and searches.

1. If we use an array, then we can use Binary Search to find the place where `data` should go — this takes $O(\log n)$. But after that, we have to shift/copy data to make room for the insertion, and in the worst case, this will take $\Theta(n)$, for instance, every time the element needs to be inserted in the first half of the array. Thus, the time for inserting is $\Theta(n + \log n) = \Theta(n)$.

   In return, the `get` function runs in $O(1)$, so we can now run Binary Search in time $O(\log n)$ any time we are looking for an element. It's a tradeoff — slower insertion vs. faster searching — but it may be worth it to keep the array sorted. In particular, it is worth it if we have many (fast) lookups of elements, and fewer (expensive) insertions. Of course, soon enough, we'll learn about data structures that are fast for both.

An alternative would be to insert a bunch of elements first (without keeping the list sorted), and only later run a sorting algorithm on the heretofore unsorted list. As we will learn very soon, an array can be sorted in $\Theta(n \log n)$; we wouldn't want to do that too often, but if there are stretches of time when we don't need the array to be sorted, this may be a worthwhile alternative.

2. Using a Linked List, inserting an element in the right position only takes $\Theta(1)$, once we know the position. But finding the right position takes $\Theta(n)$. The reason is that the `get` function is really slow on linked lists because we need to scan linearly: to read position i takes $\Theta(i)$, as we learned a few lectures ago. So linear search is actually the better choice to find the right position, and sorted insertion takes $\Theta(n)$, just like for arrays.

   What do we get in return? Absolutely nothing! Because the `get` function takes $\Theta(n)$, if we were to implement Binary Search on top of a linked list implementation of a Sorted List, it would take $\Theta(n)$ for each step of the Binary Search, which would give a total of $\Theta(n \log n)$. In other words, Binary Search is much slower than Linear Search, and there is absolutely no point in implementing it on liked lists. For that reason, there is also pretty much no reason to keep a linked list in sorted order (unless it's really important for printing it in order). Of course, we will see in Chapter 31 that a more elaborate version of linked lists called Skips Lists actually does justify a sorted linked list.

Chapter 17

Sorting Algorithms

[Note: this chapter covers material of about 2 lectures.]

Next, we will learn how to sort items. In order to sort items, we need to be able to compare them, i.e., to determine whether some item x is smaller, greater, or equal to some other item y. The goal of sorting is to put an array/list/vector of such items into non-decreasing or non-increasing order. Non-decreasing is basically the same as increasing, except that we allow multiple equal numbers. For example, `2 3 3 5 7 9` is an array of integers in non-decreasing order (but not increasing, because it repeats an item).

Formally, to say that an array or list is sorted means that $\forall i \in S : a[i+1] \geq a[i]$, where $S = \{0, 1, 2, ..., \text{size} - 2\}$ is the set of all indices in the array. Furthermore, in order to claim that an algorithm *sorts* an array, not only does the final array need to be sorted, it also has to still contain the same elements as before. Otherwise, we could use the following silly algorithm to obtain a sorted array:

```
for (int i = 0; i < n; i ++)
    a[i] = 0;
```

Clearly, this is not what we intended.

17.1 Applications of Sorting

Sorting is useful for a number of reasons, including the following:

- Understanding sorting algorithms helps to illustrate central algorithm design and analysis concepts which will be covered in more depth in an algorithms class.
- Humans usually prefer sorted data to read.
- A sorted array is much easier to search in, e.g., using Binary Search.
- Sorting makes it much easier to discover patterns or statistics of data items, such as the median or other moments.
- Sorting often helps in comparing lists (or sets), and performing operations like intersection of sets, finding out if two lists contain the same elements, finding if there are duplicates in a list, etc.

As an illustration of the last type of problem, we solved in class the following problem: given two lists of numbers, find if the two lists contain the same numbers. Half of the class was asked to solve this problem with unsorted lists, while the other half was using sorted lists. The ones with sorted lists were much faster than those with unsorted lists.

If the lists are sorted, we can simply go through both lists in parallel. If we ever discover a position where the lists differ, that's all the evidence we need to conclude that the lists are not the same. If we reach the end without finding such a position, the lists are the same. The running time is $\Theta(n)$ when the lists have size n.

When the lists are unsorted, we can't really do anything much better than going through one list, and for each element, look for it in the other list, which requires a linear search. Since we need to go through every element in the second list for every element in the first list, the runtime is $\Theta(n^2)$.

Thus, sorting really speeds up the goal of computing whether two sets are the same. This is true for many other similar problems on one or two lists, where sorting improves the performance from $\Theta(n^2)$ to $\Theta(n)$. These types of questions are also classic interview questions, since they test both knowledge of sorting, and problem solving skills.

We will learn soon that there are algorithms sorting an array of n elements in $\Theta(n \log n)$ time. Thus, sorting both lists first is actually faster in our set identity example than trying to compute the intersection on unsorted lists. In general, when an interviewer tells you to solve a problem in time $O(n \log n)$, there is a good chance that his intended solution uses sorting of an array. (Of course, there are other problems that can be nicely solved in time $O(n \log n)$. But among the interview questions for students early in their career, sorting is very prominent among $O(n \log n)$ algorithms.)

17.2 Stability of sorting algorithm

We said above that two properties are absolutely essential for sorting algorithms: (1) The output must be sorted, and (2) It must still contain the same elements. A third property is not essential, but often useful. It is called *stability*: an algorithm is stable if every two elements that have the same value have the same relative order after sorting as before. As an example, consider the following input: `3(red) 5 1 3(blue)`: we have two distinct elements, both with the value 3. The following would be the *stably sorted* output: `1 3(red) 3(blue) 5`. The following output is also sorted, but *unstably*: `1 3(blue) 3(red) 5`.

Stability of an algorithm can be very useful when we have multiple sorting criteria, which happens routinely when implementing a Spreadsheet or Database system. For example, suppose that you want to sort all USC students by GPA; if two students have the same GPA, the two students should be ordered alphabetically.

One solution of this problem would be to define the relationship of `a` and `b` to be: `a < b` if `(a.GPA < b.GPA || (a.GPA == b.GPA && a.name < b.name))`. This would work, but doing things this way requires us to define more and more sorting rules whenever we want another tie breaker.

An alternative, perhaps more convenient, solution would be to first sort by name, then sort by GPA. If we are using a stable sorting algorithm, the alphabetical order among students will still be in place, i.e., will be the tie breaker among students with the same GPA.

17.3 Bubble Sort

The first sorting algorithm we came up with in class was *Bubble Sort*. In Bubble Sort, we compare the first with the second entry and swap them if they are out of order, then the second with the third, swapping if necessary, etc. Once we reach the end of the array, we know that the largest element is there — it has "bubbled up" to the top. Now, we start again with the first element, and so on, terminating one spot earlier. This gets repeated at most $n - 1$ times. The code is as follows:

```
for (int i = n-1; i > 0; i--) {
    for (int j = 0; j < i; j++) {
        if (a[j] > a[j+1]) {
            a.swap(j, j+1);
        }
    }
}
```

This algorithm is stable, since it only swaps two items if the latter one is strictly greater, so equal-valued items will stay in their original order.

To formally prove correctness of an algorithm based on `for` loops, the typical technique is to use induction on the iterations. The induction hypothesis for this type of proof is also called the *loop invariant*: it captures a property of the variables that is true after each iteration of the loop when one runs the algorithm. While we will not do a formal proof by induction here, it is worth thinking about the loop invariant, since it also sheds insight into how an algorithm works. Here, the loop invariant is that after k iterations, the following are true:

- The last k positions of the array contain the largest k elements, and are sorted. (The first $n - k$ positions are not necessarily sorted yet.)
- The entire array still contains the same elements as at the beginning.

We would prove this claim by induction on k. It holds trivially for $k = 0$, and when we establish it for $k = n$, it implies that the entire array is sorted. A pictorial representation of the loop invariant of BubbleSort is given in Figure 17.1.

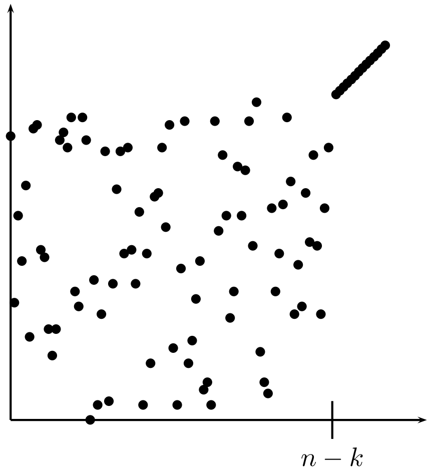


Figure 17.1: A pictorial representation of the loop invariant of Bubble Sort.

To analyze the running time of the algorithm, we start — as with any other loop-based algorithm we analyze — from the innermost loop. The inner `for` loop contains one statement, and it is always going to run in constant time regardless of size of input, giving us $\Theta(1)$ The `for` loop causes this statement to run $\Theta(i)$ times, so the inner loop has a total run time of $\Theta(i) \cdot \Theta(1) = \Theta(i)$.

Notice that `i` in the inner `for` loop runtime is really dependent on which iteration the algorithm is currently on, and so is the time that the inner loop takes. For example, the first time that the loop is run, `i` is $n - 1$, so the loop takes n steps. The last time the loop is run, `i` is 1, meaning that the inner loop only runs over 1 or 2 steps. To analyze the running time of the entire algorithm, we need to take the total time for the outer loop. That time is obtained by summing the execution time of the inner loop over all iterations of the outer loop. Thus — as always — when analyzing a loop, we get a sum in our formula:

$$\sum_{i=1}^{n-1} \Theta(i) = \Theta(\sum_{i=1}^{n-1} i) \;=\; \Theta(n(n-1)/2) \;=\; \Theta(n^2).$$

Most of these steps are very simple manipulations, and the key step is the applications of the arithmetic series (which you should have down pat, along with the geometric one).

So we have seen that Bubble Sort takes time $\Theta(n^2)$, i.e., it is a quadratic algorithm. Notice that it also takes a quadratic number of swaps, not just comparisons. Sometimes, people consider comparisons a little cheaper and distinguish carefully between the two. In practice, Bubble Sort is actually quite bad, and it is the worst of the three quadratic algorithms we will see in this class. In fact, as you saw from the link that was posted on the course website, even President Obama knows not to use Bubble Sort for large arrays.

17.4 Selection Sort

The basic idea of Selection Sort is to find the smallest element, and bring it once and for all to its correct position (first place in the array), then continue with the second position and second smallest element, and continue this way until all elements are in their correct position.[1] So we can write Selection Sort as follows:

```
for (int i = 0; i < n - 1; i++) {
    int smallestNumIndex = i;
    for (j = i + 1; j < n; j++) {
        if (a[j] < a[smallestNumIndex]) { smallestNumIndex = j; }
    }
    a.swap(i, smallestNumIndex);
}
```

Selection Sort as implemented is not stable. Suppose that we have the number 5 occuring in positions 1 and 2, and the number 3 in position 3. Then, we will swap positions 1 and 3, so that the order of the two elements numbered 5 is now reversed. To make Selection Sort stable, the easiest way would be to use a `List<T>` data structure, and replace `a.swap(i, smallestNumIndex)` with

```
T temp = a[smallestNumIndex];
a.remove (smallestNumIndex);
a.insert (i, temp);
```

Notice that this will now result in $\Theta(n^2)$ write steps total (as the `insert` and `remove` operations of lists take $\Theta(n)$ writes to shift the array), so it will slow down the algorithm.

Again, we would like to think about the loop invariant we would need to prove this algorithm correct. Here, it looks similar to Bubble Sort, only for the beginning of the array instead of the end. After any number k of iterations, the following holds:

- The first k positions of the array contain the smallest k elements, and are sorted. (The last $n - k$ positions are not necessarily sorted yet.)

- The entire array still contains the same elements as at the beginning.

Again, we would use induction on k to prove this claim. Pictorially, we can represent it as in Figure 17.2:

In the analysis, the innermost part takes time $\Theta(1)$, and the inner loop therefore has running time $\Theta(n - i)$. So the total running time is $\sum_{i=0}^{n-2} \Theta(n - i)$. In order to evaluate this sum, the bets way is to look a but by hand what happens for different values of i. For $i = 0$, we have $n - i = n$. For $i = 1$, we get $n - i = n - 1$, and so on. Finally, for $i = n - 3$, we have $n - i = 3$, and for $i = n - 2$, we get $n - i = 2$. So the sum is the same as $\sum_{i=2}^{n} \Theta(i)$. Now, we can add the $i = 1$ term (because it only adds $\Theta(1)$ to the sum), and get that the sum is $\Theta(\sum_{i=1}^{n} i) = \Theta(n^2)$ (as we did for Bubble Sort). In practice, Selection Sort is a little better than Bubbble Sort, since it only has $O(n)$ swaps (though still $\Theta(n^2)$ comparisons).

[1] The textbook describes this algorithm as finding the largest element, then putting it in the last position, and continuing this way. Obviously, it is pretty easy to trade off between those two.

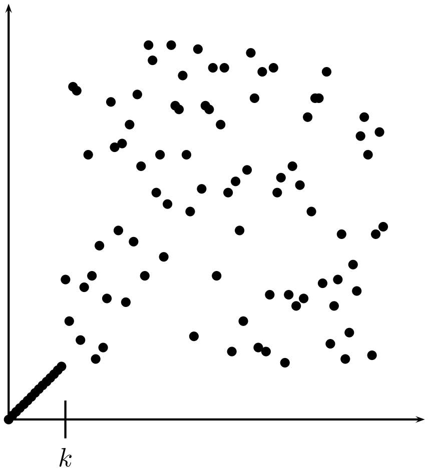


Figure 17.2: A pictorial representation of the loop invariant of Selection Sort.

17.5 Insertion Sort

When we analyzed Selection Sort, and thought about the loop invariant, it was that after k iterations:

- The first k positions of the array contain the smallest k elements, and are sorted. (The last $n-k$ positions are not necessarily sorted yet.)
- The entire array still contains the same elements as at the beginning.

Let's think about what algorithm or invariant we would get if instead we had just "the first k position are sorted," without thinking about the fact that they also contain the smallest k elements. This would give us the following visualization:

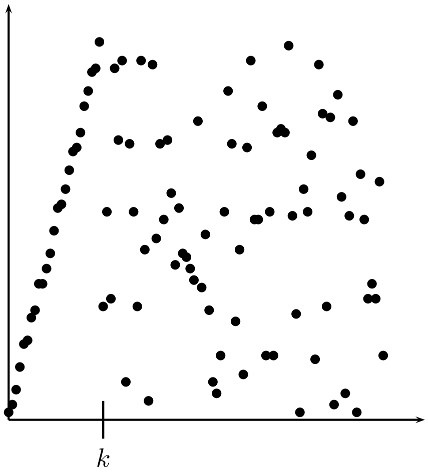


Figure 17.3: A pictorial representation of the loop invariant of Insertion Sort.

Notice the difference to the visualization of Selection Sort and Bubble Sort. Here, the sorted area is sorted internally, but may contain elements that are larger than some elements in the unsorted area. This is the loop invariant for an algorithm called *Insertion Sort*. Again, after k iterations:

- The first k positions of the array are sorted.
- The entire array still contains the same elements as at the beginning.

The Insertion Sort Algorithm works as follows: for each of the positions in order, pretend that you just "discovered" element $a[i]$, and put it in its correct position in the array between positions 0 and i. Keep doing that until the entire array is sorted. In fact, this is how many people will sort a hand of cards, picking them up one by one, and inserting them into the correct position with the current cards in hand. In code, it looks as follows:

```
for (int i = 1; i < n; i++) {
    int j = i;
    while (j > 0 && a[j] < a[j-1])
         {
            a.swap(j, j-1);
            j --;
         }
}
```

This algorithm is also stable. The reason is that it never swaps equal elements.

Next, let's analyze the running time of Insertion Sort. The commands inside the `while` loop take time $\Theta(1)$, so the inner `while` loop, which runs from i until 0, takes time $\Theta(i)$. Therefore, the entire algorithm takes time $\sum_{i=1}^{n-1} \Theta(i) = \Theta(n^2)$, a calculation which by now should be second nature.

While Insertion Sort is thus also a quadratic algorithm, it is actually not so bad in practice, and is considered the fastest sorting algorithm for $n \leq 10$. In fact, implementations of the faster recursive algorithms we see next often switch to Insertion Sort for smaller array sizes.

The implementation can also be optimized a bit. As you see, we have a lot of `swap` operations in the inner loop. One can do a little better by storing $a[i]$ in a separate variable t, then just copying each of $a[j-1]$ to $a[j]$, and finally copying t into its correct position. This replaces each `swap` by just one assignment, which should speed up the loop by about a factor of 3.

17.6 Merge Sort

Next, we learn about two classic $O(n \log n)$ algorithms: Merge Sort and Quick Sort. Both use recursion and the Divide&Conquer paradigm. Both algorithms are quite fast, both theoretically and in practice, and they also illustrate some very central algorithmic ideas.

In general, the Divide&Conquer paradigm for algorithm design considers algorithms in three phases:

Divide: Partition (split up) the input into one or more smaller inputs. These inputs may overlap, but in the simpler examples, they usually don't.

Recurse: Solve the problem on each of the smaller sets recursively.

Combine: Combine these solutions into one to solve the original problem. This is also called the "Conquer" step.

We have already seen one very simple example of Divide&Conquer earlier, namely, Binary Search. There, the Divide step consisted of comparing the searched-for element x to the median element of the array a (i.e., the element in position $n/2$). This divided the array into one smaller input, namely the half of the array in which x was now known to lie (unless we were lucky and found the element already). The Recurse step was the recursive call for just that one half, and the Combine step was trivial: it just returned the result of the Recurse step without any further work.

The Merge Sort algorithm fits into the Divide&Conquer paradigm as follows:

Divide: Do nothing much, just divide the array into two (roughly) equal-sized halves.

Recurse: Recursively sort the two halves.

Combine: This is where all the work gets done: the two sorted halves get merged in one linear-time pass.

More formally, the code looks as follows:

```
void MergeSort(T a[], int l, int r)
{
    if (l<r) { // otherwise, just one element, which is sorted
        int m = floor((l+r)/2);
        MergeSort(a, l, m);
        MergeSort(a, m+1, r);
        Merge(a, l, r, m); // this is a separate function given below
    }
}
```

Figure 17.4: The MergeSort Algorithm

The Merge function is implemented as follows:

```
void Merge (T a[], int l, int r, int m)
{
  T temp[r+1-l];
  // trace through the two subarrays, copying into a temporary one
  int i = l, j = m+1, k = 0;
  while (i <= m || j <= r)  // at least one subarray contains another element
       {
         if (i <= m && (j > r || a[i] <= a[j]))
            // next smallest element in left subarray
            { temp[k] = a[i]; i ++; k ++; }
         else { temp[k] = a[j]; j ++; k ++; }
            // next smallest element in right subarray
       }
  // now copy over the merged array into the original
  for (k = 0; k < r+1-l; k ++)
      a[k+l] = temp[k];
}
```

Figure 17.5: The Merge Subroutine

Like for many recursive algorithm, the invariant for MergeSort is actually just the correctness condition of the algorithm, and is expressed as follows:

> After MergeSort(a,l,r) executes, a is sorted between l and r, and contains the same elements as the original array.

The most interesting visualization explaining the progress of the algorithm is now drawing the array right after the two recursive calls, but before the Merge step.

Of course, since all the actual work happens inside the Merge function (the rest is just recursive calls, and no actual computation), presumably all the hard work in proving the invariant would come from analyzing the Merge function. We capture the way it works with the following lemma.[2]

[2] A lemma is a theorem that you don't really prove for its own sake, but mostly so that it helps you prove a bigger goal.

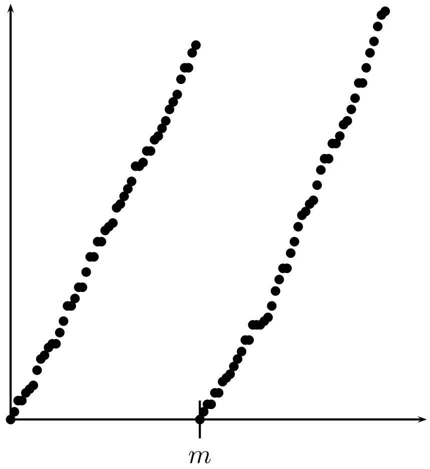


Figure 17.6: A pictorial representation of the state of Merge Sort before the actual `Merge` call.

Lemma 17.1 *If `Merge(a,l,r,m)` is called such that `a` is sorted between `l` and `m`, and separately between `m+1` and `r`, then after `Merge` runs, the array is sorted between `l` and `r` and contains the same elements.*

To prove this lemma, since `Merge` uses mostly one loop, we would have to phrase a careful loop invariant, and then prove that by induction on a suitable loop counter. Here, that would be $i+j$ in the `Merge` function. A detailed proof would be somewhat tedious, though not really hard.

Once we have proved the lemma, the correctness proof for Merge Sort is actually quite easy. We won't do it here in class, but it really just consists of plugging in the induction hypothesis and the lemma.

17.6.1 Running Time of Merge Sort

If we look at the Merge Sort algorithm more closely, we notice that the running time on an array of size n accrues as follows:

1. First, we spend time $O(1)$ for computing m.
2. Then, we make two recursive calls to Merge Sort, with arrays of sizes $\lfloor (n-1)/2 \rfloor$ and $\lceil (n-1)/2 \rceil$.
3. Finally, we call `Merge`. `Merge` goes through the two subarrays with one loop, always increasing one of i and j. Thus, it takes time $\Theta(n)$.

Let's use $T(n)$ to denote the worst-case running time of Merge Sort on an array of n. We don't know yet what $T(n)$ is — after all, that's what we're trying to work out right now. But we do know that it must satisfy the following recurrence relation:

$$\begin{aligned} T(n) &= T(\lfloor (n-1)/2 \rfloor) + T(\lceil (n-1)/2 \rceil) + \Theta(n), \\ T(1) &= \Theta(1). \\ T(0) &= \Theta(1). \end{aligned}$$

The last two cases are just the base case where the recursion bottoms out. The first equation is obtained as follows: We worked out that the running time for an array of size n is the time for `Merge` (and the computation of m), which is $\Theta(n)$, plus the time for the two recursive calls. We don't know how long those two take yet, but we know that they must be the function T applied to the respective array sizes.

Having worked out the recurrence, with a bit of experience, we actually realize that in this type of recurrence, it doesn't really matter whether one rounds up or down, and whether it is $(n-1)/2$ or $n/2$.

If you are worried about this, you can work out the details and verify them. There are certainly cases where this would matter, but until you start analyzing pretty intricate algorithms and data structures (at which point you'll have learned the material so well that you don't need these lecture notes), you can always disregard, for the purpose of analysis, such small details. So we get a simpler recurrence:

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

This type of recurrence pops up very frequently in the analysis of Divide&Conquer algorithms. The more general form is $T(n) = a \cdot T(n/b) + f(n)$, for some constant numbers a and b, and some function f. You will learn in CSCI270 how to solve this more general case, including by a theorem called the Master Theorem (which really isn't very hard, the name notwithstanding). But it's actually not too hard to do by hand. The typical way to solve such recurrences by hand is to draw a recursion tree, work out the amount of work on each level and the number of levels, and then add them up. This gives you a conjecture for the formula for $T(n)$. This conjecture can then be verified using (strong) induction on n. After a bit of experience, one may omit the induction proof (since it's always very similar), but for now, verifying by induction is quite important.

The recursion tree is given in Figure 17.7:

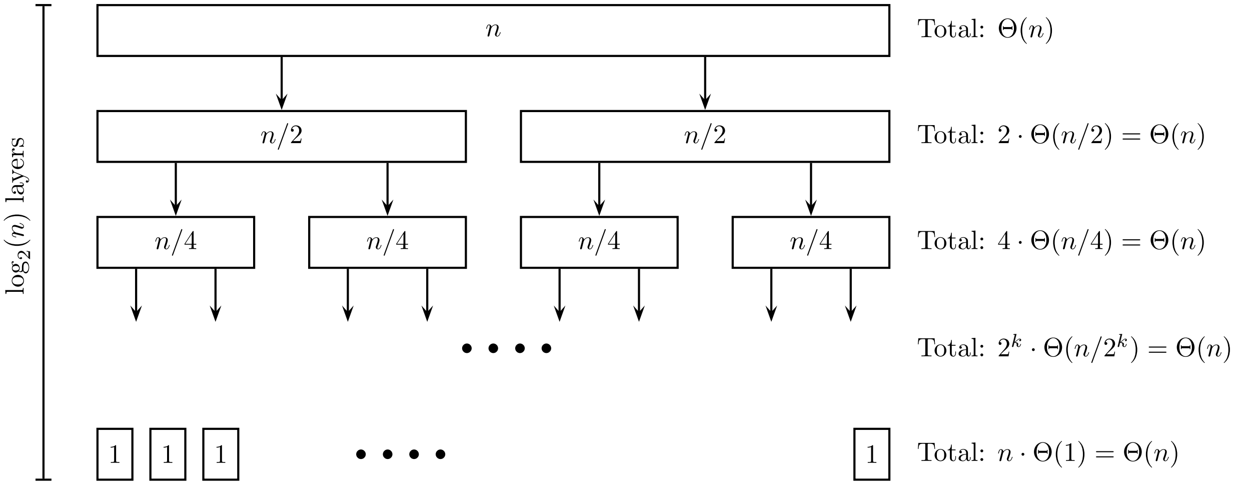

$\log_2(n)$ layers
n
$n/2$
$n/2$
$n/4$
$n/4$
$n/4$
$n/4$
1
1
1
1
Total: $\Theta(n)$
Total: $2 \cdot \Theta(n/2) = \Theta(n)$
Total: $4 \cdot \Theta(n/4) = \Theta(n)$
Total: $2^k \cdot \Theta(n/2^k) = \Theta(n)$
Total: $n \cdot \Theta(1) = \Theta(n)$

Figure 17.7: A recursion tree for Merge Sort. The numbers in the boxes are the array sizes, and we know that the work for `Merge` for an array of size s is $\Theta(s)$. In layer k, there are 2^k subarrays to process in the separate recursive calls, and each of them has size $n/2^k$.

Each level corresponds to one level of recursion. The top (root, level 0) is the call on an array of size n. This causes two calls with arrays of size $n/2$, at the next lower level (level 1). Each of those causes two calls with arrays of size $n/4$, for a total of 4 such calls at level 2. More generally, at level k, we have 2^k recursive calls, each on an array of size $n/2^k$. This bottoms out at the level where the array sizes are 1.

Now, if we look at the total work done by the calls to `Merge` at level k, we see that we call the function 2^k times, on arrays of size $n/2^k$ each. Since the running time for `Merge` is linear in the array size, we get $2^k\Theta(n/2^k) = \Theta(n)$. Thus, the total work at each level is $\Theta(n)$.

Next, we calculate the number of levels. Since the array size halves with each extra level, and it starts with n and finishes with 1, the number of levels is $\log_2(n)$. (Technically, it is $\lceil \log_2(n) \rceil$, but such details don't affect the running time analysis.) So the total work, summing up over all levels, is $\Theta(n \log_2(n))$. Remember that all logarithms are the same up to constant factors (base conversion), so we can just write $\Theta(n \log n)$, and leave the base unspecified.

So now, we have a pretty well-founded conjecture that $T(n) = \Theta(n \log n)$. But we want to prove this conjecture very formally. Whenever we want to formally analyze the running time of a recursive algorithm, the proof technique of choice is induction, because to prove something for bigger arrays, we'll want to rely on the same result for smaller arrays. This requires us to write a formal induction hypothesis and statement. First, to avoid mistakes we might make with $\Theta()$ notation (there are some subtleties when combining recursion and $\Theta()$), let's pretend that the recurrence is actually:

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

getting rid of all $\Theta()$ notation. Then, we also want to make the precise form of the conjecture concrete, by saying that

$$T(n) = n(1 + \log_2(n)).$$

You may wonder where the "1+" came from suddenly. When looking at the base case $n = 1$, we notice that $T(1) = 1$ is what we want, but if we just had $n \log(n)$, because $\log(1) = 0$ (regardless of base), we would have 0. Adding "1+" is a bit of a trial-and-error result.

We will now prove the conjecture by (strong) induction on n. For the base case $n = 1$, we get that $T(1) = 1$ by the recurrence, and our formula gives us $1 \cdot (1 + \log_2(1)) = 1 \cdot (1 + 0) = 1$, so the base case worked.

Next, we state the induction hypothesis. Because we are doing *strong* induction, we get to assume that *for all* $k < n$, the statement $T(k) = k(1 + \log_2(k))$ is true. We want to prove that $T(n) = n(1 + \log_2(n))$. Notice here the difference between normal induction and strong induction. In normal induction, we would only get to assume that the hypothesis holds for $k = n - 1$, whereas using strong induction, we can assume it for *all* $k < n$, including $k = n - 1$. This is useful when, as here, the recurrence for n is based on values for parameters other than $n - 1$; in our case, this is $n/2$.

To actually prove this, we begin by using the only thing we know for sure about $T(n)$, namely that

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

Now, we need to deal with those $T(n/2)$ terms. Here, we apply the induction hypothesis with $k = n/2$. We are allowed to do so, because $n \geq 2$ implies that $n/2 < n$. Then, we get that

$$T(n) = 2T(n/2) + n \overset{I.H.}{=} 2\frac{n}{2}(1 + \log_2(n/2)) + n = n(1 + \log_2(n) - 1) + n = n(1 + \log_2(n)).$$

This is exactly what we wanted to show, so the induction step is finished, and we have completed the induction proof.

17.7 Quick Sort

Merge Sort was our first illustration of a Divide&Conquer sorting algorithm. The other classic representative is Quick Sort. Merge Sort does practically no work in the Divide step — it only calculates m, the middle position of the array. Instead, the Combine step is where all the work happens. Quick Sort is at the other extreme: it does all its hard work in the Divide step, then calls itself recursively, and literally does nothing for the Combine step.

The Divide step in Quick Sort makes sure to move all of the smaller numbers to the left side of the array (but not sort them there), all of the larger numbers to the right side of the array (again, not sorted further), and then call itself recursively on the two sides. This division is accomplished with a *pivot element* `p`. The left side will contain only elements that are *at most* as large as `p`, while the right side contains only elements *at least* as large as p. (Depending on the implementation, elements equal to p may end up on either side, or the implementation may choose to put them all in one side.) Once we do this Divide step, we know that no elements of the left will ever need to end up on the right side, or vice versa. Thus, after we recursively sort the two sides, the entire array will be sorted.

Note that the left and right sides of the array will not necessarily be the same size, not even approximately. In Merge Sort, we carefully ensured to divide the array into two equal halves. In Quick Sort, we may also end up with two halves, but that would require choosing the median of the array as the pivot. More formally, the Quick Sort algorithm looks as follows.

```
void QuickSort (T a[], int l, int r) {
    if (l < r) {
        int m = partition(a, l, r);
        QuickSort(a, l, m-1);
        QuickSort(a, m+1, r);
    }
}
```

As you can see, basically all the work must be done in the partition function, which is as follows:

```
int partition (T a[], int l, int r) {
    int i = l; // i will mark the position such that everything strictly to
               // the left of i is less than or equal the pivot.
    T p = a[r];
    for (int j = l; j < r; j++) {
        if (a[j] <= p) {  // found an element that goes to the left
            a.swap(i, j); // put it on the left
            i++;
        }
    }
    a.swap (i, r); // put the pivot in its place
    return i;
}
```

The partition function runs one loop through the array, and moves to the left side any element that is smaller than the pivot, keeping track of the boundary (i) between elements that are smaller than the pivot, and elements that may be (or are) larger. This is a perfectly adequate implementation of the partition function, but it uses about twice as many swaps as necessary. (In big-O notation, that does not matter, of course, but in practice, such a factor of 2 can be very important.) The slightly more clever implementation is to have two counters i, j, one starting at the left, the other at the right. Whenever a[i] > p and a[j] < p, the two elements at i and j are swapped. Otherwise, i is incremented, j is decremented, or both. When the counters cross each other, the function is done. One has to be a little careful with the indices i such that a[i] = p, which is why in class, we present the simpler and slower version. But it's not too hard to work out.

Again, because Quick Sort is a recursive algorithm, the correctness statement is simply the overall correctness condition, and we don't need a loop invariant:

> After QuickSort(a,l,r) executes, a is sorted between l and r, and contains the same elements as the original array.

To prove this condition, we would again use induction over the array size $n = r + 1 - l$, just as with Merge Sort. Also, as with Merge Sort, since all the actual work is done by a "helper function" — here, the partition function — the correctness proof would mostly rely on a lemma about the behavior of that helper function.

Lemma 17.2 *When `partition(a,l,r)` returns the value `m`, the array `a` still contains the same elements, and has the following property: (1) Each position $l \leq i < m$ satisfies $a[i] \leq a[m]$, and (2) Each position $m < i \leq r$ satisfies $a[i] \geq a[m]$.*

We can visualize this lemma as in Figure 17.8, covering the main insight of the Quick Sort algorithm visually (like we did with the other sorting algorithms):

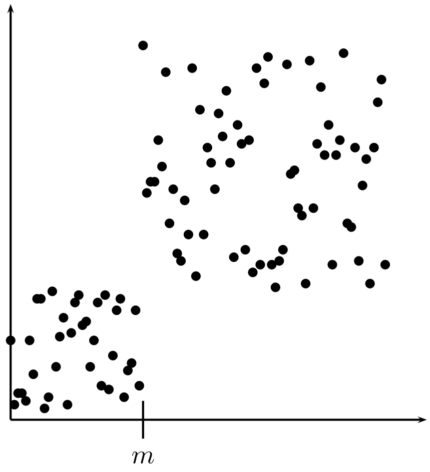


Figure 17.8: A pictorial representation of the state of Quick Sort after calling `partition`.

To prove the lemma, we would again need induction. Since `partition` consists mostly of a loop, we would need a loop invariant, capturing formally the outline of how `partition` works. We won't do that here, but it isn't too hard. Once we have the lemma, the correctness proof for Quick Sort is very straightforward. It simply uses strong induction on the array size, and applies the lemma and the induction hypothesis. This is one you should be able to work out pretty easily on your own.

17.7.1 Running Time

To analyze the running time of Quick Sort, we use the same approach as we did for Merge Sort (and is common for many recursive algorithms, unless they are completely obvious). We let $T(n)$ represent the worst-case running time of the Quick Sort algorithm on an array of size n. To get a hold of $T(n)$, we look at the algorithm line by line. The call to `partition` takes time $\Theta(n)$, because it runs one linear scan through the array, plus some constant time. Then, we have two recursive calls to Quick Sort. We let $k = m - 1 - l$ denote the size of the left subarray. Then, the first recursive call takes time $T(k)$, because it is a call on an array of size k. The second recursive call will take time $T(n-1-k)$, because the size of the right subarray is $n-1-k$. Therefore, the total running time of Quick Sort satisfies the recurrence

$$\begin{aligned} T(n) &= \Theta(n) + T(k) + T(n-1-k), \\ T(1) &= \Theta(1). \end{aligned}$$

This is quite a bit messier-looking than the recurrence for Merge Sort, and if we know nothing about k, we cannot really solve this recurrence. But in order to get a feel for it, we can play with it a bit, and explore different possible values of k.

1. For $k = \frac{n}{2}$, the recurrence becomes much simpler: $T(n) = \Theta(n) + T(n/2) + T(n/2-1)$, which — as we discussed in the context of Merge Sort — we can simplify to $T(n) = \Theta(n) + 2T(n/2)$. That's exactly the recurrence we have already solved for Merge Sort, and thus the running time of Quick Sort would be $\Theta(n \log n)$.

2. At the other extreme is $k = 0$ (or, similarly, $k = n - 1$). Then, we get only that $T(n) = \Theta(n) + T(0) + T(n-1)$, and since $T(0) = \Theta(1)$, this recurrence becomes $T(n) = \Theta(n) + T(n-1)$. This recurrence unrolls as $T(n) = \Theta(n) + \Theta(n-1) + \Theta(n-2) + \ldots + \Theta(1)$, so $T(n) = \Theta(\sum_{i=1}^{n} i) = \Theta(n^2)$.

The running time for $k = 0$ or $k = n - 1$ is thus just as bad as for the simple algorithms, and in fact, for $k = 0$, Quick Sort is essentially the same as Selection Sort. Of course, this quadratic running time would not be a problem if only the cases $k = 0$ and $k = n - 1$ did not appear in practice. But in fact, they do: with the pivot choice we implemented, these cases will happen whenever the array is already sorted (increasingly or decreasingly), which should actually be an easy case. They will also happen if the array is nearly sorted. This is quite likely in practice, for instance, because the array may have been sorted, and then just messed up a little with some new insertions.

As we can see, the choice of pivot is extremely important for the performance of Quick Sort. Our favorite pivot would be the median, since it ensures that $k = \frac{n}{2}$, giving us the best solution $T(n) = \Theta(n \log_2 n)$. There are in fact linear algorithms for finding the median; they are not particularly difficult (in particular, the randomized one is quite easy; the deterministic algorithm is a bit more clever), but belong more in an algorithms class.

Of course, we don't have to find exactly the median. As long as there exists some *constant* $\alpha > 0$ with $\alpha n \leq k \leq (1 - \alpha)n$ for all recursive calls, we will get that $T(n) = \Theta(n \log n)$. However, the constant hidden inside the Θ gets worse as $\alpha \to 0$, because the array sizes in Quick Sort become more and more imbalanced.

So we would be quite happy if somehow, we could always pick a pivot p such that at least 25% of the array's entries are less than p and at least 25% are more than p. Notice that half of all entries in the array would actually satisfy this, namely, the entries which (in the sorted version) sit in array positions $n/4 \ldots 3n/4$. Unfortunately, right now, we don't really know how to find such a pivot, either. (It can be done with basically the same idea as finding a median.)

But one thing we can do is pick a *random* element of the array as a pivot. That will not *always* guarantee that the pivot satisfies this nice 25% property, but it happens on average half the time. So, half the time, the subarray sizes shrink at least by 25%, which is enough to ensure that we only have $O(\log n)$ levels of recursive calls, and thus running time $O(n \log n)$. The analysis of *Randomized Quick Sort* is not particularly difficult, but would take us about a lecture, so we'll skip it here — you will likely see it in CSCI270. But one can show that the expected running time $E[T(n)] = \Theta(n \log n)$. Notice that when the algorithm makes random choices, like Randomized Quick Sort does, the running time becomes a random variable. One can show that not only in expectation is it $\Theta(n \log n)$, but in fact, this happens most of the time.

In practice, Randomized Quick Sort performs quite well. Another way to achieve the same result is to scramble the array truly randomly first, and then run the default Quick Sort algorithm from above on the scrambled array. That is mathematically equivalent.

As an aside, here is how you randomly scramble an array:

```
for (int i = n-1; i > 0; i --)
     a.swap (i, rand()%(i+1));
```

This ensures that each permutation of the array is equally likely in the end. Don't try to scramble it by repeatedly swapping random pairs of elements, like the following:

```
for (int i = 0; i < MAXSWAPS; i ++)
    a.swap (rand()%n, rand()%n);
```

This does eventually give you a truly random array, but it takes way more swaps than you would normally run. This is actually an interesting area of mathematics (Analysis of Mixing Times of Markov Chains and Random Walks, specifically for card shuffling), and the main result is that you need MAXSWAPS $= \Omega(n \log n)$ pairwise swaps before the array actually looks random.

Chapter 18

Templates

[Note: this chapter covers material of about 0.5 lectures.]

Once we have carefully implemented a class like `List` or `Stack` or `Queue`, we may discover that it is quite nice, and we would like to also have a List or Stack or Queue of strings. And one for users, and for web pages, and so many other types of objects. The obvious solution would be to copy the code we wrote for integers, and then replace the word `int` with `string` everywhere. This will cause a lot of code duplication. In particular, imagine now that after making 20 different copies, we discover that the original implementation of `List` actually had a few bugs. Now we have to fix them in all copies.

What we'd really want is a mechanism for creating a "generic" `List` class, which allows us to substitute in any type of data, rather than just `int`, or just `string`. This way, we avoid code duplication and all the problems it creates (in particular in terms of debugging and keeping versions in synch).

The C++ mechanism for doing this is called *templates*. You've already used this when using the C++ STL (Standard Template Library), and even earlier when using `Vector<...>`. The syntax for creating your own template classes is a little clunky, and because of the particular way in which C++ implements it, it unfortunately also forces us to give up some of our good coding practices. (It was not originally part of the C++ design, but rather grafted on top later, which explains why it does not fit very smoothly.)

The basic way of defining templates classes is explained first via an implementation of a generic `struct Item`:

```
template <class T>
struct Item
{
    T data;
    Item<T> *prev, *next;
}
```

This tells C++ that we are defining a template class, which will be generally based on another class. We call that class `T` for now. By writing this, we can treat `T` as though it were an actual name of an existing class.

What really happens is the following. Suppose that in some later code, we want to create an `Item` for strings. We will now write:

```
Item<string> *it = new Item<string>;
```

When the compiler sees this code, it will copy over the template code, and wherever it sees `T`, it will instead substitute `string`. In other words, it will exactly do the text replacement that we wanted to avoid doing by hand. Of course, in this way, we only maintain one piece of code, and the rest is generated only at compile time, and automatically. That's how templates save us work.

We can now apply the same ideas to our LinkedList class:

```
template <class T>
class LinkedList {
  public:
    LinkedList ();
    ~LinkedList ();
    void append (T value);
    void remove (Item<T> *toRemove);
    void printlist ();

  private:
    Item<T> *head;
}
```

When we implement class functions of template classes, the syntax is as follows:

```
template <class T>
LinkedList<T>::add (T item) {
     //code
}
```

Note the `template<class T>` line and the `<T>` in the class name. You have to put these in front of *each* member function definition; otherwise, how is the compiler to know that you are implementing a member function of the template class? Usually, if you get a "template undefined" error, you might have missed a `<T>`. (Note that the identifier `T` is arbitrary — you can use `X` or `Type` or whatever).

By the way, the keyword `template` cannot be used just with classes, but also with other things, such as functions. For instance, we could write the following:

```
template <class Y>
Y minimum (Y a, Y b)
{ if (a < b) return a; else return b; }
```

Another thing worth noting about templates is that you can't just use one type: you can use multiple types. For instance, remember that a `map` has two types: one for the key, and one for the value. We could specify that as follows:

```
template <class keyType, class valueType>
class map
{
  // prototypes of functions and data go here
}
```

Templates were kind of grafted on top of C++, and not really part of the initial design. That is why the syntax is rather unpleasant, and the "obvious" way of doing things causes all kinds of compiler and linker problems. In order to get things to work, you will sometimes need to deviate from good coding practices, for instance by having `#include` of a `.cpp` file. Check the course coding guide for detailed information on how to deal with some of the most common problems. Seriously, read it very carefully before attempting to code anything with templates. It will save you many hours of debugging - promised!

18.1 Some other considerations

Earlier on, in Chapter 12, we learned about friend functions. Friend functions require some extra care when you combine them with defining your own template classes.

When the function you want to declare as a friend takes a template parameter (because your class is templated), you need to say so inside the class definition, and give it a different symbolic name to avoid ambiguity.

For instance, suppose that you want to implement a generic "multiplication" of an integer with an array — maybe it concatenates the array with itself n times. So you'd need to overload the `*` operator and declare that operator a friend of your `ArrayList` class.

```
template <class T>
class ArrayList {
  // other stuff
  template <class TT>
    friend ArrayList<TT> operator* (int n, const ArrayList<TT> & oldArray);
}
```

Notice that we named the other template parameter something other than that `T`; here, we used `TT`.

Chapter 19

Qt and Event-Based Programming

[Note: this chapter covers material of about 1 lecture.]

Qt (pronounced: cute) is a cross-platform application development framework for developing Graphical User Interfaces (GUIs), working with many different languages (such as C++, Java, Python, Ruby). There are three main reasons why we want to learn a little bit about programming with Qt in this class:

1. It can make your applications look much nicer.
2. GUIs developed in Qt are necessarily based heavily on inheritance and composition, so they are a great and practical illustration for why these concepts are useful.
3. In CSCI 201, you will learn in more depth about event-driven GUI programming, and having seen it here for a little bit may make it much more intuitive later.

In writing event-based GUI code, there are a few ways in which code design is a little different from the way you typically design your `cin, cout` applications. Specifically, we will look at (1) layout of graphical objects, (2) event-based programming, and (3) putting it all together (and compiling).

19.1 Layout of Graphical Objects

When designing GUIs, there are many graphical objects that commonly appear in applications, such as buttons, text fields (both for display, and for entering), radio buttons (for selecting exactly one option from many), check boxes, etc. What is different is which exactly are used, how they are labeled, how they are arranged, and what happens when you press them or enter stuff. But since enough of the functionality stays the same (as does much of what is shown), it makes sense to have a class for each of the common types of graphics objects. The graphics objects that users can see or interact with are usually called *widgets* in GUI contexts, so we stick with this name here.

There are two basic concepts that you combine to build user interfaces: widgets and layouts. The widgets do the actual work, while the layouts determine where the widgets appear relative to each other.

19.1.1 Layouts

A *layout* is an abstract concept capturing a way of arranging widgets. Common layouts would be to arrange all the widgets horizontally, vertically, in a 2D array of fixed dimensions, or as a "form" with a label and an input field for each row. The layouts that will be most relevant to you are probably the following:

QHBoxLayout: a layout in which all the items you add are put next to each other horizontally (left to right).

QVBoxLayout: a layout in which all the items you add are put on top of each other vertically (top to bottom).

QGridLayout: a layout in which the items are arranged in a two-dimensional grid of given dimensions. Individual items can occupy more than one cell of the grid.

QFormLayout: a somewhat more specialized layout with exactly two columns, where the first item is a descriptive label, and the second a field for entering something. This captures forms in which you enter a value/string for each of several parameters.

For adding widgets to a layout you have already generated, you can use the function

```
void addWidget (QWidget *w);
```

You can also add layouts inside layouts, by using the function

```
virtual void addItem (QLayoutItem *item);
```

This works because all layouts inherit from the abstract class `QLayout`, which in turn inherits from `QLayoutItem` (and similarly for the widgets).

Why would you want to put layouts inside other layouts? For instance, you may want a row of 4 buttons on the top (basic control). Below that, maybe you want some text fields to enter the values of different parameters, and below that a place where messages or file contents are displayed. You'd do that by having a high-level vertical layout, and nesting some horizontal and form layouts inside. Designing a good user interface with nice layouts is not always easy, but these basic primitives give you a lot of flexibility. There are also IDEs in which you can create these layouts by clicking and dragging, the way you would for Excel tables with nested tables.

Layouts have a number of parameters that you can use to change the way they appear. This is really not so much something you learn in class as something you experiment with when you need it by looking at the class definitions online. We just wanted to make you aware of it.

19.1.2 Widgets

The widgets are the things that the user actually interacts with. All widgets inherit from the base class `QWidget`. This means that for any layout, you can pass in any widget you want, and the layout won't mind. At this point, we recommend that you pause and think back to how simple some things become once you have the concepts of inheritance and base classes. Try to imagine how you would program, without using inheritance, a generic toolkit that would let programmers design their own arrangements of arbitrary buttons, text boxes, etc. Seriously, we encourage you to interrupt your reading at this point for 5–10 minutes, and think about how you would plan this out without inheritance.

Ok, you've thought about it for some time? Not easy, right? On the other hand, once we have the idea of a base class, and many different widget classes inheriting from it, it becomes very clean. Because each layout class inherits from `QLayout`, they all have the function `void addWidget (QWidget *w)`. And because each widget class inherits from `QWidget`, each of them can be passed as the argument `w` here. So arbitrary widgets can be added into arbitrary layouts.

How does the layout know whether something is a button or a text field? It doesn't, and it doesn't need to know. The object itself knows, and because the important functions are virtual, the right functions get called when — say — a user clicks on it, or the object needs to be drawn. All that the layout needs to know is that there is an object, and the object has a function to tell the layout how big it is (so the layout can arrange it properly). Notice the beauty of object-oriented design here, and the benefits of hiding information except for what must be known.

So what widgets are there already for your use? Here's a list of some of the more common ones — this list is not intended to be complete, and if you need something particular, you should look around a bit in documentation of Qt. To use any of the widgets, you `#include` the header file with the same name.

QPushButton: A button you can press (typically with text on it).

QToolButton: A quick-access button to commands or options.

QCheckBox: A box which you can check, usually with text to label it. Check Boxes are typically used when you can choose multiple options.

QRadioButton: A button you can check, usually with text to label it. Radio Buttons are typically used when you select one out of several given options.

QComboBox: Combined button and drop-down list, e.g., for selecting one of many options (like a state for an address).

QLabel: Place to display text or an image.

QLineEdit: One-line text editor.

QScrollArea: A way to surround another widget with scroll bars.

QTabBar: Creating tabbed dialogs.

QSlider: Vertical or horizontal slider to control a display or enter a value.

QSpinBox: A way to enter a value by incrementing/decrementing or entering it directly.

QMenu: A widget for a whole menu (such as menu bars, context menus, and others).

QMainWindow: A widget for a whole main window of your application. It already creates a menu bar, status bar, and several other areas for you to put content. You can access those objects and add to them directly, and don't have to create everything from scratch.

There are also more complex pre-written interfaces such as ones for entering a date, time, or both, or selecting from a calendar, choosing fonts or colors, etc. As you design your own applications, check out what's already there.

The constructors for these classes allow you to pass the key information, such as the text to label a button and others. Like with layouts, there are a number of parameters that you can set or change for widgets and that will change the appearance. These can be widget-specific (such as colors or fonts, or the extent to which a button gets shown as "depressed" when you click on it), or higher level, such as the style in which everything is displayed. (E.g., does the interface look like Windows or Mac?) You will probably learn about these parameters as you use Qt yourself.

Suppose that you need a widget that doesn't already exist. For instance, suppose that you want a button that changes color based on the values of other things (e.g., whether the user has checked the box that agrees to pay you a lot of money). This one doesn't exist yet. Do you now have to write a whole new button class from scratch?

The answer is "No." Again, object-oriented programming comes in to help you. As you learned, you can modify existing code without having access to it, by using inheritance. What you would do is inherit from the `QPushButton` class and write you own `ColorChangingPushButton` class, which keeps almost everything but overwrites one or a few virtual functions.

Most often, the key function to overwrite here is the `paintEvent` function, which is called any time the object needs to be painted. Here, you will often call the parent class's `paintEvent` first (so that the basics of the button or other object are correctly drawn), and then add some of your own code to show what you wanted to show.

19.2 Event-Based Programming

So far, we know how to arrange the layout of widgets, and how to select widgets to display. But how do we specify what actually *happens* when a user clicks a button, or enters something into a text box, or hovers the mouse over a particular area?

In our `cin, cout` model so far, it was pretty simple. The program waited until the user entered something; that stuff went into a `string` or `int` or similar, and we resumed computing. But here, it's not like we wait for just one particular entry. There are a number of different things the user could do. And in many cases (e.g., games), we want the program to continue doing something even if the user is not entering anything right now.

The way GUIs typically do stuff is using *event-based programming.* The way this works is typically as follows. You write your own function, say `foo`. What you would like is for `foo` to be called any time the user clicks on a particular button. Now the conundrum is the following: the folks who wrote the `QPushButton` class had no idea about the function `foo`, so they can't have added any code anywhere in `QPushButton` to call `foo`. How then do you get the code for calling `foo` in there?

The way you do it is to *register* `foo` with the button: you tell the compiler to connect the event of pressing the button with the function `foo`. The following is not exactly how Qt does it, but perhaps it illustrates the underlying concepts more cleanly for now. We could add to our `QPushButton` class a function:

```
void addFunctionToCallWhenPressed (void (*f)(void));
```

(Remember how you saw function pointers before? This would be where they come in handy.) Then, we could add the following code:

```
myPushButton.addFunctionToCallWhenPressed (foo);
```

Now, `myPushButton` is a `QPushButton`, which could internally store a list of function pointers, and all of them get called any time someone presses the button. So long as our function `foo` is a function of type `void` with no parameters, this will all work out fine.

There are some reasons not to do it this way, and a somewhat more elegant solution is the following (which is essentially how Java AWT does it). We can define an interface (i.e., completely abstract class) `Runnable` as follows:

```
class Runnable {
  virtual void run () = 0;
}
```

In other words, any object can be of type `Runnable`, so long as it has a `run()` function. Now, we could add in `QPushButton` the following function:

```
void addObjectToCallWhenPressed (Runnable *r);
```

Now, instead of calling our function `foo` (and making it a global function), we could define a class as follows:

```
class FooClass : public Runnable {
  virtual void run () {
    // code here that was previously in void foo ()
  }
}
```

Now, if we define an object `fooObject` of type `FooClass`, we can add

```
myPushButton.addObjectToCallWhenPressed (&fooObject);
```

Internally, the QPushButton could keep a list of objects of type Runnable. Any time the button is actually pressed, the QPushButton object could go through its list, and for each member of the list call the function run() (which must exist, because the object is of type Runnable). This would be an elegant way to establish the connection between the button that is pressed and the function to execute.

You should pause here for a moment (again) to understand this, and to notice the elegance of the approach. You have buttons which were programmed before the functionality they are supposed to cause. All they know is that there will be some other objects whose functions they are supposed to call. Similarly, you have objects (of type Runnable) which will implement the actual functionality you want. They don't need to be aware at all whether they will be called by buttons or menu items or even normal cin, cout code. All they know is that whenever the run() function gets called, they should do some useful work. So we have cleanly separated the GUI from the actual functionality, yet we can connect them because everyone is implementing a particular interface of functions (adding an object to call, and the run() function). This kind of paradigm is at the heart of much event-based programming.

Ok, we've talked at length about related ways that aren't exactly how Qt implements event-based programming. So how *does* Qt implement it?

The approach is based on what is called *signals* and *slots*. Signals are emitted (fired) by the widgets, and slots are the functions that get called when the signals are emitted. Qt then needs to *connect* these two with each other. It's important to remember that one signal can be connected with many slots (e.g., when you press a button, many functions could get called), and a slot can be connected with many signals (e.g., the same function could get called when you press a button or select a command from a menu).

19.2.1 Signals

To define a signal inside your object, you use the keyword signals: (which is used the way you currently use public: and private:). For instance, you could define a class

```
class Sender : public QObject
{
  Q_OBJECT
public:
   Sender () {}
   sendASignal (int number) { emit send(number); }
signals:
   void send (int k);
}
```

A few things to note here. First, the Q_OBJECT is just a keyword that you need to put in any time you want Qt to do some pre-compilation of Qt syntax (see also the discussion in the next section). Second, the keyword signals is not actually C++ — if you just ran g++, it would not compile. Qt will replace it with other code in its pre-processing. By using the signals keyword, you declare a signal, but you don't actually need to provide a function body, as it's just a symbolic reference. Finally, the interesting stuff happens in sendASignal. Here, we *emit* the signal, which will make the signal come into existence, so a slot can take care of it.

Roughly speaking, what will happen is that wherever you say emit send (number), the compiler will substitute in the function (from another object) that you *actually* want to call.

19.2.2 Slots

To declare a slot, i.e., a function which can be called in response to a signal, you use the keyword slots:, as follows:

```
class Receiver : public QObject
{
  Q_OBJECT
public:
   Receiver () {}

public slots:
   void receive (int k)
   { std::cout << k; }
}
```

This looks just like a normal class definition, except for (again) the keyword Q_OBJECT, and the fact that receive is defined not just as a public function, but as a public slot. This means that it is "eligible" to be connected with a signal from another object.

19.2.3 Connections

So far, we can create objects of type Sender and Receiver, but the sender cannot signal anything to the receiver yet. What we would like now is to connect the emission of a signal (happening with emit signal(number)) to the reception of something (in receive (k)).

The syntax for that is as follows:

```
int main ()
{
   Sender s;
   Receiver r;

   QObject::connect (&s, SIGNAL(send(int)), &r, SLOT(receive(int)));
   s.sendASignal(5);
}
```

connect is a static function in the class QObject (which basically means that it does not access any member variables); you therefore don't need to have an actual object of type QObject, and can call the function directly on the class.

It has four arguments: the pointer to the object to which the *signal* belongs (here, that's s), the signal within that object (here, it's the function stub send(int)), the pointer to the object to which the *slot* belongs (here, r), and finally the slot within that object (here, receive(int)). What this function does is what we've been talking about all along: it will basically replace any occurrence of the line emit send (n) with r->receive(n). Then, exactly the right function will be called in the right places.

What happens in this code is thus that the number 5 is printed. Once you really understand why, you probably get most of event-based programming.

19.3 Putting it Together

The GUI layout and event-based approach are the key pieces to know about. But there are a few other things that we haven't talked about so far.

19.3.1 Getting at data from widgets

First, how do you get at the information from the fields in your form? For instance, suppose that you have a form with an "Ok" button, and a few fields where people enter their name and e-mail address. Probably, entering things by itself shouldn't trigger any action, only once you press the button. But the button doesn't know about the values of those fields. So when the "Ok" button emits a signal, how can the corresponding slot know about the values of the text field?

The way we would do it is to connect the signal that is emitted by the button to a slot in the main window. The main window contains all the other widgets, so it can query their contents, and then process them further, either itself, or by calling another method that is just in charge of processing. (Notice that because you yourself will have written the main window class, inheriting from QWidget or something related, you have full control over which functions your class calls, and you won't need to use any signal-slot approaches for it — though of course, you can.)

To see how to get at the data inside your widgets, you can look at the documentation for individual widgets. For instance, if you have a QLineEdit object for entering a string, it has a function text() which returns the string you actually entered. (However, notice that it is returned not as a standard C++ string, but as a QString object. Fortunately, QString provides a method toStdString() which returns the string as a standard C++ string, so you can get it pretty easily.)

19.3.2 Control flow and main function

So what exactly does your main function do once you've written all these windows and signals and slots and connected everything up? It turns out, pretty much nothing. Typically, your main function will look as follows:

```
int main (int argn, char **argv)
{
   QApplication a (argn, argv);
   MyMainWindow w(arguments of constructor);
   w.show ();
   return a.exec();
}
```

We assumed here that you wrote your own MyMainWindow class. Even if you generate your own window (statically, as here, or dynamically), it isn't shown until you tell it to, which you do by calling its show() function.

QApplication is a specific type of Qt object (you need to #include<qapplication.h>); its job is to handle everything behind the scenes for you. So what you do is generate one of those objects (it likes to be given the command line parameters, so it can find out about any arguments that would change the appearance), and then hand control over by calling its exec() function. At this point, Qt takes over, and the button presses on windows will call the corresponding functions.

The exec() function will return a value based on what happened during its execution, i.e., it will signal whether the execution was successful.

19.3.3 Compiling Qt

Because Qt is not exactly standard C++, in order to compile it, you can't just run g++. Instead, you first run it through a pre-compiler, which will generate a bunch of extra files from your code to incorporate all the windows and event-based stuff; it also adds a bunch of code to work behind the scenes. After that, you can run your normal compiler.

To compile a Qt program (assuming Qt is installed correctly), you do the following:

1. Call qmake -project. This will scan the current directory for code containing Qt syntax, and generate a platform-independent project file (with extension .pro).

2. Call qmake. This will read the .pro file that Qt generated (or you edited by hand), and generate a real Makefile for compiling your code and linking it with all the Qt libraries.

3. Call make. This will do the actual compiling and linking, and reveal your errors, if any. For most debugging, you'll just need to run make again, without the first two steps, but if you changed the dependencies more fundamentally, you may need to repeat the first two steps, too.

Chapter 20

Graphs: An Introduction

[Note: this chapter covers material of about 2 lectures.]

20.1 The Basic Definitions and Examples

A *graph* is a set of "individuals" and their "pairwise relationships". The individuals are called *nodes* or *vertices* (singular: *vertex*), and sometimes also *points* (mostly by mathematicians). The relationships are called *edges* (or also *arcs* if they are directed), and sometimes also *lines*.

Many things in the real world can be very naturally represented by graphs. Examples include:

- Computer networks (including the Internet)
- Social networks (such as friendship, enemies, job supervision, family ties, sexual contacts, crushes, ...). Notice that some of these relationships (such as friendship, enemies, or sexual contacts) are by definition undirected, i.e., automatically reciprocated, while others (job supervision, crushes) are not necessarily so.
- Road systems or other transportation networks (train routes, flights between cities, ...). Again, notice that some edges go both ways (2-way streets), while others don't.
- Financial networks, such as investments between companies or financial obligations, overlap among boards of directors, and others.
- Supervision between different branches/entities of government.
- The WWW and other hypertext.
- Many more, including physical proximity, matches played between sports teams, symbiotic or predator behavior between species, reactions in biological/chemical systems.

Before getting too carried away and wanting to model everything as graphs, we should keep in mind that graphs only capture *pairwise* relationships. For example, suppose that you are trying to model a set of students (nodes), and whether they take classes together. There are three students, A, B, and C. If you have an edge between all three pairs $(A, B), (B, C)$, and (A, C), that could mean that all three are in a class together, or that there are three different classes, one which A and B are taking, one which B and C are taking, and one which A and C are taking. A graph does not let you distinguish between these two real-world scenarios. If we really wanted to model the difference, there would be two different approaches.

1. One would be to move from graphs to *hypergraphs*: hypergraphs have *hyperedges*, which may contain more than two nodes. Then, a hyperedge of $\{A, B, C\}$ could capture that all three students are in the same class together. In most of your standard college classes (including here at USC), hypergraphs are

not covered in depth; the main reason is that there are a lot of very beautiful and useful results about graphs, and most extensions to hypergraphs aren't nearly as useful or beautiful.

2. A different way would be to include in our graph two completely different types of nodes: students and classes. Then, we draw an edge between a student node and a class node if the student is enrolled in the class. We would not have any edges between students, or between classes. This would completely capture the scenario we are interested in. Such graphs (two different types of nodes, with edges only between nodes of different types) are called *bipartite*. They are often very useful, and there are many really interesting results about them. You may see some of them in CS170, CS270, and possibly higher-level classes.

In order to talk about graphs, we need to learn some terminology and agree on some notation[1]:

- The set of all nodes is usually denoted by V, and the set of all edges by E. Their sizes are $n = |V|$ and $m = |E|$. In talking about graphs, the use of n and m in this sense is very standard, so you should avoid deviating from it. Graphs are often denoted as $G = (V, E)$.

- Vertices are often named u, v, w, edges e, e', f.

- Edges can be *directed* or *undirected*. Undirected edges model relationships that are automatically reciprocated (such as being friends, siblings, married, in the same class, or connected with a 2-way street). Directed edges model relationships that are not necessarily reciprocated (such as having a crush on, being a parent of, being a supervisor of, or being connected with a one-way street). Directed edges are also frequently called *arcs*.

- A graph in which all edges are undirected is an *undirected graph*. A graph in which all edges are directed is a *directed graph*. A graph that contains both types is sometimes called a *mixed graph*.

- To visualize graphs, we will often draw the nodes as circles (or points or rectangles), and edges as lines (not necessarily straight). When edges are directed, we draw them as arrows.

- When there is an undirected edge (u, v) between nodes u and v, we call u and v *adjacent* (think: neighbors). When the edge is directed, people usually avoid the term "adjacent" to prevent confusion.

- In an undirected graph, the *degree* of a node v (written as $\text{degree}(v)$, or $\deg(v)$, or sometimes just $d(v)$ or d_v) is the number of edges that v is part of. In directed graphs, we usually carefully distinguish between the *out-degree* (number of outgoing edges), denoted by $\text{outdegree}(v)$ (or $d_{\text{out}}(v)$ or $d^+(v)$), which is the number of outgoing edges, and the *in-degree* (number of incoming edges), denoted by $\text{indegree}(v)$ (or $d_{\text{in}}(v)$ or $d^-(v)$).

When you do some basic calculations (counting), you see that a graph with n nodes can have at most n^2 (or $n(n-1)$ or $n(n-1)/2$) edges, depending on whether we allow a node to have an edge to itself, and whether edges are directed or undirected. In any of these cases, the maximum number is $\Theta(n^2)$. We call a graph with $\Theta(n^2)$ edges *dense*, and a graph with much fewer than n^2 edges *sparse*.[2]

[1] This list is of course far from complete: also read up in the textbook for some more terminology. You'll also likely learn much more in CS170 and CS270.

[2] For this class, the "intuitive" description will have to suffice. The attentive student comfortable with big-O notation will notice that it does not make sense to speak for a single graph about the number of edges being $\Theta(n^2)$, since the notation of O, Ω are only defined for functions. We'd really be talking about a *family* of graphs, including arbitrarily large graphs, and whose edge sets grow as $\Theta(n^2)$. For "sparse graphs", we will keep it deliberately underspecified. In different contexts, different definitions come in handy. Sometimes, we may just mean that the number of edges is *not* $\Omega(n^2)$ (which we denote by it being $o(n^2)$ with a little o). In other contexts, we may actually want the number of edges to be $O(n)$ or $O(n \log n)$ or $O(n^{1.5})$.

20.2 Paths in Graphs

One of the most useful and central concepts in modeling the world with graphs is a *path*: it captures one's ability to get from one node to another not just with one direct edge, but by following a *sequence* of edges. The formal definition of a *path* is a sequence of $k \geq 1$ nodes $v_1, v_2, \ldots, v_k$ such that for each i, there is an edge from v_i to v_{i+1} (directed or undirected). In this sense, a path exactly captures our ability to traverse multiple edges in sequence. Notice that we explicitly allow the case $k = 1$, i.e., a node by itself is also a path. Even though this path is often not particularly interesting, it usually helps us avoid having to deal with special cases in proofs. We will learn next lecture how to actually compute paths between vertices.

As defined so far, a path may repeat the same node or edge multiple times. If we want to rule this out, we can talk about *simple paths*: a path is *simple* if it does not contain the same node more than once. A *cycle* (sometimes also called *circuit*) is a path that starts and ends at the same node. We say that two nodes u and v are *connected* if there is an undirected path between them. (There are similar definitions for directed graphs, but those terms are used less frequently.) Thus, two nodes are connected if it is possible to get from one to the other.

An undirected graph is called *connected* if every pair of vertices in the graph is connected. A directed graph is called *strongly connected* if for every pair u, v of vertices, there is a directed path from u to v and a directed path from v to u.

Paths between nodes are extremely useful in many settings. In road networks, they are the main concept that we need for any kind of route planning (MapQuest, Google Map driving recommendations, GPS). In computer networks, they are where packets are routed from one computer to another. In social networks, they tell us whether you are connected to someone else by a chain of friends. You'll probably find useful applications in most other examples of graphs we talked about.

20.3 The Abstract Data Type Graph

In implementing graphs, we want to again think of them as an abstract data type: the information that is stored (internally) as well as functions to interact with the data. Internally, we will need to store the nodes and the edges. In both cases, we may want to associate some data with them. For nodes, this could be some information on a user of a social network, or a computer in a network, or an intersection on a road map. For edges, this may be the length or direction of a road, or the strength of a friendship (measured in number of e-mails exchanged or something else), or the amount of money one bank owes another, or the cost of an airline flight. When such data become more relevant later in the course, we will return to them; for now, we'll just focus on the basic graph structure, and keep in mind for the future that we'd often want to store more information at nodes or edges. The functions that the abstract data type should provide us are (at least) the following:

- adding and deleting a node.
- adding and deleting an edge.
- testing if a particular edge (u, v) exists.
- for a node u, listing all of its outgoing/incoming edges or all adjacent nodes.

The latter functions are particularly useful in the context of finding paths between nodes (as well as a few others, as we'll see later). A good implementation for them would be via iterators, i.e., the function returns an iterator that will eventually output all outgoing edges. (A separate function would return an iterator over all incoming edges; for undirected graphs, we may instead want an iterator over all adjacent nodes.)

By using an iterator implementation, we can continue to hide from other classes how the abstract data type stores information about the graph internally, and will only reveal the minimum amount of information necessary.

20.3.1 How to Implement the ADT internally?

There are two natural ways to store a graph internally. In both cases, we would store nodes themselves in an array or perhaps a linked list or List or Set.

1. Via *adjacency lists:* for each node, store a list of all other nodes it is adjacent to. (This could be using the ADT Set, the ADT List, a Linked List, or a dynamically growing array.) If the graph is directed, we would store two separate lists: one for outgoing edges and another for incoming ones.

   The elements of the list would be either pointers to the other nodes, or — if nodes themselves are stored in an array — integers, i.e., the indices in the array where the other node is stored.

2. Via an *adjacency matrix:* Store an $n \times n$ matrix (two-dimensional array) A. In position $A[u, v]$, store whether there is an edge from u to v. (This could be a boolean value, or perhaps an integer storing the length, cost, or other information.)

   What we store in position $A[u, u]$ depends on what our graph is modeling. In some cases, it makes sense to treat it as though there were an edge from u to itself, in other cases not so much. There is no rule that forces us to choose one or the other, and we should use whatever makes our computational task easiest.

In comparing the two approaches, we should always take into account which operations we expect to be performed more frequently. Let us compare which operations are more or less expensive in the two implementations.

1. For adding or removing nodes, an adjacency matrix has a bit more overhead, since changing the size of a matrix involves a bunch of reallocation and copying. For many applications that a computer scientist is called upon to solve, changes in the set of nodes tend to be a bit rarer while other processing is happening.

2. Testing whether the edge (u, v) exists in the graph is the specialty of adjacency matrices. It only involves one lookup in a known position of a 2-dimensional array, and thus takes $O(1)$ time.

   For an adjacency list, we don't have that information readily available. Instead, we need to go through the list of all outgoing edges of u, and see if v is in that list. That will take $\Theta(\text{outdegree}(u))$, which can be much larger. (As we learn about better implementations of sets later, this becomes faster, but even then, the time will not go down to constant.)

3. Listing all outgoing/incoming edges of u is the specialty of adjacency lists. Since they explicitly store this information, they just have to go through their Set/List, which takes time $\Theta(\text{outdegree}(u))$ or $\Theta(\text{indegree}(u))$.

   For an adjacency matrix, we don't have this information stored, so we have to loop through the entire row (or column) of the node u, and find all the entires that are 1 or `true`. This will take $\Theta(n)$, which can be much worse if the degrees are pretty small.

4. We can also compare the memory requirements of the two implementations. For the adjacency matrix, we need to store an $n \times n$ array, which obviously requires $\Theta(n^2)$ memory.

   For adjacency lists, we store all incoming and all outgoing edges, which gives us a total memory requirement of $\Theta(\sum_v(\text{indegree}(v) + \text{outdegree}(v)))$. To evaluate this sum, notice that when we sum all in-degrees, we count each edge exactly once, since it contributes 1 to the indegree of exactly one node. So the sum of all indegrees is m, and similarly for the sum of all outdegrees. Thus, the sum above is equal to $2m$, which is $\Theta(m)$. Thus, the total storage requirement is $\Theta(n + m)$ (since we also need to store information for all nodes).

   Thus, for sparse graphs, adjacency list are much more economical with space than adjacency matrices, whereas for dense graphs, it doesn't really matter too much in terms of memory.

We saw above that each way of storing a graph has its own advantages and disadvantages. If memory isn't too big of a concern (it rarely is — computation time is the bottleneck much more often than memory nowadays), one possible approach is to store the entire graph twice internally. When a user queries whether an edge (u, v) exists, we answer it by using the adjacency matrix, while when the user queries all neighbors of a node u, we use adjacency lists.

The downside of this approach (besides using twice as much memory) is that it requires us to execute each update to the graph twice: once on the adjacency matrix and once on the list. Thus, update operations (such as adding or removing nodes or edges) will take twice as long as before. However, this may well be worth it: for many graphs, updates are much less frequent than queries. For instance, when building a GPS, it is much rarer to have roads or intersections added to a road network than to look for routes between two locations. Similarly, in a social network, users add/remove friends much less frequently than reading their friends' updates. In those cases, the extra investment in updates is well worth it to have faster responses in queries.

As an aside for the interested student, this idea of doing more "pre-processing" during update time to speed up later operations at "query time" is an important and active direction in data structures. Many papers are trying to find useful internal representations to answer queries about connectivity or short routes faster than with the "default" representations we considered above.

20.4 Graph Search: BFS and DFS

One of the questions most frequently asked about graphs is some variant of the following:

- Is there a path from u to v?
- What is the shortest path from u to v? (Either in terms of number of hops, or distances or costs which may be stored on edges.)
- What is the distance from u to every other node in the graph (or every node that can be reached from u)?

All of these problems fall under the broad area of *graph search* or computation of *shortest paths* (or just paths). These problems have many important applications:

1. Finding fast or cheap ways to go from one place to another, by utilizing road networks (optimizing distance or time), or airline or train networks (optimizing time or cost).
2. Finding social distance in a social network. One prominent example of this is the *Kevin Bacon Game*, in which the players try to construct short sequences of movies that connect a given actor or actress to the actor Kevin Bacon. There is an edge between two actors iff they co-starred in at least one movie.[3]
3. In a game (usually a puzzle or logic game), is there a way to manipulate the game according to the rules (sliding boxes, squares, changing switches, moving around, etc.) to get from a given initial state to a given target state?
4. The idea of planning to get from one state to another is more pervasive, and extends beyond games. Robots need to plan sequences of moves to get them from one configuration to another. Many systems need to plan sequences of actions to execute.

One can come up with many more examples: a huge number of real-world problems are extremely naturally modeled as shortest path searches in suitably defined graphs. Therefore, graph search algorithms are one of the most central concepts for a computer scientist to be familiar with.

As we briefly mentioned above, there are a few parameters along which concrete instances can differ:

[3] The mathematicians' version of this is the Erdős Number, where two mathematicians are connected iff they co-authored at least one paper, and one is interested in the number of hops to the legendary Hungarian mathematician Paul Erdős.

1. Do we just want to know *whether* a path exists, or do we need to find it?
2. If we need to find a path, do we want the shortest path, or will any path do?
3. If we don't need to find it, do we need the exact distance between nodes, or just whether a path exists?
4. Do edges have lengths/costs associated with them, or are we just interested in the number of hops.
5. If edges have costs associated with them, can they be negative?

For the first three questions, it turns out that generally, the problem doesn't get much easier by asking just *whether* a path exists, so the algorithms we will investigate will actually find a path; and the most "natural" algorithm (BFS) actually finds a *shortest* path. On the other hand, edge lengths/costs make the problem a bit more challenging, and we will see later in class how to deal with them. Negative edge costs are not terribly difficult, but are a little bit beyond this class — you will likely learn about them in CSCI 270.

20.4.1 Breadth-First Search (BFS)

Breadth-First Search (BFS) is a fairly simple algorithm that finds the shortest path (in terms of number of hops) from a given node u to all nodes v. The idea of BFS is to "explore" the graph in layers.

- Layer 0 is the node u itself.
- Layer 1 consists of all nodes v with a direct edge $(u, v) \in E$.
- Layer 2 consists of all nodes w with a direct edge $(v, w) \in E$ from some node v in layer 1. However, it excludes nodes that were already in Layer 1 themselves.
- More generally, Layer k consists of all nodes w with a direct edge from some node v in Layer $k - 1$, but such that w itself was not already in an earlier layer.

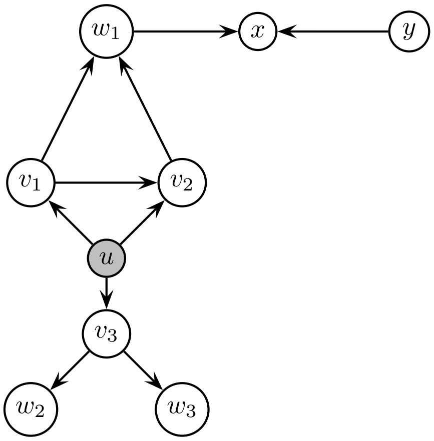


Figure 20.1: A directed graph. Here, layer 0 is just node u (the source). The nodes v_1, v_2, v_3 form layer 1. The nodes w_1, w_2, w_3 are layer 2. Notice that node v_2 was already in layer 1, so it's not also in layer 2. Layer 3 contains just node x. Notice that node y is not reachable from u, and is thus at infinite distance.

The recursive definition of layers is quite nice. It's not too difficult to prove with this definition that the nodes in layer k are exactly at distance k from u. However, to implement this algorithm, we will have to process nodes one by one, as processing an entire layer at once is not standard programming functionality.

When we process nodes sequentially, we would like to make sure that all nodes from layer k have been processed before we get to the nodes in layer $k + 1$. Because we "discovered" (with the algorithm) the nodes in layer k before those in layer $k + 1$, this means we should process nodes in the order they were discovered.

We have seen a data structure supporting exactly that: a FIFO queue. Indeed, the FIFO queue is the central part of the Breadth-First Search algorithm.

For the description and the analysis, we will let $\hat{d}(v)$ denote the *actual* distance from u to v, and `d[v]` the distance the algorithm computes. Of course, we hope that those will be the same, but we need to actually prove that. We will assume that nodes are numbered with integers $0, 1, \ldots, n-1$, so that we can simply store values associated with nodes in arrays of size n. In addition to the array of distances `d[v]`, the algorithm will also compute an array of *predecessors* `p[v]`: for each node v (other than u), this is a node in the previous layer which has an edge to v. For instance, in Figure 20.1, $p[w_3] = v_3$, and $p[x] = w_1$. On the other hand, $p[w_1]$ could be either v_1 or v_2, depending on the order in which those two nodes were explored. We will consider the arrays as global variables, just to keep notation simple.

```
int d[n];  // will store distances from u
int p[n];  // will store predecessors of nodes on shortest paths from u

void BFS (int u) {
  bool visited[n] = {false};  // no node is visited yet.
  Queue<int> q ();  // empty queue to start.
  visited[u] = true; d[u] = 0;
  q.enqueue (u);
  while (!q.empty()) {
     int v = q.peekfront();
     q.dequeue ();
     for (all nodes w with an edge (v,w) in E)  // use some iterator
         if (!visited[w]) {
            visited[w] = true;
            d[w] = d[v] + 1;
            p[w] = v;
            q.enqueue(w);
         }
   }
}
```

The idea of the algorithm is as follows: we start with just the seed node u. Its distance from itself is obviously 0. Then, the `for` loop adds all of u's neighbors to the queue.

Whenever we process a node v (dequeuing it), we look at all its outgoing edges. The edge could lead to a node we have already seen, in which case we should not process it again — if we did, we might accidentally increase the distance label. If we have not seen the node w before, then we mark it as "visited" (so it isn't processed again[4]), and set its distance and predecessor correctly. The predecessor is the node v from which the edge (v, w) allowed us to discover w, and the fastest way to go from u to w is to first go to v, then take one more hop, so the distance is one more than that of v. Finally, we add w to the queue, so it's processed later.

While we won't do a formal correctness proof of BFS in this class, we want to roughly think about how BFS ensures correctness. Clearly, the FIFO queue is essential, and we should think what exactly it guarantees. A loop invariant that works would be the following. At each point in the `while` loop, the following are true:

1. For all nodes v with `visited[v] == true`, the values of `d[v]` and `p[v]` are correct. That is, $d[v] = \hat{d}(v)$, and $p[v]$ is a last hop node on a shortest path from u to v.

2. The distances of nodes in the queue are sorted. Let $v_1, v_2, \ldots, v_k$ be the nodes in the queue, sorted by when they were inserted. (v_1 has been in the queue longest, and v_k was added most recently.) Then, $d[v_1] \leq d[v_2] \leq \ldots \leq d[v_k]$.

[4] Forgetting this part is a commonly made mistake when coding BFS.

3. The nodes in the queue are all from just two adjacent layers. That is, $d[v_k] \leq d[v_1] + 1$.

While this may seem a little convoluted, if you think about it carefully, you'll hopefully see how that captures exactly our intuition that the FIFO queue gives a close emulation of processing nodes in layers. A correctness proof would now establish the loop invariant by induction over iterations of the `while` loop.

Next, let's analyze the running time of the BFS algorithm. First, we notice that the initialization of the `visited` array, while written as one line, actually takes $\Theta(n)$. All other individual commands take time $\Theta(1)$. So, as usual, we'll analyze loops inside out. The `for` loop goes through all outgoing edges of node v. If our iterator is implemented carefully (e.g., we used an adjacency list for our graph), then this takes $\Theta(\text{out-degree}(v))$ for node v. All the rest of the code inside the `while` loop takes time $\Theta(1)$, so the total time inside one iteration of the loop is $\Theta(1 + \text{out-degree}(v))$. (Normally, we would drop the 1. The reason we are keeping it here for the moment is that it is possible that out-degree$(v) = 0$, in which case our analysis would claim that the iteration takes 0 time, which is not true.) Now, as usual, we notice that the `while` loop may run over all nodes, so the running time is a sum

$$\sum_v \Theta(1 + \text{out-degree}(v)) \;=\; \Theta(\sum_v 1 + \sum_v \text{out-degree(v)}) \;=\; \Theta(n + m).$$

Together with the $\Theta(n)$ for initialization, the total running time of BFS is $\Theta(n + m)$, which is linear in the size of the graph (the time it takes just to read the graph as input). So BFS is a fast algorithm.

20.4.2 Depth-First Search (DFS)

Breadth-First Search processes the graph by layers of increasing distances from the start node u. That is what FIFO queues are great for. The downside is that the search algorithm jumps all around over different areas of the graph. For instance, if you trace the execution on the graph in Figure 20.1, you see that after processing u, v_1, v_2, v_3, rather than staying with v_3 and its neighbors, the algorithm next jumps to w_1. When you want just shortest paths, that's of course not a problem, but sometimes, you want to explore a graph by staying local — this is sometimes needed as part of other algorithms. To explore a graph locally, we would want to first explore all the nodes "around v" before switching to other parts of the graph.

We can accomplish this by replacing the FIFO Queue in the BFS algorithm with a LIFO Stack instead. That way, the most recently added node will be the one explored next, which ensures that the algorithm stays in a neighborhood of a node. Apart from that one-word change, the algorithm is exactly the same. This algorithm is called Depth-First Search (DFS), because it first explores the neighborhood of a node going deeper into that area, before going for other parts of the graph.

Of course, DFS will *not* find shortest paths any more necessarily. For instance, in our Figure 20.1, it will first reach v_2 from v_1, assigning it a distance of 2, and never revisiting this choice. Notice that this is fine — DFS is not used when one wants *shortest* paths. For that, you would use BFS. But since the `d[v]` values don't really capture anything particularly useful any more, we could simplify the algorithm a bit by removing those arrays altogether.

The running time of DFS is obviously also $\Theta(n + m)$, since we just plugged one data structure in for another, and all operations take the same amount of time.

There is an alternative (perhaps even simpler) implementation of DFS using recursion instead of a stack.

```
bool visited[n] = {false};

void DFS (int u) {
  for (all nodes v with an edge (u,v) in E)   // again use an iterator
     if (!visited[v]) {
        visited[v] = true;
        p[v] = u;
        DFS(v);
     }
}
```

In this implementation, we don't have to explicitly worry about stacks — the recursion automatically takes care of the stack for us.

20.5 PageRank

Students familiar with linear algebra (hopefully most of you) will remember "matrices" as the central concept in that field. Is it a pure coincidence that we are interested in the adjacency *matrix* of graphs? Not really.

There are a lot of interesting things one can do with matrices, such as adding, multiplying, finding eigenvectors and eigenvalues, and more. It turns out that some of these have really useful meanings in computing properties of graphs, and some of the most exciting research in graph theory these days is based on interesting computations with adjacency matrices (and slight variations of them). The area is known as *spectral graph theory*, and some of the results are quite complicated. But other cases are pretty directly accessible, and we will look at one of the easier and more useful ones now.

One of the many things naturally modeled by graphs is hyperlinked text, such as the World Wide Web. If we think about the task of writing a web search engine, one of the biggest problems is how to identify not just pages containing a particular word, say, "graph", but to find the best ones. (Google currently reports about 86 million results, which is a bit too many for a user to check by hand.) Of course, the ideal solution would be if the search engine could actually *understand* the text and find out what the page is about, and whether it's useful. But understanding natural languages is a notoriously difficult task, and even today, the mere task of determining the *topic* of a piece of text is quite difficult, let alone finding out whether the text is *useful* on that topic.

In fact, in the early days of the web (mid-1990s), most search engines were really quite bad, since they were exclusively text-based. The key insight which gave Google a huge edge was to look at the link structure of the web to determine which pages were good. Google started as a research project by two grad students at Stanford, but was so much better than the competitors that it quickly became a serious product. The idea to use links is obvious in retrospect, but wasn't at the time.

The idea behind using links is that if page A links to page B, then this must to some extent express an endorsement from A of B.[5] Thus, all things equal, if we are looking at two pages A and B both containing the search term, and A has more inlinks than B, then we would think that A is better than B. This would be our draft 1 of using links.

Once we start thinking in those terms, we realize that not all links are created equal. An inlink from the NY Times is probably a stronger endorsement of a page than an inlink from a friend or relative. In other words, links from pages which are themselves good should contribute more to a page being considered good. Of course, now, our definition has become self-referential: in order to know whether a page is good, we need to know whether the pages linking to it are good. That seems circular, but as we'll see in a moment, it actually admits a nice solution.

The other way in which links are not created equal is in terms of the number of outgoing links. If we have determined that A and B are equally good pages, and A has just one outgoing link, to C, while B has 10,000 outgoing links, one of them to D, then we would expect that the link from A to C confers more support (because it was chosen carefully) than the one from B to D (which is just one among many, maybe part of a directory or "phone book").

Putting all of these together, we could say that each page i has a quality score q_i, and that these must satisfy the following equation:

$$q_i \;=\; \sum_{j:j\to i} \frac{1}{\text{out-degree}(j)} \cdot q_j.$$

Thus, each page j confers equal fractions of its own quality on all the pages it links to. This captures all of the things we wanted to capture earlier. Notice that in order to make this work out, i.e., for the system of linear equations to have a solution, we need to assume (or make sure) that each page links to itself.

[5] Sometimes, links are made to mock or otherwise disparage another page, but those are definitely in the minority.

We an also get this system of linear equations into more standard matrix-vector system notation. Let A be the adjacency matrix of the directed graph, with $A = (a_{i,j})$ and $a_{i,j} = 1$ if i links to j, and 0 if not. (As we mentioned above, this works better if $a_{i,i} = 1$ for all i.) Then, we can write

$$M = \begin{pmatrix} \frac{1}{\text{out-degree}(1)} & 0 & \cdots & 0 \\ 0 & \frac{1}{\text{out-degree}(2)} & \cdots & 0 \\ 0 & 0 & \ddots & 0 \\ 0 & 0 & \cdots & \frac{1}{\text{out-degree}(n)} \end{pmatrix} \cdot A.$$

Then, we can rewrite the previous system of linear equations as $\vec{q} = M^T \cdot \vec{q}$, where you may remember that the T stands for taking the transpose of the matrix, i.e., mirroring it along the main diagonal. This says that $\vec{q}$ is an eigenvector of M for the eigenvalue 1.

We can interpret the same system of linear equations in a different way. Suppose that a person, whom we will call a random surfer, starts at some node i. In each step, he clicks on a uniformly random outgoing link from the current page, and follows that link. Then, he continues from there. Because each outgoing link is taken with probability $\frac{1}{\text{out-degree}(i)}$, he is at each of the endpoints with that probability after 1 step. We then continue in this way, and we see that the vector $(M^T)^k \cdot (0, 0, \ldots, 1, 0, \ldots, 0)$ captures exactly the probability of being at each of the nodes after k steps.

But this also reveals a flaw in our approach so far: Once the surfer reaches a node j with no outgoing links (except to itself), he will never go anywhere else. Those are the only places to get stuck, and as a result, in the long run, the only states that have non-zero probability are those with no outgoing links. That's not exactly what we wanted.

The solution is a small hack. Thinking still about our random surfer, to get him unstuck, we also allow him to jump to a random location. In each step, with some probability α, the surfer jumps to a uniformly random new node (i.e., any node, whether connected by an edge or not); with the remaining probability $1 - \alpha$, the surfer follows a random outgoing link from the current page. In practice, people typically choose $\alpha = 15\%$ or similar values. The number $1 - \alpha$ is also called the *damping factor*. We can now rewrite our linear system, as follows. Let

$$B = (1-\alpha)M + \alpha \cdot \frac{1}{n} \cdot \begin{pmatrix} 1 & 1 & \cdots & 1 \\ 1 & 1 & \cdots & 1 \\ 1 & 1 & \ddots & 1 \\ 1 & 1 & \cdots & 1 \end{pmatrix}.$$

This is the new transition matrix describing the modified surfer process. We can now write $\vec{p} = B^T \cdot \vec{p}$ as our system of equations. In other words, the quality vector we want is an eigenvector of B with eigenvalue 1.

The vector $\vec{p}$ is called the *PageRank* vector for the graph G whose adjacency matrix is A. To use it for web search, one can first compute the PageRank vector, and then sort all eligible pages (e.g., all pages containing the search term) by their PageRank values. The better ones will typically end up on top. PageRank was the key insight for Google at the time it got started. Of course, by now, Google has a lot of additional ideas built into it, with many special case treatments, stuff it learned from billions of searches, etc.

Notice that one can apply PageRank in other settings, too. It can be used any time we believe that links confer some kind of status or importance. For instance, we could use it to identify important individuals in a social network, or important servers in a computer network.

In order to actually *compute* the PageRank vector, we can use pretty much any general-purpose linear system solving technique, such as the Gauss elimination method you learned in middle school. However, thanks to the relatively large value of α, iterative methods will converge quite fast, and are probably a superior approach, at least in terms of computation speed.

You start with an arbitrary vector $\vec{p}_0$. In each iteration, you compute $\vec{p}_{t+1} = B^T \vec{p}_t$. As $t \to \infty$, the $\vec{p}_t$ will always converge to the eigenvector $\vec{p}$ we are looking for. In fact, this works for almost any matrix —

basically, any matrix C for which the corresponding graph (with edges (i, j) whenever $c_{i,j} \neq 0$) is connected. For general matrices C, the convergence speed of this iterative method could be very slow. However, for PageRank specifically, iterative methods will converge fast, typically giving good approximations after 30–100 iterations already (even for very large graphs).

Chapter 21

Trees and Tree Search

[Note: this chapter covers material of about 1 lecture.]

21.1 The Basics

Trees are a special type of graph. We can think of them in two different ways, arriving at the same definition in the end.

- A tree is an undirected, connected graph without cycles.
- A tree is "like a" linked list, with each node having at most one `prev` pointer (exactly one node having none), and being allowed to have *multiple* `next` pointers.

An undirected graph without cycles that may or may not be connected is called a *forest.* In other words, a forest consists of one or more trees.

In the real world, we can model quite a few things using trees: family trees (either by going from one person to their parents, grandparents, etc., or from one ancestor to his/her children, grandchildren, and so forth), file system hierarchies, evolutionary trees among species (sort of like family trees), parsing of human language or formulas or programming languages, shortest paths in a graph as computed by BFS, and a few others.

Even more importantly in this class, trees are very useful as the basis of many more complex data structures, and often offer much better tradeoffs between running times of different operations than linear structures like arrays or linked lists. When using trees in the design of data structures, we usually think of the trees as directed. There is a designated *root node* of the tree, and all edges point away from it.

The terminology for trees is a somewhat inconsistent mix of botany and family trees.

- If node u has a directed edge to node v, then we say that u is a *parent* of v, and v is a *child* of u. If u has a directed edge to nodes v_1, v_2, then v_1 and v_2 are *siblings.*
- The *root node* is the one node that does not have a parent. Since every other node can be reached from the root, if we have all the edges, it's enough to have access to the root to find all other nodes.
- Nodes that can be reached from u with a path of length 1 or more are called *descendants* of u. Nodes that can reach v with a path of length 1 or more are called *ancestors* of v.
- A *leaf* is a node without children. A node with at least one child is called an *internal node.*
- When talking about rooted trees, the *degree* of v refers to the number of edges out of a certain node. For example, if a node has one edge from its parent, and two to its children, its degree is 2 (even though if we thought of it as an undirected tree, we would call the degree 3).

- A *subtree* of a tree is a subset of nodes and edges that are (by themselves) connected. The most frequently used subtrees are those consisting of a node v and all its descendants. Those are called the *subtree rooted at* v.

- It is frequently useful to think about the *levels* of nodes. For any node v, the level of v is the number of nodes in the path from the root to v. Thus, the root itself is at level 1, its children are at level 2, its grandchildren at level 3, and so on. (Some sources may start with level 0 — make sure you use the same notation as whoever you are talking with.)

- The *height* of a tree is the largest level of any of its nodes.

Much like other structures in this class, we can use recursion to say formally what a rooted tree is.

1. A root r by itself is a rooted tree. (Depending on how we feel about calling an empty tree "rooted", we could instead use the empty tree as our base case.)

2. If $T_1, T_2, \ldots, T_k$ are rooted trees, rooted at $u_1, u_2, \ldots, u_k$, then by adding a node r and directed edges $(r, u_1), (r, u_2), \ldots, (r, u_k)$, we obtain a rooted tree.

This recursive definition of a tree often aligns very naturally with recursive algorithms for processing data on trees, as we will see soon enough.

There are specific subclasses of rooted trees that are frequently used in designing data structures, so we emphasize them here:

1. A tree is *d-ary* if each node has degree exactly 0 or d. A *binary tree* is a 2-ary tree. We emphasize that we sometimes allow an exception for one node to have only one child, as we will see below.

2. A d-ary tree is *full* if all leaves are at the same level (so adding one more node would require a new level to be formed).

3. Being *complete* is slightly less restrictive than being full. A complete d-ary tree has all its leaves at level h or level $h-1$. Usually, when talking about complete trees, we also assume that there is a natural "left-to-right" order among the subtrees, and we require that the leaves at level h are as far to the left as possible.

Many trees we will use for implementing data structures will be binary, but there will be an important exception of so-called 2-3-trees, in which each internal node has degree either 2 or 3.

21.2 Implementing trees

Trees are special types of graphs, so we could just use our general-purpose graph implementations (adjacency matrix or adjacency list) to implement them. Adjacency matrices are not very natural, for two reasons:

1. We rarely need to find out if two specific nodes are connected by an edge, but we frequently need to explore all children of a given node.

2. Trees are extremely sparse ($n-1$ edges for n nodes), so adjacency matrices would be extremely wasteful with space.

Adjacency lists are a more natural fit. But we can simplify them a bit, since we know that each node has exactly one incoming edge (except the root, which has 0). So we won't need a whole list of incoming edges, and can just store one pointer to the parent (which is `NULL` for the root). This gives us the following as the structure for a node.

```
template <class T>
class Node {
   T data;
   Node<T>* parent;
   List<Node<T>*> children;
};
```

Depending on whether the order of the children matters, we may use a `Set<Node<T>*> children` instead of the `List`. For a parse tree of an arithmetic expression, the order of children clearly matters, as $5 - 2$ is not the same as $2 - 5$. For some other trees, it doesn't matter as much.

Many of our trees will be binary, in which case we don't need a list of children, and can instead have two pointers.

```
template <class T>
class Node {
    T data;
    Node<T> *parent;
    Node<T> *leftChild, *rightChild;
};
```

In both cases (binary or more general), notice that we are storing pointers to other nodes, rather than something like `Node<T> parent`. This is important: ideally, we'd like to generate just one object for each node, and then have others point to it. If instead, we stored nodes themselves (rather than pointers), we would be creating a new copy of a node for each neighbor, and following around the structure would be hard.

An alternative to generating dynamic objects for nodes is to store all nodes in one array. Then, instead of storing pointers to the parent and children, we can just store their indices as integers. This would give us the following for a binary tree (and a similar idea for general trees):

```
template <class T>
class Node {
    T data;
    int parent;
    int leftChild, rightChild;
};
```

If the tree is a *complete binary* tree, this can be simplified even further. If we start numbering the nodes at 1 (for the root node), then by a little bit of experimentation, we find that the parent of node i is always node $\lfloor i/2 \rfloor$, and the two children are $2i$ and $2i+1$. The formula looks a little different if we number the root with 0, but it's not much more difficult. It also generalizes to d-ary trees quite naturally.

21.3 Traversing a tree

Traversing a tree means visiting each node of the tree exactly once. This is naturally done recursively, following the recursive definition for a tree. Traversing a leaf is pretty easy — we just do whatever we want to do with it (such as print it or do some computation). Traversing an internal node v involves visiting the node itself, and recursively visiting each of the subtrees rooted at its children $u_1, u_2, \ldots, u_k$ (for $k \geq 1$). The main distinction is then the relative order: do we traverse the subtrees first, or do we visit the node v itself first? This is exactly the difference between *post-order* traversal and *pre-order* traversal. If the tree is binary, it also makes sense to traverse the left subtree first, then visit the node v, and then traverse the right subtree. This order is called *in-order.* We will illustrate all three with a traversal of the following tree:

In *post-order traversal*, we visit all the subtrees first, then process the root. Thus, the pseudo-code looks as follows:

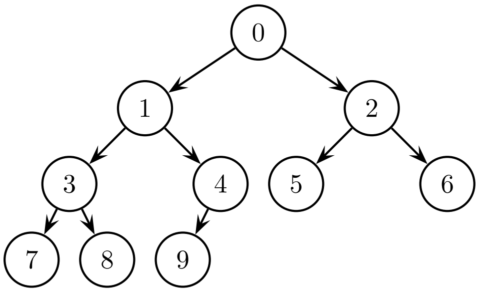


Figure 21.1: A tree T on which to illustrate different traversal orders. We would consider T a complete binary tree, even though technically, node 4 has only one child, violating the definition. But the concept is useful enough that we'd like to not worry about this small detail.

```
void traverse (Node<T>* r) {
   for each child u of r
       traverse(u);
   process r's data, e.g., output it or something;
}
```

If we apply it to our example tree, we get the following sequence: 7 8 3 9 4 1 5 6 2 0.

In *pre-order traversal*, we process the root first, then visit all of the subtrees. The code is obtained by just swapping the order of the two parts in the post-order traversal pseudo-code.

```
void traverse (Node<T>* r) {
    process r's data, e.g., output it or something;
    for each child u of r
        traverse(u);
}
```

For pre-order traversal, the visit order in our tree is: 0 1 3 7 8 4 9 2 5 6.

Finally, for binary trees, there is also *in-order traversal*, in which we visit all nodes of the left subtree, then the root, and then all nodes of the right subtree. We get the following pseudo-code:

```
void traverse (Node<T>* r) {
    traverse (r->leftChild);
    process r's data, e.g., output it or something;
    traverse (r->rightChild);
}
```

Here, the visit order for our example tree is: 7 3 8 1 9 4 0 5 2 6

In-order traversal is most natural for binary trees. If a node has more than 2 children, one would have to make a decision what is the right point to process its own data. If a node has d children and $d-1$ pieces of data (instead of just one), then it makes sense to alternate between children and pieces of data, and indeed, we will see that when talking about 2-3 trees later.

21.4 Search Trees

The key property that makes a (binary) tree a *search tree* is that the following holds at *every* node v:

> Let k be the key in node v, and T_1 and T_2 the left and right subtrees at v. Then, all keys in T_1 are less than (or equal) k, and all keys in T_2 are greater than (or equal) k.

An example tree to illustrate this concept is given in Figure 21.2:

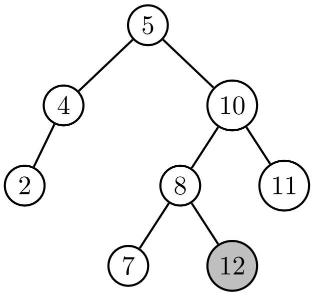


Figure 21.2: An illustration of the Search Tree property. The property is satisfied almost everywhere. The exception is the gray node labeled "12". It is in the left subtree of the node labeled "10", which violates the property that all keys in the left subtree of a given node are smaller than the key in the node itself.

Let's figure out how to search for a value in a tree Suppose that we are looking for a key `k` in a tree rooted at `v`. There are three cases:

1. If the tree is `null` (i.e., an empty tree), then `k` wasn't in the tree, which we report (e.g., with an exception).

2. If `v.data == k`, then the key is at the root node, and we can just return the root note in some form.

3. If `k < v.key`, then the search tree property guarantees that `k` is either in the left subtree of `v`, or not in the tree at all. So we recursively search in the left subtree.

4. In the final remaining case `k > v.key`, we recursively search for `k` in the right subtree T_2.

Notice the similarity between this search and Binary Search. We repeatedly query a "middle" value, then decide to recurse in one subpart or the other. Indeed, it is quite easy from a Search Tree to obtain a sorted array of all entries: perform an in-order traversal of the tree. The advantage of Search Trees over sorted arrays is that we can rearrange trees just a little bit at a time, rather than having to shift huge numbers of items around for every insertion. Thus, search in a Search Tree is as fast as Binary Search (which is very fast), but as we will see later, insertions and removals are very fast, too.

So far, we have asserted that search in a Search tree is fast, and based on our example in Figure 21.2, it looks like it is. As we do the analysis of the search algorithm above, we see that each step takes constant time, and increases the level we are searching by one. Thus, the time to search for an item is $\Theta(\text{height}(T))$. Whenever the height is small, say, $O(\log n)$, Search Trees will perform great. But will the height always be small? Consider the example in Figure 21.3.

This tree doesn't look like a tree at all — it's basically a linked list. But of course, technically speaking, it is a tree. Its height is n, the number of elements, and so a search would be really slow.

In order to keep the height small, ideally, our tree should be close *balanced*: for any node, the difference in heights of its subtrees should not be too big. That way, the tree will look almost like a complete binary tree, and it is easy to see that a complete binary tree has height $O(\log n)$. But how do we make sure a search tree remains somewhat balanced? We'll learn about it soon enough — stay tuned.

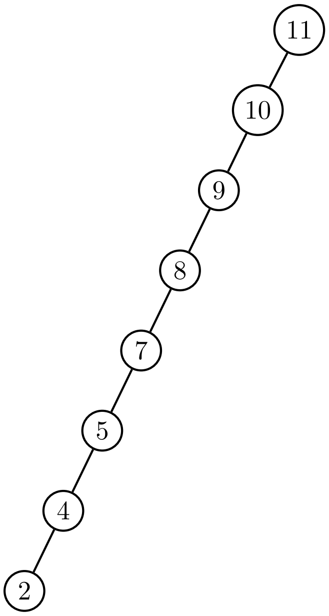


Figure 21.3: A degenerate search tree. Here, a search for the number "1" would take time linear in the number of elements, as it would just become a linear search.

Chapter 22

Priority Queues and Heaps

[Note: this chapter covers material of about 1 lecture.]

Earlier in class, we have seen two simple structures that manage access to shared resources: queues and stacks. Stacks access the data in a LIFO (last-in-first-out) order, in contrast to the FIFO (first-in-first-out) order in queues. In the real world, we often employ queues to achieve some notion of fairness, because we feel it is right to first serve those who arrived first. Examples include:

1. A line at a restaurant or grocery store. When customers arrive, we want to be fair to them, so we serve them in the order in which they arrive.

2. An operating system. Often, when the operating system is running, there are different programs that need access to the same resources (memory, processor, printer, ...). Perhaps, they should receive access in the order in which they requested it.

These queues process items in the exact arrival order, and do not naturally include different priorities. For instance, a restaurant may want to give priority to customers who have made a reservation. The operating system should grant higher priority to the code for handling inputs from mouse and keyboard, as opposed to some long-running scientific calculation. Additional examples would include the following:

- Airport landing rights. Planes that are at risk of running out of fuel or are having emergencies should have high priority for landing. Planes that are ahead of their scheduled time might be given lower priority.

- Emergency room access in a hospital. While in general, patients should perhaps be processed in order of arrival, patients in dire need of medical attention (gunshot victim? heart attack?) should be given priority over broken legs or high fever.

So we would like a data structure that supports more flexibility, namely, assigning priorities to items, and processing in order of priority, while adding and removing items.

22.1 Abstract Data Type: Priority Queue

The *priority queue* is a data type supporting exactly these types of operations. The key abilities are:

1. Adding an item (with a priority).

2. Returning the item of highest priority currently stored.

3. Deleting the item of highest priority from the queue. (If there are ties for highest priority, then the returned and deleted item should be the same.)

Notice that there is deliberately no way to return or delete any item other than the one of highest priority. Priority queues serve a particular purpose, which is to process items by priority; for this goal, access to other elements is not necessary. This is just like for queues and stacks, where we could only access or remove one particular item at a time.

In order to find the item of highest priority, we need to be able to compare the priorities of two items, both of the type `T` stored in the priority queue. There are (at least) two natural ways of implementing this comparison.

1. The data type `T` itself allows comparison of priorities of objects, e.g., by overloading the comparison operators. Thus, for any two objects `T a, b`, we can directly test if `a < b`, which returns a comparison of their priorities. Thus, priority is stored *inside* the object.

2. Priorities are kept separately, for instance as integers. Then, when we add a new item to the priority queue, we also need to tell the priority queue what the item's priority is. Then, the queue needs to store two things for each item: `T data`, and `int priority`. Through this approach, the priority is determined only when the item is inserted.

The first method is perhaps easier to implement, but the second might be more flexible. In particular, if you want to have the same items have different priorities based on the context (imagine people who will both visit an emergency room and go to a restaurant, with or without reservation), the priority cannot be an inherent property of the item itself.

For the purpose of these lecture notes, to keep notation simple and focus on the essentials, we will present the abstract data type under the first approach, i.e., we assume that `T` overloads the comparison operators. In practice, the second approach is perhaps a better choice.[1] Now that we have discussed how objects are compared, we can formalize the functions that the ADT Priority Queue should support:

```
template <class T>
class PriorityQueue {
    void add (const T & item); // adds an item to the priority queue
    T peek() const;            // returns the highest priority item
    void remove();             // removes the highest priority item
    bool isEmpty();            // determines if the priority queue is empty
    void changePriority (T & data);
             // changes the priority of an item.
             // The textbook does not include this, but it can be very
             // useful in many applications, as we will see later
}
```

Above, we discussed landing rights, hospital room emergencies, and operating systems as some application areas of priority queues. Truth be told, computer scientists are rarely called upon to implement hospital admissions systems; and even in operating systems, it is not particularly important to have the best data structures for dealing with the priorities of processes — there just aren't that many of them.

The true reason to study priority queues is for their role in search algorithms, which are the key part of much of the work in Artificial Intelligence and such applications as route planning. Building an AI (for many games) often involves exploring a state space (for a game, this could be the positions where all pieces or characters are located, their individual status, etc.). Some states are good, some are bad, and we we would like to find a way to get from the current state to a good one. Since there is usually a huge number of states, exploring them in an intelligent order is crucial — this is what algorithms like A^* search and Dijkstra's Algorithm do. They assign numerical values to states, and always next explore the most promising one. From that state, several new states may be discovered, and they need to be considered for exploration, depending on their priority.

[1] Another approach, probably even better, is to implement a separate comparison function on objects of type `T`, and pass that into your data structure at initialization. This can be done by passing either a pointer to your comparison function, or a Comaprator object.

This application also suggests why a function changePriority could be useful. For instance, suppose that during the exploration so far, you've found a way to get your game character to a certain place, at the cost of losing almost all energy. If that place is surrounded by monsters, it may not be worth exploring for now. But suppose that by exploring something else, we now discover a way to get to the same place with almost all energy still in place. Now, exploring from that state should have higher priority, as it looks more promising. In other words, we'd like to now change the priority of this state.

As we discussed above, depending on how we think about our application, we can think of priority as inherent in an item, or determined only when the item is added to the data structure. In the former case, the priority is assigned at creation of the item, while in the latter case, it is assigned when add is called.

One natural question is whether we should allow items with the same priority in the priority queue at the same time. If we do, then there is no guarantee which of them will be returned by peek (and removed by remove, though usually, you would want to guarantee that it's the same one). After all, if they have exactly the same priority, by definition, each is equally important. If that's not what you want, then you should change your definition of priority to break ties in the way you want them to be broken. For instance, if you want to break ties in FIFO order, then the priority should be a pair (originalPriority, additionTime), and item a has higher priority than b if it has higher originalPriority, or the same originalPriority and earlier additionTime.

22.2 Simple Implementations of a Priority Queue

Notice that even though "Priority Queue" has the word "Queue" in it (because there are some conceptual similarities), it is not a good idea to implement it as a queue; in fact, it's not clear how you would even do that.

The two naïve implementations would be using a (unsorted or sorted) linked list or array. For a linked list or unsorted array (or List type), the implementation would be as follows:

Add : Add the item at the tail or the head of the linked list, or at the end of the array. This runs in $\Theta(1)$.

Peek : To return the highest-priority element, we now have to search the entire array or list, so it takes $\Theta(n)$.

Remove : To remove the highest-priority element, we first have to find it (linear search). In an array, we also have to shift array contents to fill the gap. So this takes $\Theta(n)$.

So a linked list or unsorted array are great for inserting elements, but not good at finding high-priority elements (or removing them). An alternative is to sort the array (or List or linked list) by priority, with the highest priority at the end of the array. Then, the implementations would work as follows:

Add : Search for the correct position ($O(\log n)$ using binary search in an array or List, linear search in a linked list). Once the correct position is found, insert the element there. In an array, this involves shifting everything to the right of the inserted element over by one position. So in either case, the cost is $\Theta(n)$.

Peek : Returns the last element, so it runs in $\Theta(1)$.

Remove : Removes the last element, e.g., by decreasing the size counter, so it takes $\Theta(1)$.

Thus, a sorted array or linked list is fast at looking up and removing high-priority elements, but pays with linear insertion cost.

22.3 Implementation using a Heap

The "sorted array" implementation of a Priority Queue is going in the right direction: it makes sure we can access the highest-priority element easily, by putting it in a designated spot. But beyond that, it is somewhat overkill. Just to access the highest-priority element, it is not necessary to keep the array entirely sorted — it would be enough for it to be "kind of" sorted, so that after removing the highest-priority element, the next one can be found from among only few alternatives.

This is exactly the clever idea underlying a *heap*.[2] A heap is a *complete binary tree* with the following additional key property on the contents of its nodes:

> **Heap Property:** For each node u, the priority of the content at u is at least as high as for all of u's children.[3]

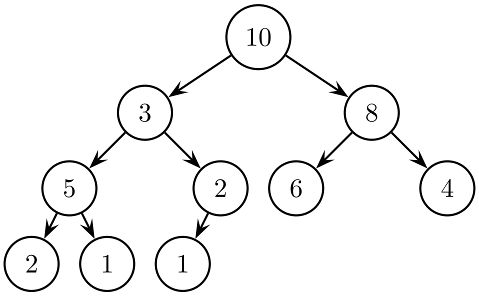


Figure 22.1: An illustration of the heap property, for a Max-Heap. The given tree is a complete binary tree. It satisfies the heap property at all nodes except one: the node with priority 3 has a child (its left child) with priority 5, which is not supposed to happen. Notice that for any node, it does not matter which of its children has higher priority, so long as both have no higher priority than the node itself.

Notice that when we are implementing a Priority Queue using a heap, it is our responsibility to ensure that the tree remains a complete binary tree, and the Heap Property is maintained.

We mentioned above that a heap should be a complete binary tree. This means that all leaves are within at most one level of each other, and all leaves at the lowest level are as far left as possible. As we discussed in previous lectures, this implies that the heap can easily be stored in an array. In order to put the root at 0, rather than at 1 (as we did before), we now get that for any node i, the parent is then located at array index $\lfloor (i-1)/2 \rfloor$, while the children are at $2i+1$ and $2i+2$. (When we started labels at 1, the parent was at $\lfloor i/2 \rfloor$, and the children were at $2i$ and $2i+1$.)

We can now proceed to implementing the functions for a priority queue. We will assume that the binary tree is stored in an array `a`, and that the root is in `a[0]`. The variable `size` captures the number of elements currently stored in the array, so it starts at 0. We will not worry about exceeding the array size — this can be taken care of by using our `List<T>` data type instead of an actual array.

`Peek` : This is particularly easy, since the highest-priority element will always be at the root node.

```
T peek() const { return a[0]; }
```

`Add` : When we add an element, we first wonder where to add it. Since we want to maintain the "complete binary tree" property, there is really only one place: as a new leaf as far to the left as possible. (In array positions, this translates to inserting it at `a[size]`.

But inserting it there may violate the heap property, if the newly added element has higher priority than its parent. So we need to fix the heap property after adding the element. We do so by swapping

[2] The data structure *heap* shares only the name with the heap memory used to allocate objects; don't confuse the two.

[3] If we build a heap using integer priorities, is is up to us to decide whether larger or smaller integers encode higher priority. A heap that puts the smallest number at the top is called a *Min Heap*, while one that puts the largest number at the top is called a *Max Heap*. Obviously, it is easy to change from one to the other by switching comparison operators, or multiplying all numbers with -1.

it with its parent, if necessary, and then continuing at that node, having the element “trickle up” until it actually has lower priority than its parent node, or reaches the root. This gives us the following:

```
void add (const T & data)
{
   size++;
   a[size-1] = data;
   trickleUp(size-1);
}

void trickleUp (int pos)
{
   if (pos > 0 && a[pos] > a[(pos-1)/2])
      {
          swap (a, pos, (pos-1)/2);
          trickleUp((pos-1)/2);
      }
}
```

`Remove` : In trying to remove the highest-priority element, our first thought would be to just delete that element from the array. But we can’t have a tree without a root. This would perhaps suggest filling the root with the one of its children that has larger priority, then recursing on the child. The problem with that approach is that by the time we reach the lowest level of the tree, we may end up swapping up a leaf from the “middle”, i.e., violating the part of the “complete binary tree” property requiring that the leaves are as far left as possible.

An improved way is to instead move the very last leaf’s content into the root first. That way, we know which leaf is being moved. The rest of the way, we just do `swap` operations, trickling down this new root to where it actually belongs. This gives us the following solution.

```
void remove ()
{
   swap (a, 0, size-1); // swaps the highest priority element with the rightmost leaf
   size --;            // we want to consider the former root "deleted"
   trickleDown (0);    // trickles down, so the former leaf will go where it needs
}

void trickleDown (int pos)
{
   if (pos is not a leaf)    // implement test as 2*pos+1 < size
   {
       i = child of pos of highest priority;
               // If you only have one child, return that child.
               // Else, use comparisons to see which has highest priority
       if (a[i] > a[pos])
          {
             swap (a, i, pos);
             trickleDown (i);
          }
    }
}
```

22.4 Running Time of Priority Queue Operations

Next, we analyze the running times of our Priority Queues operations. Since `swap`, array access in known positions, `return` etc., are all constant time, we get that `peek ()` takes running time $\Theta(1)$ — after all, the highest-priority element is known to be at the root. For both `add ()` and `remove ()`, everything except `trickleUp()` and `trickleDown()` takes constant time, so we really just need to analyze the running time of those two functions.

In both cases, a constant amount of work is done in the function (`trickleUp()` or `trickleDown()`), and then, a recursive call is made with a node at the next higher or lower level. Thus, the amount of work is $\Theta(\text{height(tree)})$. So our goal is now to figure out the height of a complete binary tree with n nodes. We will do that by first solving the inverse problem: what's the minimum number of nodes in a complete binary tree of height h?

To make the tree have height h, we must have at least one node on level $h-1$. Each node at levels $i = 0, \ldots, h-3$ has at least two children. Therefore, the number of nodes doubles from level to level, and we have 2^i nodes at each level $i < h-1$, and at least one at level $h-1$. Summing them up over all levels gives us $1 + \sum_{i=0}^{h-2} 2^i = 1 + (2^{h-1} - 1) = 2^{h-1}$. The sum we evaluated was a geometric series, and is one of the series that you really need to have down pat as a computer scientist.

So now, we know that a tree of h levels has at least 2^{h-1} nodes, so when $n \geq 2^{h-1}$ (because the tree has h levels), we can solve for h and get that $h \leq 1 + \log_2(n) = \Theta(\log n)$. So we have proved that a complete binary tree with n nodes has height $\Theta(\log n)$.

Putting it all together, we get that both `add()` and `remove()` take time $\Theta(\log n)$. We can now create a table of how long the different implementations take.

	unsorted array	sorted array	heap
add	$\Theta(1)$	$\Theta(n)$	$\Theta(\log n)$
peek	$\Theta(n)$	$\Theta(1)$	$\Theta(1)$
remove	$\Theta(n)$	$\Theta(1)$	$\Theta(\log n)$

Table 22.1: Comparison of Priority Queue implementations.

For other tasks we have seen in this class, the usual answer to "Which data structure is best?" was "It depends". Here, this is not the case. A heap is clearly the best data structure to implement a priority queue. While it looks as if on individual operations, one or the other of unsorted arrays and sorted arrays will beat a heap, with a priority queue, each element is usually inserted once, removed once, and looked at once (before being removed). Thus, a sequence of n insertions, peeks, and removals will take the other data structures $\Theta(n^2)$, while it takes a heap $\Theta(n \log n)$, much faster.

22.5 Heap Sort

So now we have an ADT that implements `add`, `remove`, and `peek` in time $O(\log n)$. Do we already know of any algorithms where we want to repeatedly find the largest element and then remove it?

Indeed, we do. If we look back at Selection Sort from a few weeks ago, we can describe it as follows[4]:

```
for (int i = n-1; i > 0; i --)
   {
     Let j be largest element of a between 0 and i;
     a.swap (i,j);
   }
```

[4] At the time, we described it as repeatedly finding the smallest element and putting it at the beginning of the array. Equivalently, we can repeatedly find the largest element and put it at the end of the array.

Previously, we ran a loop to find j. But now, we have something better. We can put all of the elements of the array in a Max-Heap first. Since there are n elements, and each takes at most $O(\log n)$ to add, this takes time $O(n \log n)$. (The first few actually take less time, as the heap is almost empty; but for most of them, it's still $\Theta(\log n)$, so we can't improve the analysis.) Then, we can repeatedly find the largest element and put it in its final position. Finding it takes $O(1)$ and removing it takes $O(\log n)$, and since we do that $n-1$ times, the whole thing takes $O(n \log n)$, too. The resulting algorithm is called HeapSort, and it's a non-recursive $O(n \log n)$ algorithm, which is kind of cool. (We implemented `trickleDown` and `trickleUp` recursively, but they are pretty easy to implement iteratively, too.)

When you look at it, you realize that you can actually use the array `a` itself as a heap. You can start by calling `trickleUp` on each element i from $n-1$ to 0. After that, the array satisfies the heap property. Then, we swap position 0 with $n-1$, and decrement `size` by one, then trickling down from 0. We repeat this — every time, we are putting one more element in its final position, and telling the heap that it now "owns" one fewer element of the array. So we don't even need any additional memory or data structure.

As a side remark, HeapSort in the obvious implementation is not stable, because array indices are given a very different interpretation by heaps compared to the "normal" one. Making it stable is quite an interesting research topic, and the consensus appears to be that it requires at least a little bit more memory $\Theta(n)$, i.e., basically another copy of the array.

Chapter 23

Dijkstra's Algorithm and A^* Search

[Note: this chapter covers material of about 1 lecture.]

Earlier on, we looked at the problem of finding shortest paths in graphs, and used Breadth First Search (BFS) to solve this problem. At the time, our graphs did not have any edge costs or weights. The task gets a little more interesting when there are edge costs: then, the equivalent algorithm is called *Dijkstra's Algorithm*[1].

Dijkstra's algorithm is the right choice when all we are given is the graph with its edge costs/weights. But often, there is more information, such as geography, which can be used to guide a shortest-path search to speed it up. The improved version of Dijkstra's Algorithm taking advantage of extra information is called A^* search, and is particularly important in the field of Artificial Intelligence.

23.1 Dijkstra's Algorithm

As we said, we now assume that each edge $e = (v, w)$ of our graph has a cost (or length) $c_e = c[v][w] \geq 0$.[2] First, we might just try to run BFS. But that's clearly not correct, as we can see from Figure 23.1.

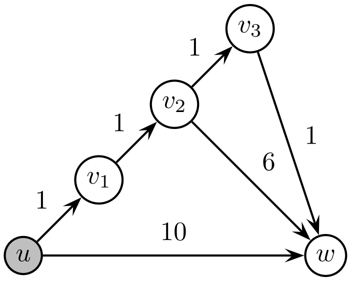


Figure 23.1: An example with edge costs in which BFS does not find the shortest path from u to w.

When we process u (the start node), we add v_1 and w to the queue. We next process v_1, and add v_2. But when we process w, we are done with it, and never revisit its distance label. So we think that it is at distance 10 from u, when it really is at distance 4.

The mistake we are making here is that processing w is premature. The node v_2 is a much better candidate to explore next, because it is closer to u; the fact that it is closer means that it may lie on an

[1] after Edsger Dijkstra, one of the key pioneers of the field of computer science

[2] When edges can have negative costs, things get a bit more complicated. Dijkstra's Algorithm doesn't work any more, but a somewhat slower algorithm due to Bellman and Ford does; you'll likely learn that one in CS270.

actual shortest path from u to w (as it does here), so we shouldn't conclude anything about the distance from u to w until we've made sure that there isn't another, shorter, path.

What this suggests is that nodes shouldn't just be stored in a queue. When a newly added node — like v_2 in our example — is closer to u, then it should be allowed to jump ahead of other nodes and be processed before them. But we've already seen a data structure built exactly for this purpose: a Priority Queue. So Dijkstra's Algorithm is obtained pretty much exactly by replacing the Queue in the BFS algorithm with a Priority Queue. Beyond that change, we just need some small modifications, mostly to take care of the fact that the estimated distance of a node may be updated multiple times. For instance, in our example in Figure 23.1, when we explore v_2, we update our distance estimate for w to 8 instead of 10, but we later update it to 4, which is the final value. The more formal algorithm we get is as follows:

```
int d[n];     // will store distances from u
int p[n];     // will store predecessors of nodes on shortest paths from u
int c[n][n];  // contains the costs of edges

void Dijkstra (int u) {
  bool visited[n] = {false};  // no node is visited yet.
  PriorityQueue<int> pq ();
     /* empty priority queue to start. We assume that the priority queue
        always returns the element v with smallest d[v] value,
        and can deal with updating the d[v] value for an element. */

  visited[u] = true; d[u] = 0;
  pq.add (u);
  while (!pq.isEmpty()) {
     int v = pq.peek();
     pq.remove ();
     for (all nodes w with an edge (v,w) in E)
         if (!visited[w] || d[v] + c[v][w] < d[w]) { // found a shorter path to w
            d[w] = d[v] + c[v][w];
            p[w] = v;
            if (!visited[w])
               {
                 visited[w] = true;
                 pq.add(w);
               }
            else pq.update(w);
         }
   }
}
```

Notice the strong similarity to the BFS algorithm. The main change is the we use a priority queue instead of a queue, and that we have an additional condition that allows us to process a node w: not only when the node hasn't been visited at all, but also when we found a strictly shorter distance to get to w. In the latter case, the node will already be in the priority queue, so instead of adding it, we need to update the associated value.

When we first learned about Priority Queues (in Chapter 22), we didn't discuss how to update an entry after its priority has changed. It's pretty clear that when its priority gets higher (i.e., its distance gets smaller), we should trickle the element up. And when the priority gets smaller, we should trickle it down. The not-so-obvious thing is how we find it in the heap in the first place, so we can trickle it up or down. A linear search through all elements would take $\Omega(n)$, and thus completely defeat the purpose of using a heap in the first place. The most obvious way to solve this problem is to store somewhere (e.g., in the `struct` for a node of the graph) an integer index describing where in the heap the element is located. Then, any time two elements swap positions in the heap, we can update their entries, at an additional constant cost. If we don't like the idea of storing heap information in a node's `struct` (since it's really not part of the node's description, but part of the algorithm), we could instead have another array inside the Priority Queue: that array tells us for each of the nodes (in their original ordering in the graph) where it is located in the heap. Either way, it is easy to implement a lookup operation so that we only incur a constant times as much cost for each step.

The correctness proof for Dijkstra's Algorithm would use induction over the iterations of the `while` loop. It requires a bit more care in the formulation of a loop invariant, and you may see it in CSCI 270 (or CSCI 570 or 670, if you take it). We won't go over it here, even though it's not all that difficult.

The running time analysis gets a little more interesting than for BFS. The `remove()` and `add()` operations now both take $\Theta(\log n)$ time (while `peek()` is still $\Theta(1)$). So the content of the `for` loop takes time $\Theta(\log n)$, and since it executes $\Theta(\text{out-degree}(v))$ times, the total time of the `for` loop is $\Theta(\text{out-degree}(v) \log n)$. This in turn gives us that the stuff inside the `while` loop takes time $\Theta((1 + \text{out-degree}(v)) \cdot \log n)$, which we now have to sum up over all nodes v, as usual:

$$\sum_v \Theta((1 + \text{out-degree}(v)) \cdot \log n) \;=\; \Theta(\log n \cdot (\sum_v 1 + \sum_v \text{out-degree}(v))) \;=\; \Theta(\log n \cdot (n + m)).$$

For Dijkstra's Algorithm, even though in principle, we could have the case $m < n$ just like we could for BFS, people usually ignore the n part of $n + m$, and simply describe the running time as $\Theta(m \log n)$. Not quite linear time, but it's still quite fast, and a pretty cool application of priority queues. In fact, Dijkstra's Algorithm and A^* search are really the main reason computer scientists need to care about priority queues.

23.1.1 Fibonacci Heap Implementation

We should also mention here that there is a data structure called *Fibonacci Heap* which allows for a faster implementation of Dijkstra's Algorithm. It's based on heaps, but changes them up quite a bit. We frequently teach it in CSCI 670. The upshot is that while the `remove` operation still takes $\Theta(\log n)$, the `insert` and `update` operations run in *amortized* time $O(1)$. We have alluded briefly to amortization before: it means that while the *actual* worst-case time of the operations could be worse, whenever an operation takes longer, it is always preceded by several cheaper operations, so that the average time is faster. Here, the average is not taken over any randomness. Even if we have a worst-case sequence of operations, for instance, if there is an $\Omega(\log n)$ update operation, that means it must have been preceded by $\Omega(\log n)$ operations with time $O(1)$. Thus, the average of those times will work out to $O(1)$.

An easier example we have seen earlier is the use of a `vector` data structure for implementing a stack. When the size of a vector doubles, pushing an element on the stack takes time $\Omega(n)$, even though it is normally constant. But since it only happens every $\Omega(n)$ operations, the average time for pushing elements is $1/n \cdot (n \cdot O(1) + 1 \cdot \Theta(n)) = O(1)$.

Once you have `update` (and also `insert`) in $O(1)$ time, the running time analysis can be improved. Each node is inserted and removed from the priority queue once, which takes a total of $\Theta(n \log n)$. Each node's value is updated at most once per incoming edge, so the total number of `update` operations is $O(m)$, and they each take time $O(1)$. Thus, the running time of Dijkstra's Algorithm with a Fibonacci Heap is $O(m + n \log n)$, which is quite a bit faster when the graph is not sparse (has more than a linear number of edges).

Implementing a Fibonacci Heap is quite a lot of work, and it takes quite a lot of overhead. But for large enough graphs — maybe beyond 100,000 or 1,000,000 nodes — a Fibonacci Heap implementation will actually speed up Dijkstra's Algorithm in practice as well.

23.2 A^* Search

If no additional information is available to guide the search, then Dijkstra's Algorithm is optimal. But often, there is more information available, and a clever algorithm should use it. For instance, imagine that you are

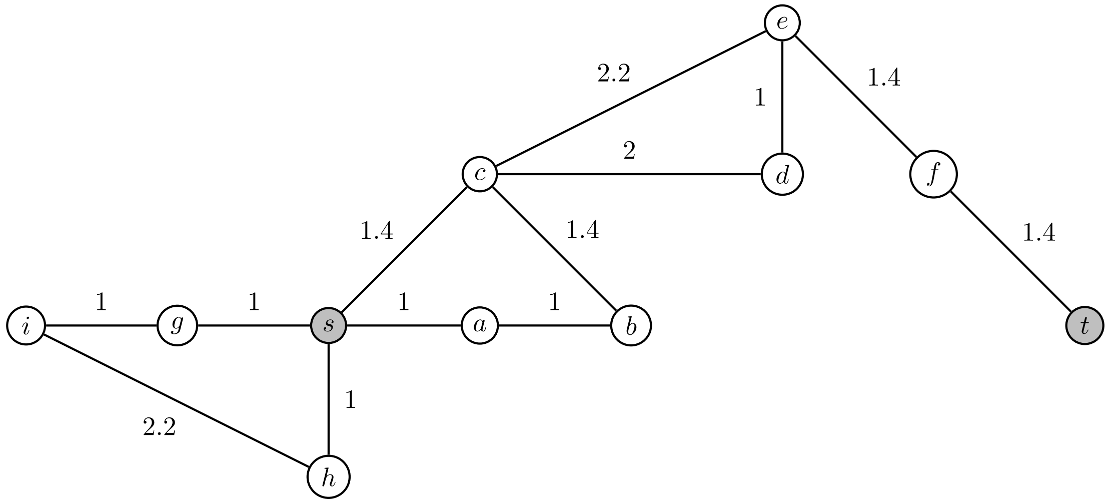


Figure 23.2: An example to illustrate using A^* search.

planning the fastest route to drive from USC to LAX. While there may be different paths that you would need to explore, you'd likely not first try routes that go to downtown LA and Pasadena. Maybe with enough traffic or constructions, that would in the end turn out best, but it shouldn't be the first thing to explore. Let's explore that with an example, shown in Figure 23.2:

Suppose that in the example of Figure 23.2, we want to find a path from s to t. The distances are roughly the Euclidean distances of the nodes.

Dijkstra's Algorithm, starting from s, would begin by putting a, c, g, h in the priority queue. It would next process, say, a, and add b. Next would be g and h. This seems like a bit of a waste. It's pretty clear to us looking at the figure that going to g or h is very unlikely to help us get to t fast. After all, they are further from t than s itself. It may still be the right move, for instance, if we added a long edge from g to t, and removed the edge from f to t. But looking at things right now, exploring b first looks much more promising, and probably also c. That's because they are closer to the target (in terms of straight-line distance, not graph distance), which suggests that we should try them first.

This idea — estimate how far a node is from the target and use that in deciding which node to explore next — is the central idea of A^* search. More formally, A^* needs an *underestimating distance heuristic* $h(v)$ defined on nodes v. The important property is that $h(v) \leq d(v, t)$, i.e., the estimated distance to the target *must always be no more than the real distance*. In our example, if we assume that the numbers written on the edges are Euclidean distances, then the straight-line distances are always no more than the shortest-path distances, which have to take a sequence of multiple edges.

The definition of the A^* algorithm is now exactly the same as Djkstra's algorithm, except the priority of each node v in the priority queue is $d[v] + h(v)$. Here, d is the distance estimate, as before. So notice that the distances are still updated to the same value, and we only change the priorities for the priority queue, i.e., the order in which nodes are explored. Let's look at three natural examples of distance heuristics if we search for paths for nodes embedded in the Euclidean plane, as in our example:

1. $h \equiv 0$. This is clearly an underestimate. Unfortunately, it doesn't help us much. In fact, you will notice that we exactly get Dijkstra's Algorithm back in this case.

2. $h(v) = d(v, t)$, i.e., $h(v)$ is the actual shortest-path distance from v to t. This would be an extremely accurate heuristic — in fact, the A^* search algorithm would find the shortest path directly, without any wrong turns ever. The downside is that computing $h(v)$ reduces back to the same problem we are trying to solve in the first place: finding a shortest path. So the problem with this heuristic is that it takes such a long time to compute that it is not useful.

3. $h(v) = \|v - t\|_2$, i.e., the straight-line distance from v to t. That is a pretty good heuristic, and fast to compute. For extra illustration, we will work through the example from Figure 23.2 with this heuristic.

The upshot to remember is that you want h to be: (1) underestimating, (2) fast to compute (much faster than the shortest-path search), and (3) as close to the actual distance as you can be.

Let's see what A^* search will do on the example from Figure 23.2. Let's estimate the distances to t from the different nodes as follows (for exact values, use Pythagoras):

s	t	a	b	c	d	e	f	g	h	i
5	0	4	3	4.1	2.2	2.8	1.4	6	5.1	7

We start with just s. When we process it, we add to the priority queue the nodes a with priority $1+4 = 5$, c with priority $1.4+4.1 = 5.5$, g with priority $1+6 = 7$, and h with priority $1+5.1 = 6.1$. So we next explore a and add b with priority $(1 + 1) + 3 = 5$. (We can see here that it is on the straight line from s to t.) So the next node to be explored is b, and we will not update the priority of c, as the new path is longer. The next node extracted from the priority queue is c, even though its edge from s is longer than those to g and h: this is where A^* is noticeably different. When processing c, we add d with priority $(1.5 + 2) + 2.2 = 5.7$ and e with priority $(1.5 + 2.5) + 2.8 = 6.8$. So we next explore d — notice that we are again trying to head straight for d. Processing d does not add any useful information. Next will be h, because its priority is 6.1. Processing h adds i with priority $(1 + 2.2) + 7 = 10.2$ to the priority queue. So next we explore e, and add f with priority $(4 + 1.4) + 1.4 = 6.8$. Notice that this is the same as e's priority, because we are on a straight line to t. So we explore f next, and find t with priority 6.8, and have found the shortest path.

Looking back, we tried to take straight routes as much as possible, but had to take some detours. But compared to Dijkstra's Algorithm, we never processed g or i, as they were in the wrong direction.

23.2.1 The 15-Puzzle

The context in which the A^* algorithm is used most often is in planning in Artificial Intelligence. When planning a sequence of actions to solve a puzzle (either a toy puzzle like Rubik's Cube, or a real-world task that involves multiple moves), we can think of the states of the world as a graph. The algorithm has actions available to manipulate the world, and each action takes the world from one "state" to another. The goal is to find a sequence of actions of minimum length or cost to get from a known start state to a desired end state.

As an example, let us look at the well-known 15-puzzle. It is played on a 4×4 grid, with 15 tiles (numbered $1, 2, \ldots, 15$, or perhaps with drawings on them) that can slide horizontally or vertically. Since there is at any given time just one free spot, only the adjacent tiles can slide, into that open spot. Figure 23.3 shows an example of a possible start (or intermediate) state and the desired end state.

12	4	3	8
9		1	14
11	5	13	15
2	6	10	7

1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	

Figure 23.3: An intermediate state and the desired final state of the 15-puzzle.

In order to model the 15-Puzzle to make it amenable to graph search, we think of any state of the board as a node. So the graph has 16! nodes, which is a lot. We can't even generate the entire graph in memory. There is an edge between two states if one can get from one to the other by sliding just one tile. Edges are by nature undirected, as one can revert a move by sliding the tile back to where it came from. Since we are only counting the number of moves, the cost of each edge is 1. Again, this technique — find the right state space to build a graph — is very common in applying graph search.

Because all edges have cost 1, we could apply BFS. But that takes time $\Theta(n+m)$, and we just realized that $n = 16!$, which is a lot. Therefore, using A^* search is pretty much a necessity here. We want to guide the search towards states in which tiles are in their final position, or close to it. The simplest heuristic h for this is to look at each tile in isolation, and count how far it is from its destination, adding the number of rows and columns. (This is called the Manhattan Distance between the two positions, or L_1 distance, and written as $\|y - x\|_1$.) Now, we add this over all tiles to get h. The reason this is an underestimating heuristic is that each move can only move one tile by one position, so it will take at least this many moves to get to the final position. Better heuristics are known, and in fact, many research papers have been written about good A^* heuristics for the 15-Puzzle and other puzzles.

Chapter 24

AVL Trees

[Note: this chapter covers material of about 1 lecture.]

In the next few chapters, we will learn of the two typical ways of implementing maps: Search Trees and Hashtables. Remember that in a map, we store associations between keys and values. We need to be able to insert and remove such associations, and to look up the associated value for a given key. We already saw a brief preview of Search Trees in Section 21.4. There, we only showed the keys in our graphic depiction. In this and the next chapter, we will do the same thing. However, even though we only show keys in our diagrams, it is implied that for each key, there is also an associated value stored, and that looking up this value is really the main reason for studying trees in the first place.

Also, for maps, one typically assumes that there can only be one copy of each key. If you explicitly want multiple copies of the same key, you would call it a multi-map. It makes some implementation details more messy, and we want to focus on the essentials here. So from now on, in all of our examples, we will not have the possibility of duplicates among the keys.

24.1 Balancing Trees and Rotations

As we discussed when we got started on search trees, the important thing is to keep the height bounded by $O(\log n)$, so that search (and insertion and deletion) is fast. In order to do that, you want the search trees to be "balanced," in the sense that all the subtrees of a given node are "similar" in height or number of nodes. The goal of constructions such as AVL Trees (this chapter) and Red-Black Trees (Chapter 26) is to impose certain rules on the trees that will trigger small-scale restructuring whenever trees get too unbalanced. "Small-scale" means that we want to spend at most time $O(\log n)$ per insertion or deletion. For AVL trees, these rules involve comparing the heights of the two subtrees at each node, and making sure they do not differ by more than 1. For Red-Black Trees, we define rules for coloring nodes (motivated by 2-3 trees), which will have a similar effect.

To get a feeling for how to make this work, let's revisit the bad tree from Figure 21.3. How could such a tree have been generated? Quite easily: If we start by inserting 11, then 10 as its left child, then 9 as 10's left child, etc., we'll get exactly that bad tree. Perhaps along the way, we should have realized that things weren't going so well, and started fixing them before they got too out of whack. Specifically, the first time something seems awry is when we insert 9 as the left child of 10. At the point, we have produced a tree of height 3 when we could have produced one of height 2 by making 10 the root. So perhaps we should fix the tree right then. What we'd be doing would be the following:

What we did here is called a *rotation*, or more specifically, a *right-rotation.* The node 10 rotated to the root, and 11, previously its parent, became its right child. Rotations can be performed for arbitrary trees, and they are our primary (or really, only) tool in fixing imbalances in search trees. More generally, they look as follows:

Notice that the rotations generalize what we did for the 3-node tree. In the right rotation, u, which was a left child of v, becomes its parent, and v becomes the right child of u. In the left rotation, v, which used

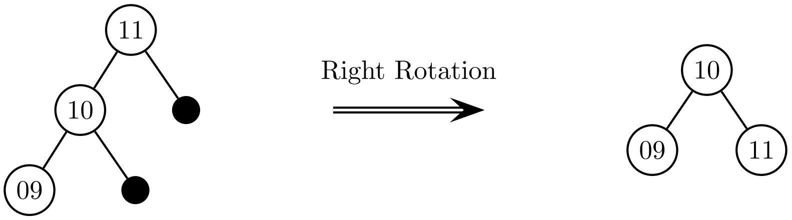


Figure 24.1: Fixing a 3-node tree.

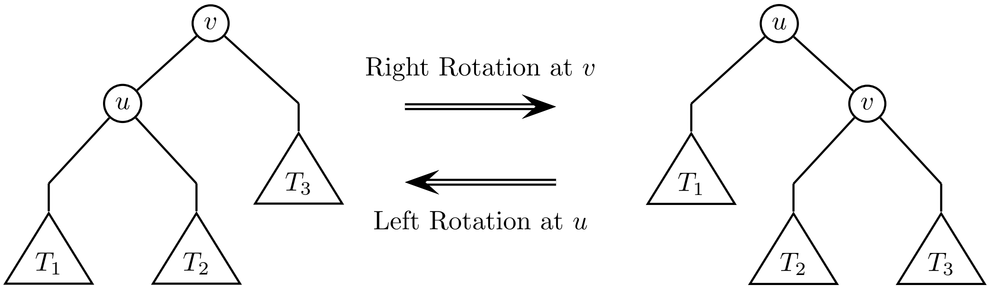


Figure 24.2: Right/Left Rotations.

to be a right child of u, becomes its parent, while u becomes the left child of u. Notice that all keys in T_1 are smaller than u, the keys in T_2 are between u and v, and the keys in T_3 are larger than v. Thus, they are all in legal positions after the rotation.

24.2 The AVL Tree Balance Property

AVL trees (named after their inventors Adelson-Velskij and Landis) were the first search tree construction to explicitly guarantee an $O(\log n)$ height at all times. The approach is to explicitly keep them "height-balanced." AVL trees are binary search trees with the property that each non-leaf node has either 0 or 2 children. All the data are stored in the non-leaf nodes. In this sense, you can really think of leaves as just `null` pointers, and the "0 or 2" requirement as there mostly to simplify the way we talk about the trees. The key property is the following:

> For every node v, let its left and right subtrees be T_ℓ^v and T_r^v. Then, the heights of T_ℓ^v and T_r^v must differ by at most 1.

Just as a thought experiment, let's replace '1' with '0' in that condition. Then, at every node, all subtrees have to have the same height. It is quite an easy proof (induction) that the only trees satisfying this condition are full binary trees, which is much too restrictive. So the condition is kind of the best one could hope for in terms of height balance.

Intuitively, it feels like a binary tree with the AVL property should be relatively shallow, i.e., have small height. Next, let's verify this intuition. Just as we did when analyzing the height of a priority queue in Section 22.4, the best way to answer the question "How high is an AVL tree with n nodes?" is to first answer the question "How many nodes must an AVL tree of height h contain?" It turns out that this analysis is most easily carried out if instead of all nodes, we focus on just the number of leaves.[1] This really is not a

[1] We could do it for all nodes, but the formulas would look a little less familiar; it's not really much harder, just not as obvious for someone early in their CS career.

problem, because for every tree, the number of leaves is one more than the number of internal nodes, so we can easily reconstruct the number of keys.

So let's denote the minimum number of leaves in an AVL tree of height h by L_h. (To be precise, we count the height without the leaves, so a single internal node with two leaves will be counted as height 1.) For height 1, the answer is $L_1 = 2$, and for height 2, it is $L_2 = 3$. For height h, we have one root node v with two subtrees T_ℓ^v and T_r^v. One of them must have height $h-1$, and the other one must have height $h-1$ or $h-2$, because the heights cannot differ by more than 1. Because an AVL tree of height $h-1$ contains more nodes than a smallest AVL tree of height $h-2$, and the leaves of the entire tree are exactly those of one subtree plus those of the other, we get that $L_h \geq L_{h-1} + L_{h-2}$. When aiming for the smallest number, we may as well write equality instead of '$\geq$', and we get a recurrence relation. So now, we want to solve

$$\begin{aligned} L_1 &= 2 \\ L_2 &= 3 \\ L_h &= L_{h-1} + L_{h-2} \quad \text{for } h \geq 3 \end{aligned}$$

Except for the initial values, this should look familiar to you: it's exactly the Fibonacci series. And if we added $L_0 = L_{-1} = 1$, we would exactly get the Fibonaccy series definition. So if F_h is the h^{th} Fibonacci number, we have shown that a smallest AVL tree with height h has at least F_{h+2} leaves.

Next, we need to figure out just how big F_h is. You probably already solved this at some point as a homework exercise. It's not that difficult to show (induction) that

$$F_h = \frac{1}{\sqrt{5}} \left(\left(\frac{1+\sqrt{5}}{2} \right)^{h+1} - \left(\frac{1-\sqrt{5}}{2} \right)^{h+1} \right).$$

This formula looks a bit ugly, but by looking closely, we can simplify it. First, $-1 < \frac{1-\sqrt{5}}{2} < 1$, so the term $\left(\frac{1-\sqrt{5}}{2}\right)^{h+1}$ will always be between -1 and $+1$. (That means it really doesn't matter much.) And because $\frac{1+\sqrt{5}}{2} = 1.618\ldots$ looks scary, let's just call it ϕ, which is its standard name. It's called the "golden ratio." Then, we get that $F_h \geq \frac{1}{\sqrt{5}} \cdot \phi^{h+1} - 1$. And from this, we get that

$$L_h \geq \frac{1}{\sqrt{5}} \cdot \phi^{h+3} - 1 \ \geq \ \frac{\phi^3}{\sqrt{5}} \cdot \phi^h - 1.$$

So the number of internal nodes (and thus keys) in an AVL tree of height h is at least $\frac{\phi^3}{\sqrt{5}} \cdot \phi^h - 2$. We can now solve this inequality for h, and obtain that an AVL tree with n keys has height at most

$$\log_\phi(\frac{\sqrt{5}}{\phi^3} \cdot (n+2)) = \log_\phi(\sqrt{5}) - 3 + \log_\phi(n+2) \ = \ 1.4404\ldots \cdot \log_2(n+2) - 1.327\ldots.$$

In particular, the height is only about a factor 1.44 larger than the height of a complete binary tree, and it is $O(\log n)$. This means that searching in an AVL tree with n keys takes time $O(\log n)$, as we would like it to.

So next, we need to see how to implement insertions and removals to maintain this height difference property.

24.3 Inserting into an AVL Tree

In order to be able to keep the subtrees balanced, it appears that we need to know the height of the subtree at each node. It turns out that storing somewhat less information is sufficient: we can store at each node v just the height difference between the two subtrees T_ℓ^v and T_r^v. This difference can only be $-1, 0$ or 1 in a legal AVL tree, depending on whether the left subtree is higher (-1), the right subtree is higher (1), or they have the same height (0). We denote the difference by $b(v)$ (for *balance*). We will see as we go through the operations that the values $b(v)$ at all nodes are enough information to implement insertion and removal. When we draw tree structure, we will put $b(v)$ next to v, to distinguish it from the key stored in the node. (We will often omit the key when it is not relevant.)

To insert a key, one always starts by searching for it. If the key is found, then one throws an error, or updates the value associated with it, or whatever else is the desired behavior. The search will end at a leaf node v, and the new key is inserted into this leaf node, turning it into an internal node with two leaf children. The new node then has balance $b(v) = 0$. However, the insertion might change the balance at nodes higher up in the tree, and we might have to fix the tree (with rotations). For instance, consider the following small tree, resulting from inserting 5 into a tree with numbers 4 and 7.

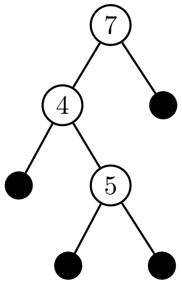


Figure 24.3: An imbalance (at node 7) is created by inserting 5.

So we now explore whether an imbalance is (potentially) created, and how to fix it if so. For the following discussion, let p be the parent of the newly inserted node v. There are three possible cases:

1. $b(p) = -1$ before the insertion. Because v replaced a leaf, this means that the tree rooted at p looked as shown in Figure 24.4 and is fixed as shown there, because v must be inserted as the right child of p.

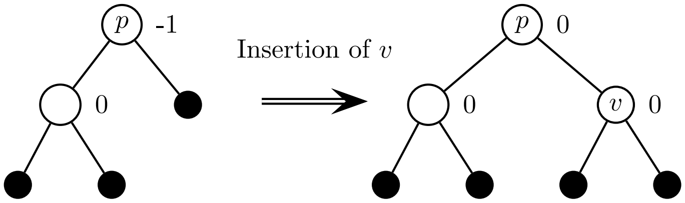


Figure 24.4: Inserting v into a subtree with imbalance -1. No further action is needed.

   Because the height of the tree rooted at p did not change (only the balance at p), no further action up the tree is needed, and we are done. The total time here is $O(1)$.

2. $b(p) = 1$ before the insertion. This case is completely symmetric to the previous one. v is inserted as the left child of p, resulting in a new balance of 0 at p.

3. $b(p) = 0$ before the insertion. This is the case we saw in Figure 24.3. Depending on whether v is inserted as the left or right child of p, the balance of p changes to -1 or 1. In either case, the subtree

rooted at p has grown by 1 in height, which creates a risk of a greater imbalance at an ancestor of p. In this case, we call a recursive function `insert-fix(p)` on the parent; we derive and analyze this function next.

24.3.1 The Insert-Fix function

We will ensure that whenever `insert-fix(v)` is called on a node v, the (new) balance $b(v) \in \{-1, 1\}$, and the tree rooted at v has grown in height by 1. The easiest case is when v is the root of the tree; then, we're done. Otherwise, let p be the parent of v.

For the following description, we will assume that v is the left child of p. The other case is completely symmetric; just look at these notes in a mirror, or substitute 'right' and 'left' for each other everywhere they occur. (Also, you need to substitute some '-1' and '1' for each other.)

We distinguish three cases, based on the balance at p.

1. If $b(p) = 1$ before the insertion, then the right subtree of p was one level higher than the left subtree, and the left subtree has grown by one level. So now, the two subtrees have the same height, and we can just set $b(p) = 0$, and we're done. This is because the height of the subtree at p has not grown (only its smaller tree has).

2. If $b(p) = 0$ before the insertion, then the subtrees had equal heights. This means that now, $b(p) = -1$, because the left subtree has grown in height. But this also means that the height of the entire subtree rooted at p has grown by 1. So the imbalance at p is not too large, but there is still a chance that a problem exists further up in the tree. Hence, we recursively call `insert-fix(p)`. Notice that the conditions for doing so are met: the new value of $b(p)$ is -1 or 1, and the subtree rooted at p has grown in height by 1.

3. If $b(p) = -1$ before the insertion, then the left subtree was already one level higher, and it has grown by one level. Thus, the imabalance at p is too large, and we have to actually fix something. How exactly we do the fixing depends on whether the balance at v is -1 or 1.

   (a) The first case, when the balance at v is -1, is slightly easier. The situation is as shown on the left in Figure 24.5.

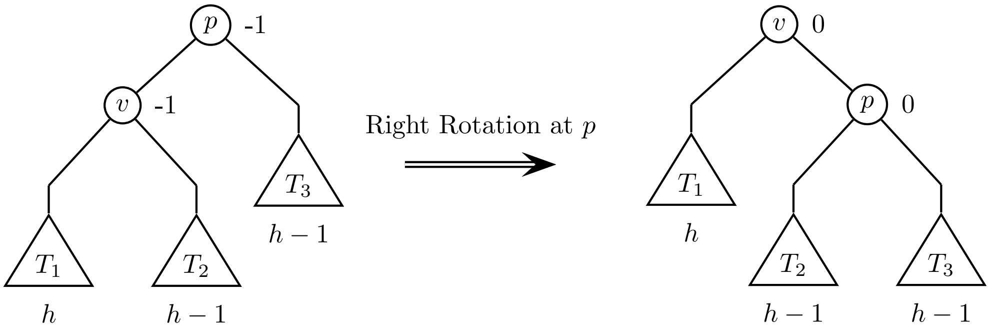


Figure 24.5: A right rotation fixes the imbalance when both v and p have balance -1.

   Because the balance at v is -1, we know that T_1 is one higher than T_2; let's use h to denote the height of T_1. And because the balance at p was -1 before the insertion, the height of the subtree rooted at v, which is $h+1$ is two larger than the height of T_3. In the figure, we have denoted the heights.

   Now, we perform just a right rotation at p. This gives p two subtrees (T_2 and T_3) of height $h-1$, and v two subtrees of height h each. As a result, the balance at both becomes 0. Furthermore, the height of the entire tree (now rooted at v) is $h+1$, which is exactly the height of this subtree before the insertion. Hence, as far as the rest of the tree is concerned, this subtree hasn't changed, and we need no further recursive calls.

(b) When the balance at v is 1, the situation is as shown on the left in Figure 24.6.

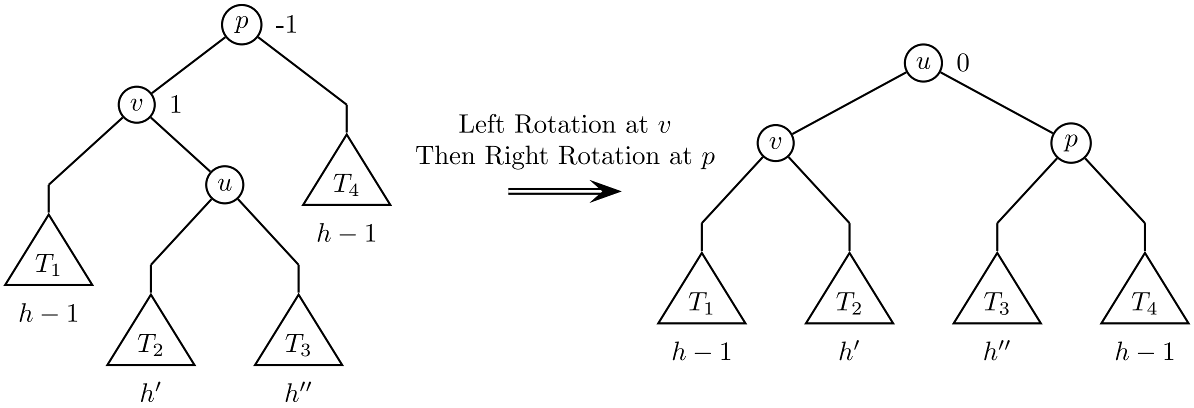


Figure 24.6: A left rotation at v followed by a right rotation at p fixes the imbalance when v has balance 1 and p has balance -1.

Here, the relationship between the heights needs a bit more thought. Let h be the height of the subtree rooted at u. Because the balance at v (after the insertion and any adjustments we have made) is 1, the height of T_1 is $h-1$. In order for the subtree at u to have height h, at least one of T_2 and T_3 has height $h-1$; so h' or h'' is equal to $h-1$, and the other is $h-1$ or $h-2$.[2] Because the subtree rooted at v had height h before the insertion, and the balance at p is -1, T_4 must have height $h-1$.

You can verify easily that in this situation, just a right rotation won't do, because the subtree rooted at u would be brought entirely to the right, creating a balance of $+2$ at the new root v. But instead, we can use a left rotation at v to first bring about the situation from the previous case (Figure 24.5) and then do one right rotation to fix it. The resulting double rotation is shown in Figure 24.6.

Notice that the balance at v could be 0 or -1, and the one at p could be 0 or 1, but the balance at u will always be 0, because the height of both its subtrees is h. So the imabalance has been fixed. Furthermore, the new height of the tree rooted at u is again the same as the old height of the tree rooted at p, meaning that no balance at any ancestor node can have changed. So again, no further recursive calls are needed.

24.3.2 Running Time Analysis

The initial step (creating a new node for the key) clearly takes constant time, so the running time is dominated by `insert-fix`. At each level, we just perform a constant number of comparisons (inspecting the values of $b(p), b(v)$) and possibly a constant number of rotations, which just means changing a constant number of pointers. Thus, at each level, `insert-fix` takes constant time, and the running time is just the height of the tree. And we already derived in Section 24.2 that the height is $O(\log n)$. Hence, insertion into AVL trees takes time $O(\log n)$.

[2] In fact, the other one of h', h'' must be $h-2$. For if it were $h-1$ as well, then why would we be fixing anything? As we are currently seeing, as soon as one rotation is made, the tree is all fixed. So we haven't performed any rotation yet. But then, never mind which of T_1, T_2, T_3 has grown by one level, the height of the tree rooted at v could not have increased by 1, because one of T_2, T_3 already had the same height earlier.

24.3.3 An Example of some insertions

Let's practice AVL insertions a little bit by starting from our example in Figure 24.3, fixing that imbalance, and then inserting a couple more keys.

Figure 24.7 shows the state of the tree and all its balance counters right after 5 is inserted, but before we have updated anything. Then, we see how `insert-fix` works its way up. In each step, the gray node is the one which `insert-fix` is currently working on. To make the figure more legible, we are omitting all leaf nodes. For node 4, no structural change is needed; only the balance information is updated, causing a recursive call to the root. At the root, we are immediately in the most interesting case, requiring a left rotation (at 4) followed by a right rotation at 7.

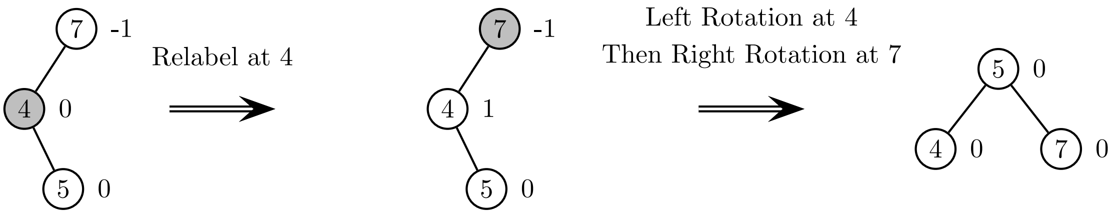


Figure 24.7: Fixing the result of inserting 5.

Next, we insert the key 8; Figure 24.8 shows how `insert-fix` relabels the tree. This case is easier. As `insert-fix` works its way up the tree, at each of the stages, it just needs to relabel the balance at some node by 1. Eventually, it reaches the root, and is done.

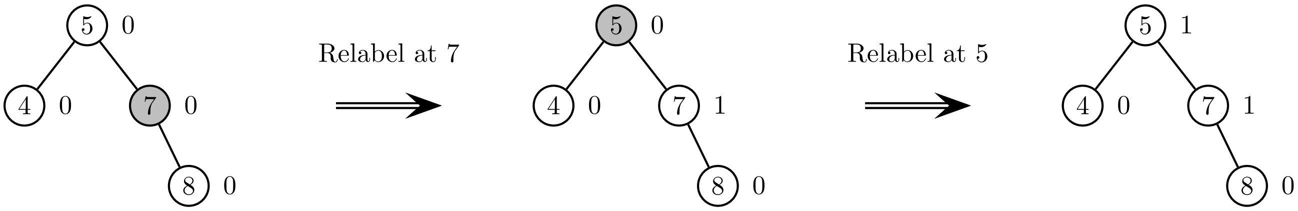


Figure 24.8: Fixing the result of inserting 8.

Finally, in Figure 24.9, we look at what happens when the key 9 is inserted. Again, we begin with relabeling its parent. Then, because the imbalance at node 7 has grown too big, we need to rotate. In this case, a simple left rotation is enough. Because it decreases the height of the subtree by 1, `insert-fix` can terminate here without even looking at the root.

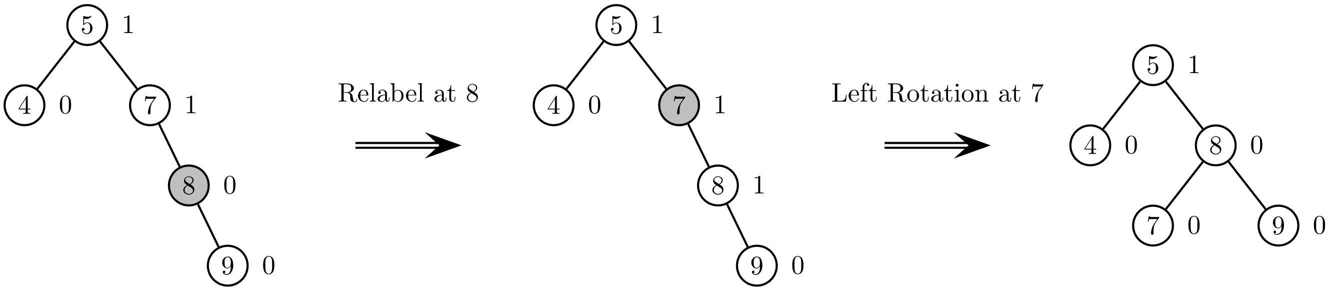


Figure 24.9: Fixing the result of inserting 9.

24.4 Removal from AVL Trees

To remove a key k from an AVL tree, we first search for it. If k is not in the tree, then we throw an error, or don't do anything, or whatever else is the desired behavior. In any case, the tree is not changed. Otherwise, let's say that the search terminated at some node v which contained the key k.

We distinguish three cases, depending on how many non-leaf children v has.

1. If v has two leaves as children, then we can just delete the key from v, turning it into a leaf (and get rid of its two leaf children). As a result, v will have new balance $b(v) = 0$, and its subtree has decreased in height by 1. Since this may cause problems further up in the tree, we call `remove-fix(v)`. In all (later recursive) calls of `remove-fix`, we will have the property that the new balance is $b(v) = 0$, and the tree rooted at v has decreased in height by 1.

2. If v has one leaf child and one non-leaf child u, then u must have two leaf children (otherwise, the AVL property would be violated at v). Then, we put u's key into v, and delete the node u from the tree, replacing it by a leaf. As a result, the new balance at v is $b(v) = 0$, and the subtree rooted at v has decreased in height by 1. As in the previous case, we now call `remove-fix(v)`.

3. If v has two non-leaf children, then we do what one (almost) always does when trying to delete a key from an internal node. We search for the successor key k', that is, the smallest key $k' > k$ in the tree. The successor key[3] is easy to find: we go to the right child of v (which we assumed exists), and then go to the left child at any subsequent node that has a left child. This will terminate at a node (call it u) with no left child, and its key k' is the successor.

   As we discussed, once we find k', we put it (and its value) into v instead of k. Then, we delete it from u. Because u does not have a left child (the search terminated at a node with no left child), we must be in one of the previous two cases, so we can just follow the description there.

This idea of deleting the successor (or predecessor) is pervasive in search trees. We will see it again in B trees, Red-Black Trees, and Splay Trees. Clearly, most of the actual work is done in `remove-fix`, which we explore next.

24.4.1 The remove-fix function

As we mentioned above, we will ensure that whenever `remove-fix(v)` is called, v is a node (possibly a leaf) whose balance after the deletion is $b(v) = 0$, and whose subtree has decreased by 1 in height. We will see how to ensure this for all recursive calls.

When v is the root of the tree, then we are done; everything is sufficiently balanced. Otherwise, let p be the parent of v. As with `insert-fix`, in our description, we will assume that v is the left child of p. For the other case, you can again look at everything in a mirror. We again distinguish three cases based on the value of $b(p)$.

1. $b(p) = -1$. In that case, the subtree rooted at v used to be one level higher than the other subtree of p. The new balance at p is then $b(p) = 0$, and because the higher one of p's subtrees has shrunk in height by 1, so has p's entire subtree. Therefore, we recursively call `remove-fix(p)`; notice that the conditions for calling it are indeed met.

2. $b(p) = 0$. Again, the balance of p increases by 1, because its left subtree become one level smaller. So the new balance is $b(p) = 1$. But because the other subtree rooted at p had the same height as the one at v, the entire subtree rooted at p has not changed in height, and we are done.

3. $b(p) = 1$. Because the balance of p increases by 1, we would now violate the AVL balance property at p, so we need to do actual work to fix it. At a high level, the situation looks as shown in Figure 24.10.

[3] We could just as well use the predecessor: the largest k' smaller than k. Finding it is symmetric to the successor, switching "left" and "right" in the preceding description.

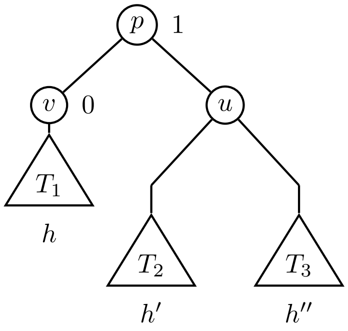


Figure 24.10: The situation when p already had balance 1.

Here, the subtree rooted at node v has height h. We now distinguish three cases, based on the balance $b(u)$ at node u (and the corresponding values of h' and h'').

(a) When $b(u) = 0$, then $h' = h'' = h+1$. In this case, as shown in Figure 24.11, we can just perform one left rotation at v.

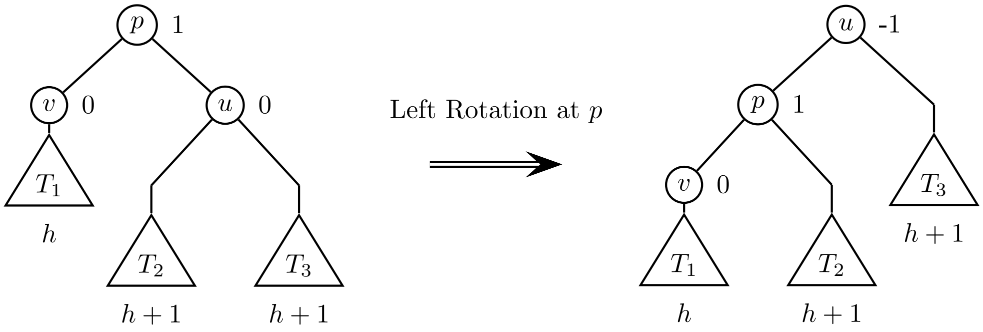


Figure 24.11: A single left rotation at p fixes the tree when $b(u) = 0$.

The AVL balance property is restored at all nodes, and the overall height of the subtree has stayed at $h+3$, meaning that no more changes are needed at ancestor nodes, and we are done.

(b) When $b(u) = 1$, we have $h' = h$ and $h'' = h+1$. We can again fix everything locally by performing just one left rotation at v, as shown in Figure 24.12.

As we can see, the balance at all of the involved nodes becomes 0. However, the overall height of the subtree has shrunk from $h+3$ to $h+2$, so it is possible that problems occur at a higher level. Hence, we need to recursively call `remove-fix(u)`.

(c) When $b(u) = -1$, we have $h' = h+1$ and $h'' = h$, we cannot simply perform a left rotation at p, because the resulting subtree at v would have height $h+2$, while T_3 only has height h. This would violate the AVL balance condition at the new root u.

Instead, we first perform a right rotation at u, giving us a higher subtree on the right than on the left. Then, the situation resembles the case $b(u) = 1$, and we can perform a left rotation. The resulting transformation is shown in Figure 24.13.

Notice here that at least one of T_2 and T_2' has height h, while the other has height $h-1$ or h. As a result, both subtrees rooted at the new root w have height $h+1$, which is one smaller than the previous height $h+2$. So while the local problems have been fixed, we need to call `remove-fix(w)`.

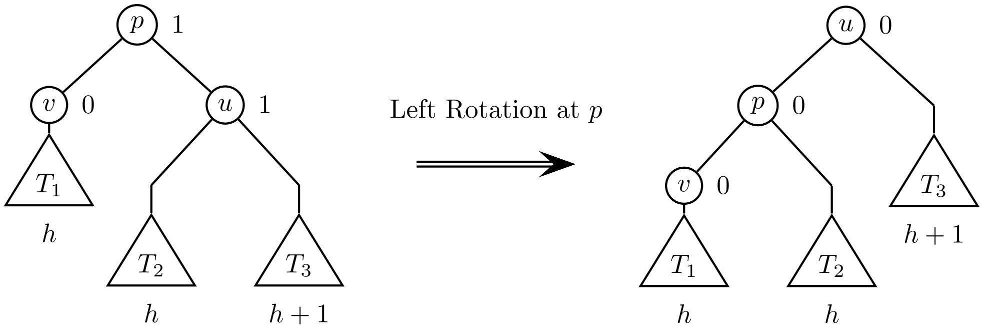


Figure 24.12: When $b(u) = 1$, a single left rotation at p fixes the local problems, but the height of the subtree shrunk, so we need to recurse to higher levels.

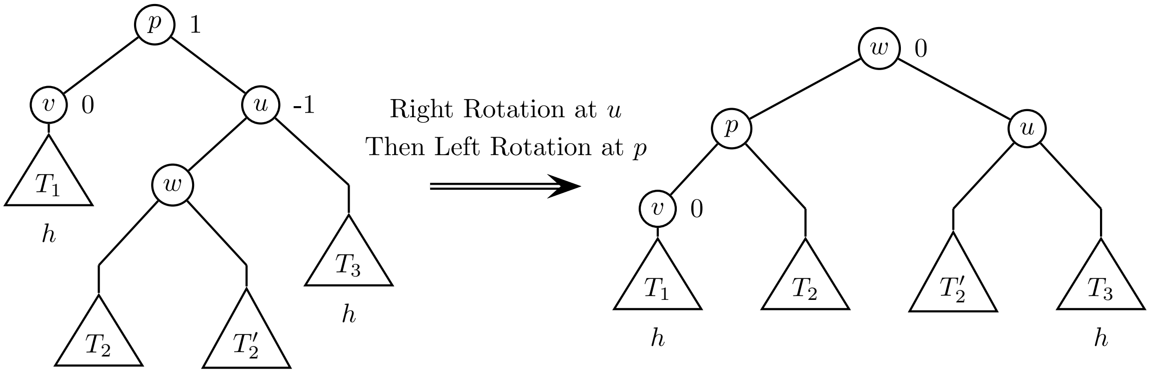


Figure 24.13: When $b(u) = -1$, a right rotation at u followed by a left rotation at p fixes the local problems, but the height of the subtree shrunk, so we need to recurse to higher levels.

24.4.2 Running Time Analysis

While the number of cases is slightly larger (and the operations a bit more complex) than for insertion, we still only perform a constant number of comparisons and rotations per level in `remove-fix`, so its running time is $O(\log n)$. The work done before in finding a key and swapping if necessary also takes $O(\log n)$, so this implementation of removal takes time $O(\log n)$.

24.4.3 An Example of some Removals

Let's also practice AVL removals a little bit. We start with the tree on the left in Figure 24.14. First, we remove the key 3 from this tree. Because 3 is not in a leaf node, we can't just remove it. Instead, we have to swap it with its successor (or predecessor, but let's go with the successor here). So we move 4 to the node, and instead delete the node that currently holds the key 4. Subsequently, we have to call `remove-fix` on the deleted node to see if anything needs to be fixed. When we check the parent (4), we see that its label was 0 before, so we don't need to rearrange the tree, just relabel the parent to -1.

Next, in Figure 24.15, we show the result of removing the key 4 from the tree. Again, 4 is located in an internal node, which only has a left child. So we swap it with its predecessor (1), then delete the leaf the used to contain 1. Again, we have to call `remove-fix`.

In this case, we have a node with label 0 (the node with key 1) whose parent has label 1 and whose right brother has label -1. This puts us in case 3c of the `remove-fix` function. As we saw there, we need to perform a right rotation at the sibling node (here, the one with key 8), follows by a left rotation at the

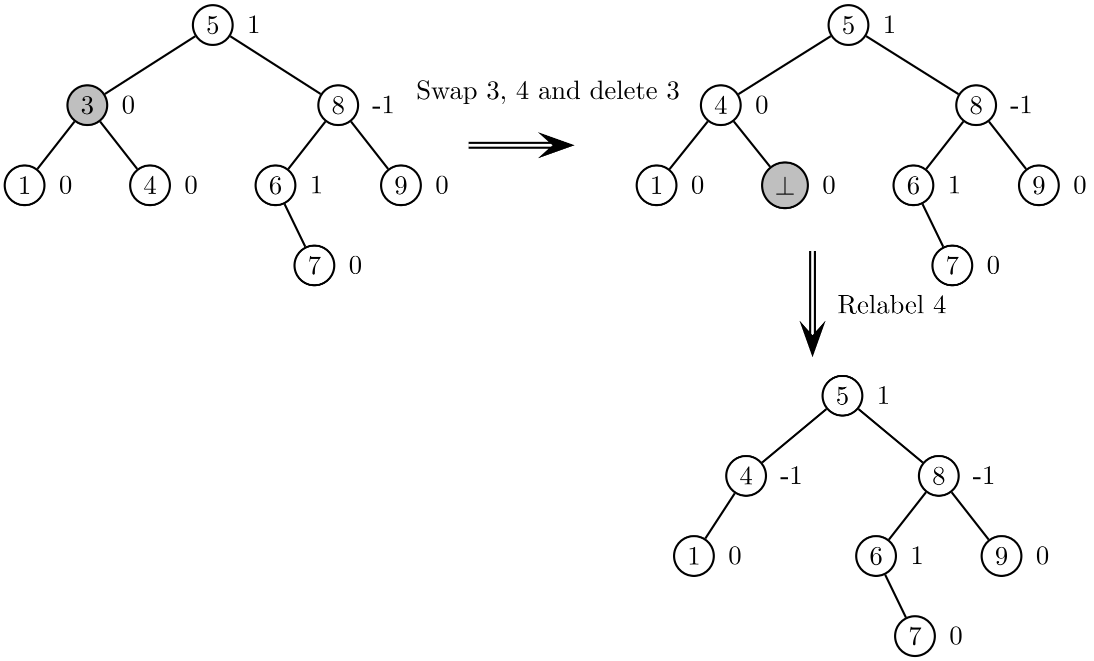


Figure 24.14: Removing 3.

parent node (here, the one with label 5). At this point, we need to recurse with the parent; here, that's the new root 6. Because it is the root, we can terminate now.

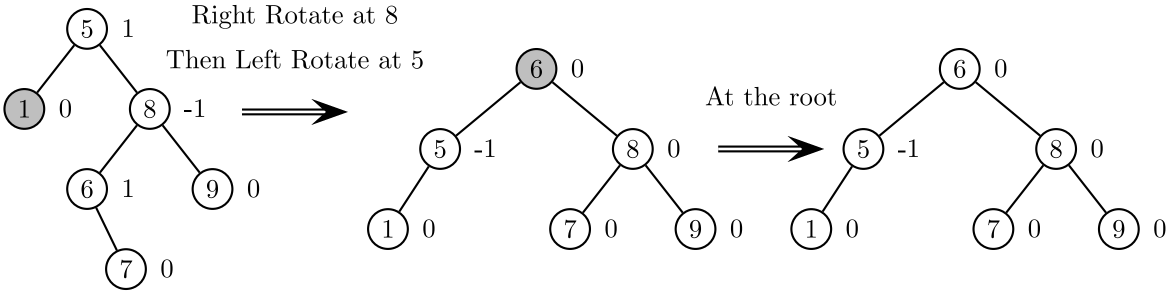


Figure 24.15: Removing 4.

Now, in Figure 24.16, let's remove 1 (which is straightforward, just involving relabeling and not shown), and then 5. Here, we again have a node with label 0 whose tree height shrunk by one, and whose parent has label 1. Because the sibling (the node with label 8) has balance 0, we are in case 3a. As we see there, a left rotation at the parent is enough to completely fix the tree. Notice that in this case, even if we were not at the root, we would not need to recursively change the tree.

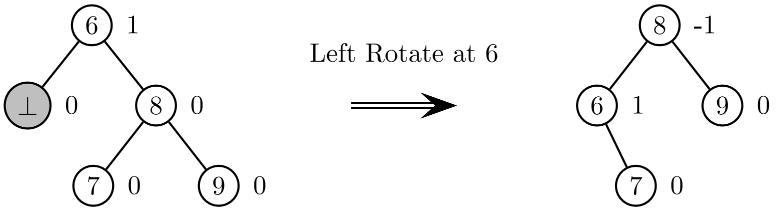


Figure 24.16: Removing 1, then 5.

Chapter 25

2–3 Trees

[Note: this chapter covers material of about 1 lecture.]

In the next few chapters, we will learn of the two typical ways of implementing maps: Search Trees and Hashtables. Remember that in a map, we store associations between keys and values. We need to be able to insert and remove such associations, and to look up the associated value for a given key. We already saw a brief preview of Search Trees in Section 21.4. There, we only showed the keys in our graphic depiction. In this and the next chapter, we will do the same thing. However, even though we only show keys in our diagrams, it is implied that for each key, there is also an associated value stored, and that looking up this value is really the main reason for studying trees in the first place.

Also, for maps, one typically assumes that there can only be one copy of each key. If you explicitly want multiple copies of the same key, you would call it a multi-map. It makes some implementation details more messy, and we want to focus on the essentials here. So from now on, in all of our examples, we will not have the possibility of duplicates among the keys.

25.1 The Basics

While many search trees (including our introductory example in Section 21.4) are binary, the ones we will analyze here in depth are not. 2-3 Trees differ from binary search trees in that each node contains 1 or 2 keys. Unless it is a leaf, a node with 1 key has exactly 2 children, and a node with 2 keys has exactly 3 children. This can be generalized further: we can build trees with m keys in which each non-leaf node has $m + 1$ children. We will see 2-3-4 trees later (where nodes have 1–3 keys), and in practice, there are reasons to use trees in which nodes have several hundred or thousand keys.

Also, we will see later that as a temporary step in adding a key to a 2-3 Tree, we sometimes have nodes with 3 keys and 4 subtrees; similarly, as part of deleting a key, we sometimes end up with a node with 0 keys and one subtree.

We'll see those exceptions soon enough. The defining properties of 2-3 Trees are the following:

- All leaves must be at the same level.
- For nodes with 1 key k, the binary search tree property holds: all keys in the left subtree are smaller than k, and all keys in the right subtree are greater than k.
- For nodes with 2 keys $k_1 < k_2$, the three subtrees T_1, T_2, T_3 satisfy the following property:

  1. All keys in T_1 are smaller than k_1.
  2. All keys in T_2 are strictly between k_1 and k_2.
  3. All keys in T_3 are greater than k_2.

It will be our job in building these trees to ensure that the defining properties hold at all times. We will see later how to do that. We will also see how to do search, and why the depth of the tree is $O(\log n)$.

To implement a 2-3 Tree, we will need a slightly revised version of a node, to accommodate multiple keys and values. The class would look as follows:

```
template <class KeyType, class ValueType>
class Node {   // variables could be public, or could add getters/setters
  int numberKeys;
  KeyType key[2];       // space for up to 2 keys
  ValueType value[2];  // space for the corresponding values
  Node* subtree[3];    // pointers to the up to 3 subtrees
}
```

Internally, the best way to store a 2-3 Tree is probably with a dynamic memory structure and pointers, storing a pointer to the root somewhere. Initially, when the tree is empty, we can set the root pointer to `NULL`. The tree will grow both in number of nodes and height as insertions happen, so obviously, we do not want to fix its size ahead of time.

We could also try to store the tree in an array (like we did for Priority Queues), but lose all of the advantages of doing so, as index calculations are not possible any more. When the tree was complete and binary, it was very easy to figure out which were the children of a given node, but here, it would depend on the degrees of many other nodes, which would take way too long to look up.

25.2 Search and Traversal

The first useful observation about 2-3 Trees is that — like other search trees — they make it really easy to search for a key, and to output all keys in sorted order.

To search for a key, we simply generalize the search procedure for binary trees. When a particular `key` is requested, and we search in a subtree with a given root `r`, we compare `key` to `r->key[0]` (and `r->key[1]`, if `r` has two keys). If we found the key, great. Otherwise, we can determine which of the two (or three) subtrees to recursively search in. The code would look as follows:

```
ValueType search (KeyType key, Node *r) const
{
  if (r == NULL) throw KeyNotFoundException;
  else {
     if (key < r->key[0]) return search (key, r->subtree[0]);
     else if (key == r->key[0]) return r->value[0];
     else if (numberKeys == 1 || key < r->key[1]) return search (key, r->subtree[1]);
     else if (key == r->key[1]) return r->value[1];
     else return search (key, r->subtree[2]);
  }
}
```

To traverse all of the keys in sorted order, we simply use depth-first in-order traversal (see Section 21.3). That is, at any node, we first recursively visit the entire left subtree, then the key (or left key, if there are two), then the middle tree (if it exists), the right key (if it exists), and finally the right subtree. This is the natural generalization of in-order traversal from binary trees to 2-3 Trees.

This describes how to implement an ordered iterator over search trees. This is one of the main advantages of search trees over Hashtables as data structures for maps. For Hashtables, it's much harder to implement an efficient Iterator. (Hashtables have other advantages to compensate.)

25.3 Inserting and Removing Keys: Overview

In implementing insertions and deletions on 2-3 Trees, we should keep in mind the following:

- The 2-3 Tree properties must always hold after we are done with the operation, so that the tree remains balanced. Thus, we must ensure that all leaves are at the same level, two-key nodes have three children, one-key nodes have two children, and we can't have any number other than 1 or 2 keys in one node.

- All insertions and removals in search trees typically (and definitely for 2-3 Trees) happen at a leaf; that's much easier to deal with than changing things at internal nodes.

- Typically, pre-processing (for removals) and/or post-processing (to restore various properties) is required, in addition to just adding or removing keys.

  More concretely, we saw for priority queues that the way to insert or remove keys was to temporarily violate the heap property, and then fix it with a recursive function. For 2-3 Trees, we will do the same thing.

  In doing this, we will *never, ever* violate the first property (having all leaves at the same level); this property would be incredibly hard to restore. Instead, we will temporarily generate nodes with 0 keys (for deletion) and with 3 keys (for addition), and then fix that systematically.

In explaining how insertions and removals work, our running example will be the tree T shown in Figure 25.1:

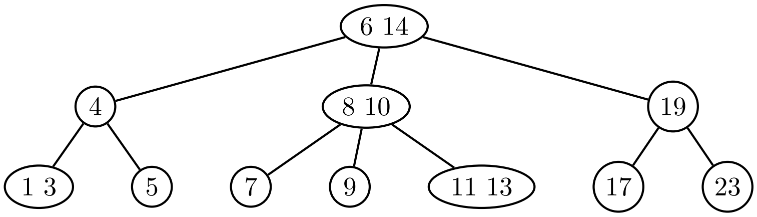


Figure 25.1: Our running example T of a 2-3 Tree.

25.4 Inserting Keys

Whenever we insert a key (or, more precisely, a key-value pair) into a tree, the first thing we do is search for it, unsuccessfully, of course. (If we found it, that would be a duplicate, so we'd throw an exception or otherwise signal that the key was already in the map.) We then insert it into the leaf node where the search terminated. If the leaf node only had one key before, it has two keys now, and everything is good. But if the leaf node already had two keys, then it now has three keys, so we'll need to fix it. We will see how to fix it by looking at the effects of inserting a number of keys into our example tree T.

First, let's look at the case of inserting 21 into T. To do so, we search for 21. When we do that, we will terminate at the node that already contains the key 23. This leaf node has only one key, so we can simply add 21. The result will only be a local change, and our tree now looks as in Figure 25.2:

This was easy. Of course, we won't always be so lucky as to insert into a node with only a single key. So next, let's look at what happens when we insert 26 into the tree we got after inserting 21. The key 26 also belongs in the node with 21 and 23, so when we add it to the node, that leaf now contains three keys, as shown in Figure 25.3:

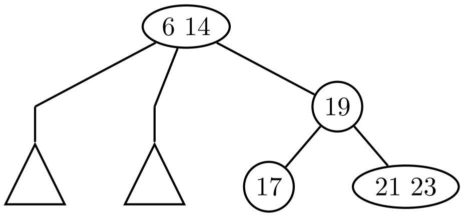


Figure 25.2: T after inserting the key 21. In this and subsequent figures, we'll just write triangles to denote parts that are unchanged or not particularly interesting.

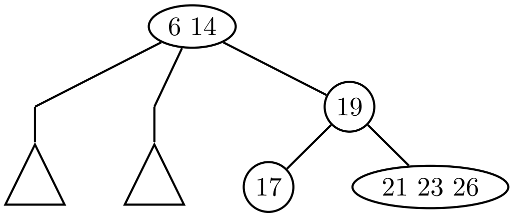


Figure 25.3: After inserting the key 26. Having three keys in a node is illegal, so we need to fix this.

To fix this, we can break up a node with 3 keys, by moving its middle key up to the parent node, and making the two other keys into separate nodes with one key each. In our example, 23 gets moved into the node that currently contains only the key 19, turning it into a node containing 19 and 23. The other two elements, 21 and 26, are split into two separate nodes (since the parent node is now a two-key node, it can support three children), and these nodes become the children nodes for the node containing 19 and 23. The resulting tree looks as shown in Figure 25.4.

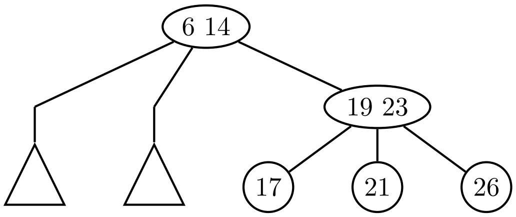


Figure 25.4: After fixing the problem from inserting the key 26.

So in this case, with just one split operation, the problem was fixed. Next, let's see what happens when we insert 12 into T. (So we're thinking of inserting it into the *original* tree, but it makes no difference in this particular case if you want to think of inserting it into the tree after we already inserted 21 and 26.)

Again, we first search for 12, ending up in the leaf that contains the keys 11 and 13 already. Again, we add it to the leaf node, resulting in 3 keys in that node. The resulting situation is shown in Figure 25.5.

As before, we take the middle key — here, 12 — and move it up to the parent's node, splitting the keys 11 and 13 into separate new nodes. But now, the parent has 3 keys, and 4 subtrees, as shown in Figure 25.6.

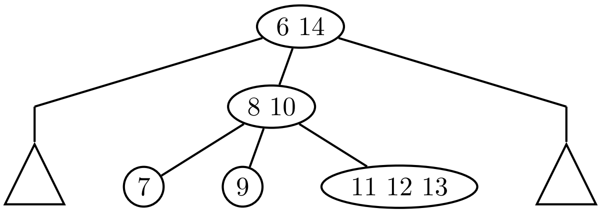


Figure 25.5: The result of inserting the key 12 into T.

So we'll have to fix that.

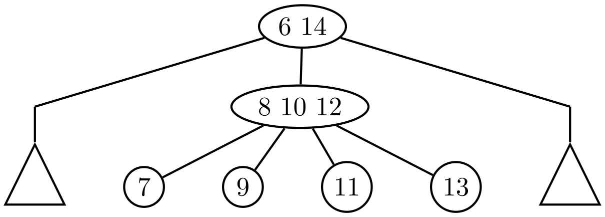


Figure 25.6: Moving the key 12 one level up.

To fix this new problem of a node with 3 keys, we again take the middle key — in this case, 10 — and move it up one level, into the parent node with keys 6 and 14. Now, the keys 8 and 12 get split and become their own nodes; the new node containing 8 obtains the left two subtrees (here, nodes with keys 7 and 9), while the node with key 12 obtains the right two subtrees, with keys 11 and 13. The resulting tree is shown in Figure 25.7.

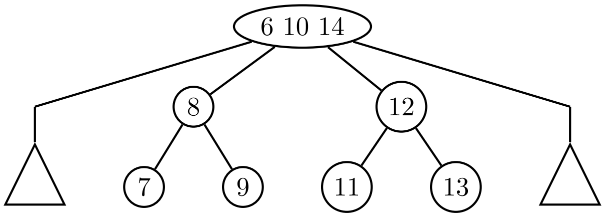


Figure 25.7: Moving the key 10 one level up.

Now, we have moved the problem yet another level up. The root node now contains three keys 6, 10, and 14. So we do the same thing: we push up the middle key (here, 10) one layer, and split the other two keys into separate nodes, each inheriting two of the subtrees. The result is shown in Figure 25.8

At this point, we finally have obtained a legal 2-3 tree again, and the process terminates. Notice that we have now increased the height of the tree by one. Some students were wondering in class how the tree can ever grow in height if we always insert at leaves. Now we know. It grows at the root, even though insertion happens at the leaves.

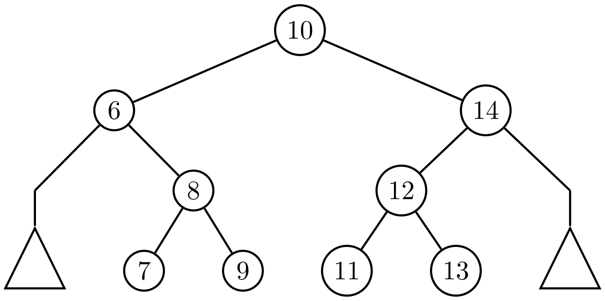


Figure 25.8: Moving the key 10 one more level up.

The important thing to keep in mind is that whenever a node has too many keys, you move up the *middle* key to the parent node, and split the remaining two keys into two separate new nodes. The left node inherits the two left subtrees, while the right node inherits the two right subtrees.

Below is pseudocode to help you understand how to insert into 2-3 Trees in general.

```
Inserting a new key

1. Search for the key. If found, deal with duplicate.
   Otherwise, we have found the leaf where the key belongs.
2. Insert the key into the leaf.
      If the leaf only had one key before, we are done now.
3. Otherwise, we must now fix the leaf.

To fix a node with 3 keys (a b c):
1. Move b up into the parent node if there is one.
   (Otherwise, create a new root for the tree, containing just b.)
2. Create a node with just a as the key, and make it the left child of the b node.
3. Create a node with just c as the key, and make it the right child of the b node.
```

Notice that insertion as we defined it maintains the properties of a 2-3 Tree: the number of levels on all subtrees is increased by one simultaneously when creating a new root, and not increased for any node otherwise.

Let's try to analyze the running time. To find the right leaf node takes $\Theta(h)$, where h is the height of the tree. To actually insert the key into the tree takes $\Theta(1)$. Breaking any three-key node into new smaller nodes takes $\Theta(1)$, and we have to do this at most once for each level of the tree, so it takes $\Theta(h)$.

So next, we want to calculate the height of a 2-3 Tree. We do this the way we have calculated tree heights before. If the tree has height h, because all leaves are at the same level, and each internal node has at least 2 children, it has at least as many nodes as a complete binary tree of h levels (plus one more), giving us an upper bound of $\log_2(n)$ on the height, as we calculated before in the context of heaps. On the other hand, a tree of h levels with maximum degree 3 has at most 1 node on level 0, 3 nodes on level 1, 9 nodes on level 2, and generally 3^k nodes on level k, for a total of at most $\sum_{k=0}^{h-1} 3^k = \frac{3^h-1}{3-1} \leq \frac{3^h}{2}$ nodes. Thus, $n \leq 3^h/2$, giving us that $h \geq \log_3(2n) \geq \log_3(n)$. Thus, h is between $\log_3(n)$ and $\log_2(n)$, and those two are within small constant factors of each other. Thus, the runtime for insertion is $\Theta(\log(n))$. (We can ignore the base of the logarithm, as they are off only by constant factors.)

25.5 Removing Keys

To delete a key (and its value) from a 2-3 tree, we of course first have to find it. Once we have found the key, deleting it from an internal node would be really complicated. Therefore, in 2-3 trees (and pretty much all search trees), we always have a first step of ensuring that we only delete keys from leaf nodes.

The way to do this is to search for the next-larger (or possibly next-smaller, but for concreteness, we'll stick with next-larger) key. This is accomplished by first going down the edge immediately to the right of the key to delete. (That is, the middle edge if the key was the left key, or the right edge if the key was the right key.) Then, we always go down the leftmost edge of all nodes, until we hit a leaf. At that point, the leftmost key in that leaf is the successor.

Once we have found the successor, we swap it with the key we wanted to delete. This is safe to do, as no other element could now be out of place — everything in the right subtrees is larger than the successor. Now, the key we want to delete is in a leaf, and we can start from there.

The deletion algorithm will start with deleting a key at a leaf, but then possibly propagate necessary "fixes" up the tree. By far the easiest case is if the leaf contained two keys. Then, we simply delete the key, and we are done.

Otherwise, we now have a leaf with no keys in it. We can't just delete the leaf, as this would violate the 2-3 tree property of all leaves being at the same level. So we need to find ways to fix the tree. The operations we perform will be the same at the leaf level as at the higher levels, so we'll phrase the problem case more generally.

At the point when we need to fix something, we have an internal node with 0 keys and one subtree hanging off. In the base case, this subtree is just `NULL`, but as we propagate up (recursively or iteratively), there will be other subtrees. Thus, the problem situation looks as shown in Figure 25.9. (The black node has no keys, and one subtree below it, which is empty for a leaf.)

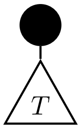


Figure 25.9: The problem case in deletion. The black node has no keys.

In order to deal with this problem case, we distinguish a few cases, based on how many neighbors the empty node has, and how many keys they in turn have.

1. If the empty node has a sibling with two keys, then the node can borrow a key from a sibling. A typical version of this case would look as shown in Figure 25.10:

   It works similarly if the empty node has two siblings. When the immediately adjacent sibling has two keys, we can do the same thing (by pushing one of the sibling's keys to the parent, and the parent's key down to the empty node). When it is the sibling two hops away that has two keys, we push one key up, a key from the parent down to the middle child, and the key from the middle child up to the parent.

2. If no sibling of the empty node has two keys, then the next case is that the empty node has two siblings (i.e., the parent has two keys). In that case, the empty node can borrow a key from the parent, with help from the siblings. A typical case is shown in Figure 25.11.

   This works pretty much the same way if instead of the right child, it is the middle or left child of the parent that was empty.

3. The final remaining case is when the empty node has only one sibling, and that sibling contains only one key. In that case, we cannot fix the problem immediately. Instead, we merge the parent and the

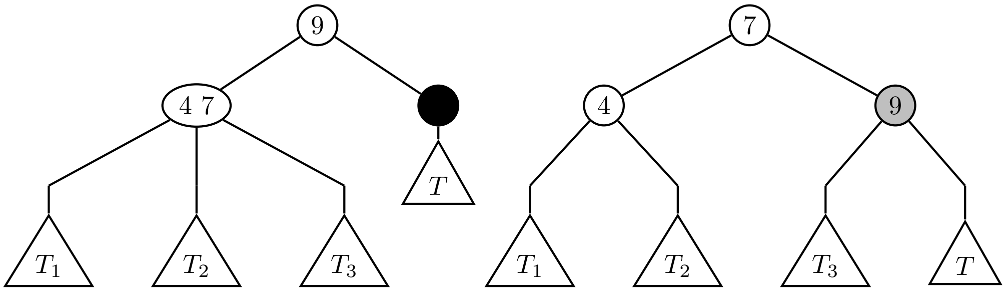


Figure 25.10: Borrowing from a sibling. The empty node borrows from its sibling (via its parent) and is shown in gray after.

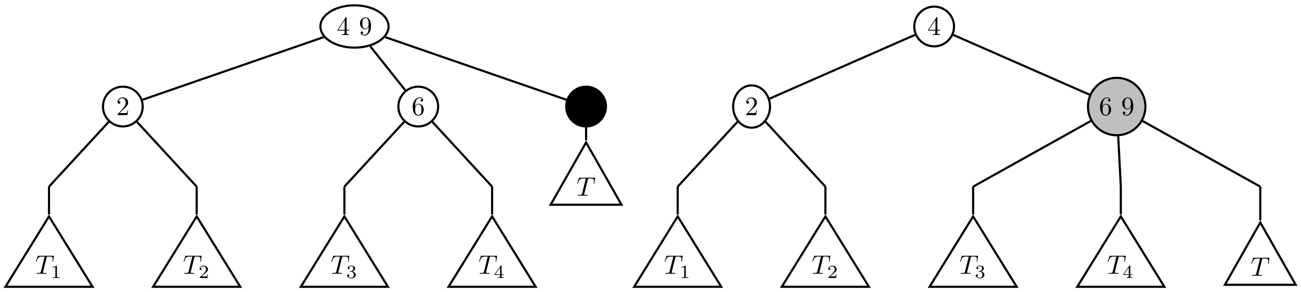


Figure 25.11: Borrowing from the parent. The empty node's sibling borrows from its parent and is shown in gray after.

sibling into one node with two keys, and push up the empty node one level, where we will try to solve it instead. Thus, this is the one case where we need recursion (or an iterative approach), while all the others solve the problem right away. This case is shown in Figure 25.12.

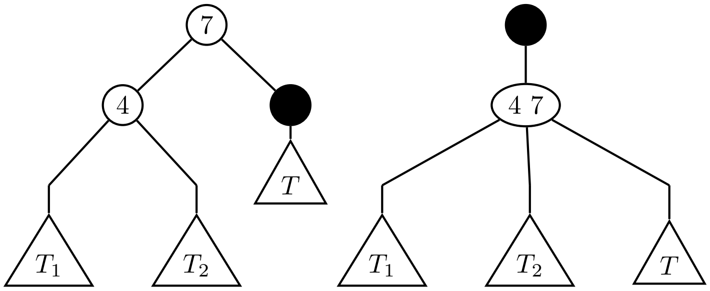


Figure 25.12: Merging two nodes and recursing. The sibling and parent are merged, and the empty node is pushed up one level, where it still needs to be dealt with.

4. There is one final case. If the empty node is the root now, then it can be safely deleted. Its one child (the root of T) becomes the new root of the tree, which is now one level smaller.

This covers all the cases; each has a few subcases, depending on which of the children is empty, but they all follow the same pattern.

Notice that these operations carefully maintain all the properties: the leaves stay at the same level, each node has one or two children once we are done fixing problems, and the tree is still a 2-3 search tree.

25.5.1 A detailed illustration

To illustrate how to apply the rules given above, let's delete a few keys from our example tree T, but with another key 16 added to it. The resulting tree is shown in Figure 25.13.

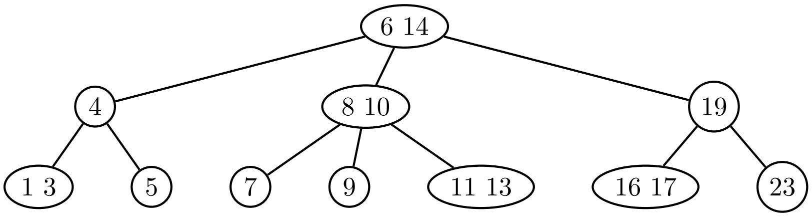


Figure 25.13: The tree T with the key 16 added.

Now, let's see what happens when we want to remove the key 14. As we mentioned earlier, removing keys from internal nodes is a glorious mess, so we swap 14 with its successor, which is 16 (go right once, then left after that). The result of swapping 14 (key to delete) with its successor (16) is shown in Figure 25.14.

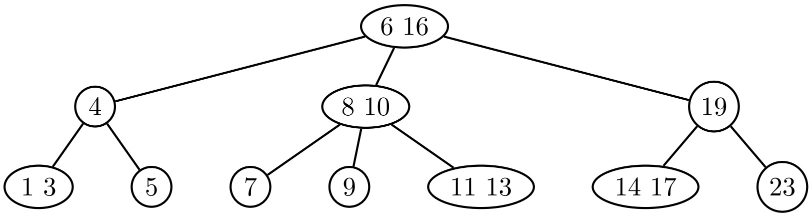


Figure 25.14: After 16 and 14 have been swapped.

Now, the key can be safely deleted from the leaf. Notice that this maintains the search tree property, as the successor was safe to take the place of the key we want to delete. The result of deleting 14 now is shown in Figure 25.15.

Deleting the key 14 was pretty easy: after the swap, its leaf node contained two keys, which made it safe to just delete a key. Next, let's see what happens if we remove the key 5. That key is in a node all by itself, so after we remove it, we have an empty leaf node. This situation is shown in Figure 25.16.

Here, the empty node has a sibling with two keys 1 and 3, so we can apply the first rule from our list above. In this case, we can move the key from the parent down to fill the node, and move one of the keys from the sibling up to the parent. The result is the tree in Figure 25.17:

Next, let's see how borrowing from a sibling works when a node has two siblings, and the one with two keys is the furthest. To see this, let's look at what happens if we next remove the key 7. The intermediate stage will be as shown in Figure 25.18.

This time, borrowing a key from the sibling still works, but takes a few more intermediate steps. We're still in the first rule case, but it works a little differently. The key 11 from the sibling gets moved up to the

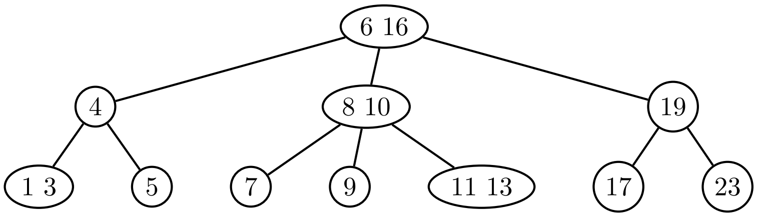


Figure 25.15: After the deletion of the key 14.

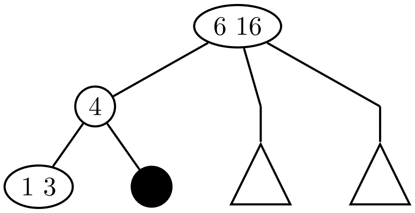


Figure 25.16: After the deletion of the key 5. The now-empty node is shown in black.

parent node; the key 10 from the parent gets moved down to the other sibling, while the key 9 from the other sibling gets moved up to the parent. Finally, we can move the key 8 down to the empty node. The result is only locally rearranged, and shown in Figure 25.19.

Next, let's see what happens when there's no sibling to borrow from. To see this, we delete the key 8 next. The resulting tree is shown in Figure 25.20.

Now, we cannot borrow from a sibling directly. But here, fortunately, the empty node has a parent with two keys, so it's possible to apply the second rule and borrow a key from the parent, and another one from the immediately neighboring sibling. The resulting tree is shown in Figure 25.21.

Next, let's look at the effect of deleting the key 17 from the tree. The first step of deletion is shown in Figure 25.22.

Now, there is no easy way to fix the problem at this level: we have to apply the third rule and escalate the problem one level up. To do so, we combine the one key in the parent node with the one key in the sibling node to form a node with two keys, and make the parent empty. In other words, we produce the tree shown in Figure 25.23:

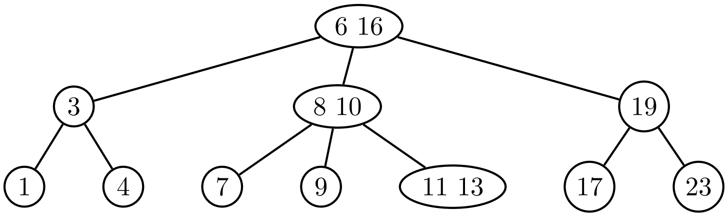


Figure 25.17: Borrowing a key from the sibling via the parent.

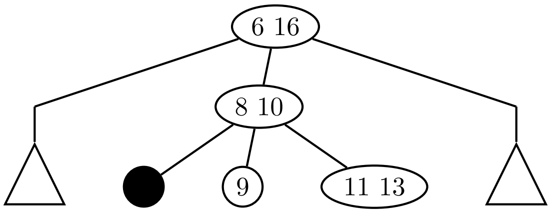


Figure 25.18: Deleting the key 7. The now-empty node is shown in black.

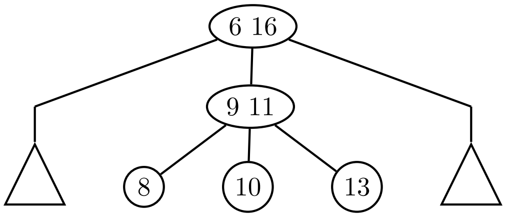


Figure 25.19: Borrowing from a 2-step removed sibling via the parent. This requires some moving up and down of keys, but only between the siblings and the parent.

At the next higher level, we now have a parent with two keys, so we can apply the second rule and borrow from the parent to fix the problem, giving us the tree shown in Figure 25.24.

Of course, we were a bit lucky — if the parent had had only one key, we may have had to pass the problem up yet another level, possibly all the way up to the root. Once the root is empty, though, it is safe to simply delete it (the fourth rule), thereby reducing the height of the tree by 1.

25.5.2 Running Time

When we look at the running time, we see that rearranging the tree is only moving a constant number of pointers and keys (and values) between nodes. Thus, all of the operations above take time $O(1)$. If we apply rules 1, 2, or 4, we are thus done in $O(1)$. In case 3, we may continue iteratively or recursively, but we perform a rearrangement operation at most once per level of the tree. Since we already worked out that a 2-3 Tree has at most $\log_2(n)$ levels, the running time is $O(\log n)$ for each of the operations. Thus, in summary,

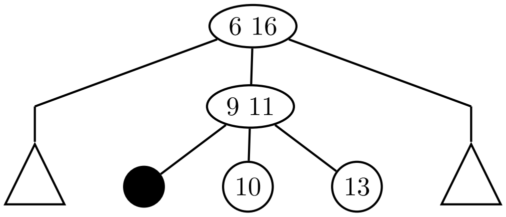


Figure 25.20: Deleting the key 8. The now-empty node is shown in black.

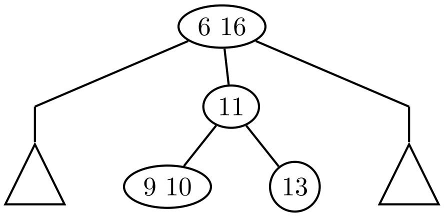


Figure 25.21: Borrowing a key from the parent.

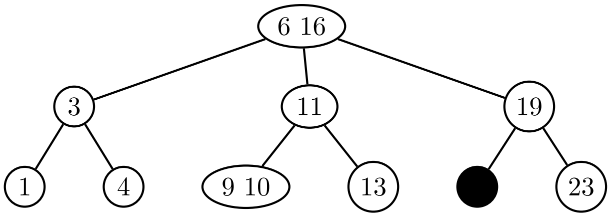


Figure 25.22: Deleting the key 17. The now-empty node is shown in black.

we get that using a 2-3 tree, all operations take time $\Theta(\log n)$. (It is not hard to construct trees on which you do need to propagate up all levels for an insertion or a removal.)

For many data structures, we say that which one to choose depends on the context. It is generally agreed that search trees (and Hashtables, which we will get to next) are simply better implementations of Dictionaries than those based on arrays, vectors, or lists. If you need an associative structure, don't use a linear structure — use a tree or Hashtable.

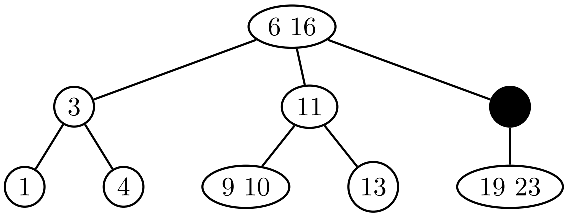


Figure 25.23: Combining a parent key with a sibling key, and passing the problem of the empty node up one level.

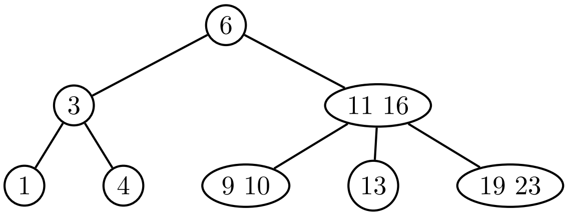


Figure 25.24: Borrowing from the parent to resolve the empty node in the middle of the tree.

Chapter 26

General B Trees and Red-Black Trees

[Note: this chapter covers material of about 1 lecture.]

26.1 More General B Trees

We've just seen 2-3 Trees as a special case of B Trees. In principle, we could implement B Trees with almost any combinations of lower and upper bounds on the number of keys per node. In general, we can make B trees with at least b children (and hence $b-1$ keys) per node and at most b' children (and hence $b'-1$ keys), whenever $b' \geq 2b-1$.

Let's see why that is, and where the $b' \geq 2b-1$ restriction comes from. First, of course, we need to allow some special cases. If we choose $b = 5$, but our tree contains only 2 keys total, then we cannot have each node contain at least 4 keys. So we allow one node to have fewer than the minimum number of keys.

Searching in a general B tree is the obvious generalization of the 2-3 Tree search. When looking for a `key` in a tree T rooted at u, we compare it to all keys in u with a linear search. If we found it, great. If not, we have at least identified two consecutive keys $k_i < k_{i+1}$ such that $k_i <$ key and $k_{i+1} >$ key. Then, we know that we need to search in the subtree T_{i+1} recursively.

To insert, as before, we find where the `key` would belong, and insert it into that leaf node. If the number of keys is still at most $b'-1$, we are all done. But if the number of keys is now b', which is too large, we need to split the node. We break it into two nodes with $\lfloor (b'-1)/2 \rfloor$ and $\lfloor b'/2 \rfloor$ keys each, while passing the middle key up to the parent. Then, we recurse or iterate on the parent, as for 2-3 Trees. Now, we can also see why we need that $b' \geq 2b-1$. After all, the two newly created nodes from splitting have to be legal, so we need that $b-1 \leq \lfloor (b'-1)/2 \rfloor$, which is ensured by $b' \geq 2b-1$.

To delete a key, we do the same initial steps as for 2-3 Trees, i.e., swapping keys if necessary, then removing a key from a node. The difficult case is again when a node has too few keys after deletion. In that case, we look to borrow keys from siblings, from parents, or merging a parent with a sibling and recursing. There are more cases now, but it works the same way. If you were to implement this for large b, instead of writing case distinctions by hand, you'd have a `for` loop to do the key swapping.

Ok, so now we know how general B trees work. But why would anyone want to use them rather than the nice 2-3 Trees? They are more complicated to implement, and generally less efficient, because you perform linear search inside each node, which can get somewhat expensive for large b.

The main reason to go to much larger b, b' (in the hundreds or thousands) is that sometimes the map cannot be entirely stored in main memory, and is instead stored on disk. In particular in the old days when memory was very scarce (think 4k of main memory), this meant a lot of loading from disk, which is several orders of magnitute slower. In particular, locating a record on disk is slow — once you have found it, reading a consecutive memory block is significantly faster. So the goal is to make the tree as shallow as possible, by giving it a larger branching factor. If you give each node an outdegree of 1000 instead of 2, the depth of the tree will be $\log_{1000}(n)$ rather than $\log_2(n)$, which is smaller by about a factor 10, so 10 times fewer disk accesses.

The idea is that we'll bring in a node with 1000 keys. The linear search in memory is still much faster, so we know where to go next, and bring in another node with a lot of keys. That way, we can do better when the tree is too large for main memory. The textbook discusses data structures for external memory (hard disk) in more detail, but we won't go into it more in this class.

One particular case of B trees we want to quickly look at is 2-3-4 Trees. So nodes can have 1, 2, or 3 keys, and correspondingly 2, 3, or 4 children. 2-3-4 Trees do have some slight advantages over 2-3 Trees, in that one can implement insertion a bit faster. (Basically, the idea is that as you search down the tree, when you see a node with 3 keys already, it looks like you might need to split this node later. So you just split it prophylactically right away, and when you get to the leaves, you can insert a key without having to propagate any insertions back up to the root.) The slight downside of 2-3-4 Trees is with implementing them: there are now more cases to consider for borrowing from siblings or parents, and the code would become a little longer.

However, for us, the actual main reason to introduce 2-3-4 Trees here is to set the stage for Red-Black Trees.

26.2 Red-Black Trees

2-3 trees and 2-3-4 trees are perfectly fine data structures. But some people prefer their trees to be binary, and there are some classic binary search tree data structures that any computer science student should have learned about. The two most common ones are AVL Trees and Red-Black Trees. In this class, we see Red-Black Trees.

As we discussed when we got started on search trees, the important thing is to keep the height bounded by $O(\log n)$, so that search (and insertion and deletion) is fast. In order to do that, you want the search trees to be "balanced," in the sense that all the subtrees of a given node are "similar" in height or number of nodes. The goal of constructions such as Red-Black Trees or AVL Trees is to impose certain rules on the trees that can be maintained easily (in time $O(\log n)$ per insertion or deletion) and ensure that the height does not grow too fast. For AVL trees, these rules involve comparing the numbers of nodes in the two subtrees, and making sure they do not get too different. For Red-Black Trees, these are rules for coloring nodes, which will have a similar effect.

There are two ways to understand Red-Black Trees: one is to present the coloring rules, which seem pretty arbitrary. The other is to realize that Red-Black Trees are exactly a way to "squeeze" 2-3-4 Trees (or 2-3 Trees) into binary trees. We will start with the second way of thinking about them, as it is more intuitive. We will then see how the strange-looking rules for Red-Black Trees are simply the consequence of this encoding.

In order to turn a 2-3-4 Tree into a binary tree, we need to figure out what to do when a node has 3 or 4 children, since that's not allowed in binary trees. The solution is quite simple: we replace the one node with a little subtree of 2 or 3 nodes. This is illustrated in Figure 26.1.

We can see that as a result of this operation, each level is split into at most two new levels, so the height of the tree at most doubles. In particular, it stays at $O(\log n)$. Also, notice that as a result, not all leaf nodes will now be at the same level, but they will be roughly at the same level (within a factor 2 of each other).

In the figure, we have also already added color coding corresponding to the way Red-Black Trees can be defined. When we split a node into 2 or 3 nodes as we did, we will color the top level *black* (in the figure, gray), and the lower level (1 or 2 nodes) *red*.

One way of defining Red-Black Trees is exactly as the trees you can get out of 2-3-4 Trees by performing the operations we just described. This is the motivation that your textbook also gives. The other definition captures the actual properties of trees you can get in this way.

Definition 26.1 *A* Red-Black Tree *is a binary search tree with the following additional properties:*

- *Each node is either red or black*

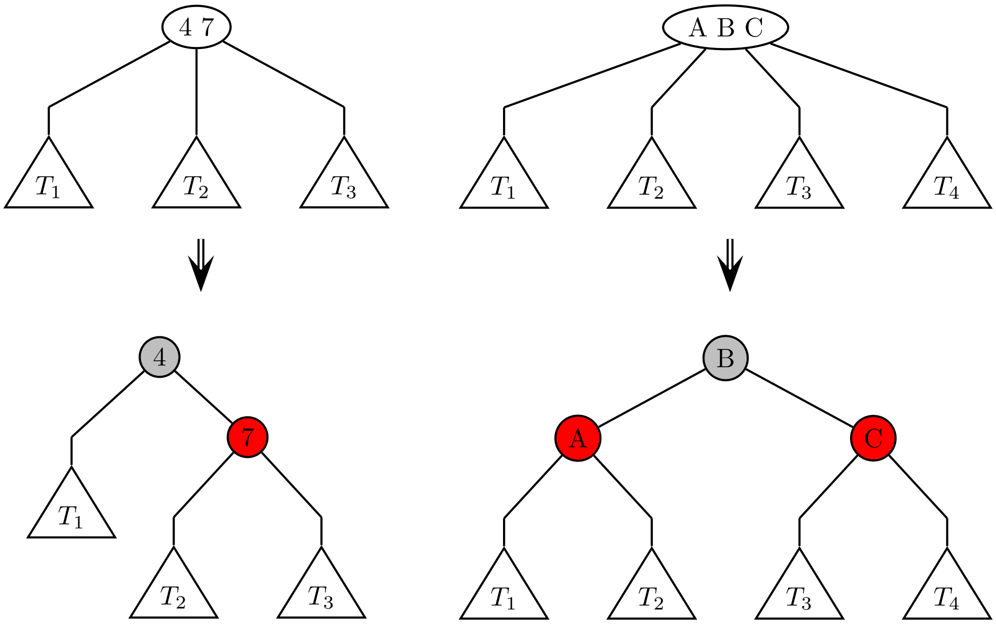


Figure 26.1: Turning 2-3-4 Trees into binary trees. The figure shows nodes with 3 and 4 children, and the corresponding little binary trees we build.

- *All `NULL` pointers (empty subtrees) are black; these dummy trees are sometimes called sentinels.*
- *A red node can only have black children. (However, a black node can have any colors among its children.)*
- *For any path from the root to a leaf, the number of black nodes on the path must be the same.*
- *The root is black.*

An implication of these properties is that every Red-Black Tree has height at most $2\log_2(n)$.

Of course, one way to get a Red-Black Tree is to start with a 2-3-4 Tree and convert it over the way we just showed. But in practice, you don't want to just build one data structure in order to convert it to another; you want your data structure to work by itself. So we'll look at how to implement the operations (search, insert — we'll skip deletion in this class) directly on Red-Black Trees.

To search for a key, you can just ignore the colors. They matter only when inserting or removing items, as that is when the tree is changing, and thus needs to be kept balanced.

26.2.1 Inserting into a Red-Black Tree

To insert a key, as always, you search for it (unsuccessfully) in the tree. Then, it is inserted as a the only content of a red leaf. If the parent of that leaf was black, all is good; we still have a valid Red-Black Tree. (Notice that in 2-3-4 Trees, this corresponds to inserting into a node that still had space for another key.)

However, the parent may actually be red, in which case we may violate the rule that a red node can only have black children. We can't just recolor the node or its parent black, because that would increase the number of black nodes on one, but not every, root-leaf path; just like for 2-3 Trees, it was important to keep all leaves at the same level, for Red-Black Trees, it is important to not violate the "number of black nodes on root-leaf paths" property, because it would be very hard to restore.

So we want to solve the situation where the node z we are currently looking at is red and its parent y is red. We will assume that y itself is the left child of its parent g (the grandparent of z). Otherwise, swap "left" and "right" in everything that follows. Notice that g must be black, because we didn't have any color violations in the tree prior to inserting the red leaf. We distinguish two cases, based on the color of z's uncle u (i.e., the other child of g besides y.

- If u is also red, then we have the situation in Figure 26.2.

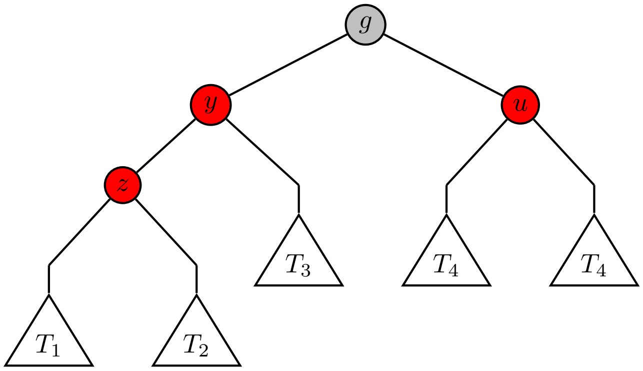


Figure 26.2: Case 1 of insertion: z's uncle u is red.

  In this case, we can recolor y and u black, and g red instead. The number of black nodes on any root-leaf path stays the same, and we've fixed the violation. Of course, if g's parent is also red, then we've created a new violation, but we can solve that iteratively, as it is two levels higher. If g was the root, we are now safe; or rather, we can recolor it black to restore that rule.

- If u is black, then the recoloring doesn't work: making g red would decrease the number of black nodes on the paths going through u. So we actually need to do some work. (So far, we've just recolored, but not changed the tree.) Let's look at the easier case first: when z is the left child of y. Then, we are in the situation shown in Figure 26.3, and we can fix it with the *rotation* shown in the figure.

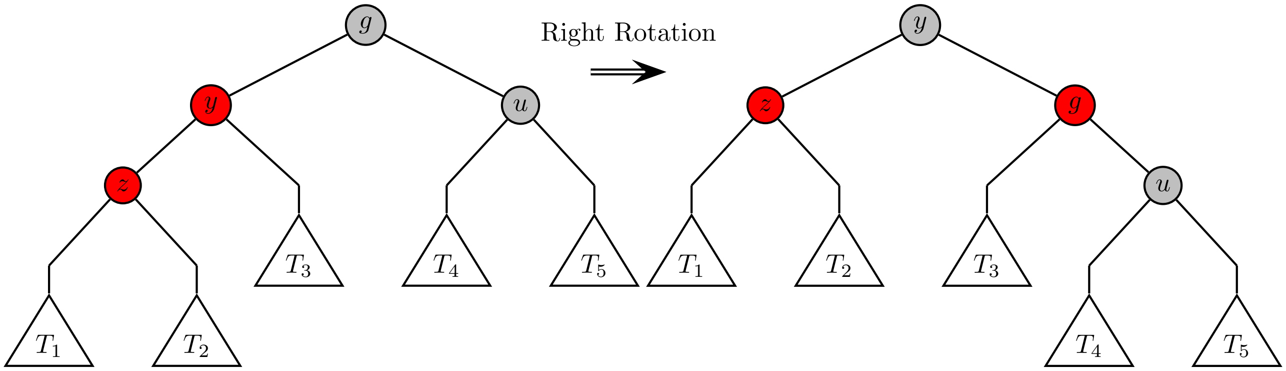


Figure 26.3: Case 2 of insertion: z's uncle u is black. We perform a right-rotation.

  Notice that as part of the rotation, y became the parent of g, and g inherited (as its new left subtree) the tree T_3 that was the right subtree of y before. We also recolored y and g. You can check that the number of black nodes on all root-leaf paths has stayed the same, and we fixed all the double-red violations. So there's no need to iterate in this case; the insertion algorithm terminates here.

So far, we assumed that z was the left child of y. What happens when z is the right child of y? That is the situation depicted in Figure 26.4. As you can see there, we deal with this with a left-rotation of z and y, i.e., one level lower than the right rotation.

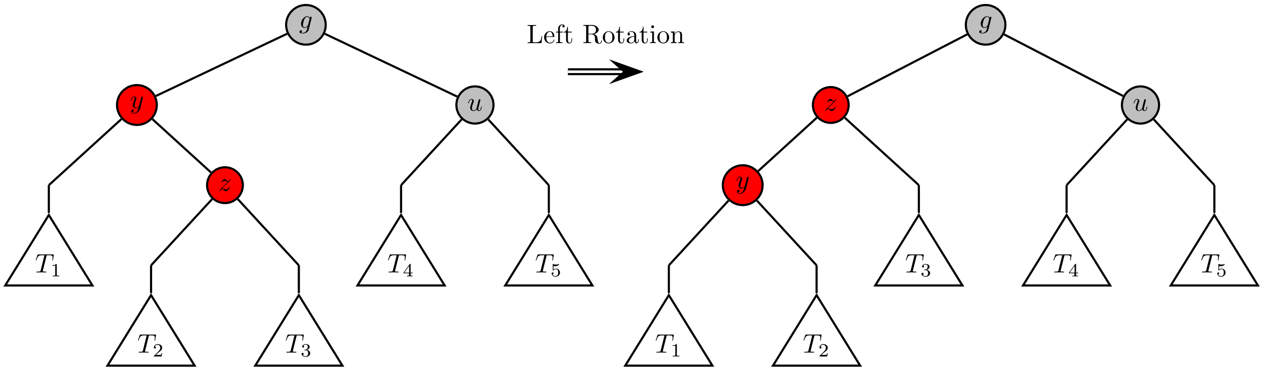


Figure 26.4: Case 2(b) of insertion: z is y's right child. We perform a left-rotation.

This does not really fix anything — we still have the same two red nodes, one of which is a child of the other. We only changed which one is the child and which one is the parent. But notice that now, we can think of y (instead of z) as the problem node, and y is now the left child of its parent. So at this point, we can apply the right-rotation from the previous case, and we're done.

What happens in Red-Black Trees during insertion is perhaps not quite as intuitive as what goes on in 2-3 Trees when you insert. As we saw in the context of AVL trees (Chapter 24), rotations are the natural way in which one fixes Binary Search Trees. But if you have trouble remembering them, you can always rederive them from 2-3-4 Trees, by asking yourself "What would a 2-3-4 Tree do?" That is, you reinterpret your Red-Black Tree as a 2-3-4 Tree, look at the correct operation, and then "translate" that operation into the Red-Black tree. That's of course not how you would implement it — converting a Red-Black Tree into a 2-3-4 Tree requires linear time, which completely ruins your running time. But it's a useful way to help you understand or remember how the operations work.

Notice that the first case (Red Uncle) corresponds to the case when you inserted a key into a full node and need to split it — that's what recoloring does. The second case captures when the node was not full, but you might need to rearrange your trees a bit locally to turn them back into a correct "translation" of a 2-3-4 Tree.

We didn't cover key removal in class, and won't include it in these notes. It contains a bunch more cases, and long case distinctions aren't particularly intuitive. As always, to remove a key, you first search for it, and swap the element with the successor in a leaf if necessary. Afterwards, there are a number of cases of rotations and recoloring, and if you really want, you can look them up in various textbooks, or derive them by asking yourself "What would a 2-3-4 Tree do?"

Chapter 27

Iterators

[Note: this chapter covers material of about 1 lecture.]

When we store a set of items in a data structure, one of the things that we often want to do is be able to output all of them. For instance, in the case of a set, while our main focus was on adding and removing items (and test membership), we want to be able to output all items as well. Ideally, we would also like the process to be fast. How should we do that?

27.1 Some first attempts

One solution would be to give the programmer (who wants to output things) access to the internals of our data structure. For instance, if it is known that we used a linked list, and we return the head of the linked list, then starting from the head, it is possible to go through all items of the linked list. But of course, this is a terrible solution: it violates everything we are trying to do by hiding the implementation; the user of our data structure should only interact with specified functions, and not know what goes on internally. His/her code would not work any more if we change the internal implementation to an array-based one.

At the other extreme would be to simply include in our implementation of the data structure another function `print()`, which prints all items to `cout`. But what if we want to print them to a file instead? Well, we could print them into a string, which could then be written to either `cout` or a file. But now what if someone would like them output in a different format? Or someone only wants to output all the entries that satisfy certain criteria? We might end up writing a huge number of different output functions. And then additional functions that might actually process the items. Clearly, that solution does not work, either.

Another solution would be to essentially provide the interface of the `List` class on top of any data structure: allow access to all elements by index, via a function `get(int i)`. This works better, but it is not very efficient: if the underlying implementation is via a linked list, then this takes time $\Theta(i)$ for element number i, for a total of $\Theta(\sum_{i=1}^{n} i) = \Theta(n^2)$. Whereas if we had just traversed the linked list, it would have been just $\Theta(n)$. It's also overkill: we don't need to be able to access elements by index; we just want to be able to go through all of them.

After thinking about this for a while, the solution one hopefully arrives at is to have some kind of a "marker" that gets pushed through the data, and remembers where it was before. If the elements of the data structure were in some particular meaningful order (such as for a `List` data structure), then our marker would traverse them in that order. If the order of the elements was not meaningful (for instance, for a `Set` data structure), then they could be output in any order.

The "marker" may be implemented differently, depending on how the data structure itself is implemented. If the data are stored in an array, then the marker may just be an integer, the index in the array that we're currently at. If the data are stored in a linked list, then the marker may be a pointer to the current element. Ideally, the implementation of the marker should hide these kinds of detail, and just expose an interface whereby another function can retrieve the actual stored elements one by one, without ever having to know about the marker.

The next question we asked ourselves was where the marker should be stored. The first "obvious" choice was that it may be stored inside the data structure itself. (That's what we did on Homework 4.) So things may look something like the following for our new modified `Set` class:

```
class Set<T> {
  ... // prior Bag functionality.
  T start(); // starts the traversal, returns first element
             // could be T or T& or T*, depending on how we want to
             // implement it.
  T next(); // advances the marker internally, returns next element
}

Set<T> set; // contains some element already, somehow

for(T elt = set.start(); end not reached; elt = set.next())
   { // process elt, e.g., by printing it;
   }
```

We'd have to add a way to test if the end is reached, which is not very difficult (e.g., return a `NULL` pointer or throw an exception). The first problem with the implementation so far is that we might want to have multiple markers in use at once. Then, we couldn't just use `start()` and `next()`, but would have to somehow index them. So the data structure would have to internally store a set of markers (e.g., as a set/map or something). It's doable, but gets a bit cumbersome.

The other issue is that because the state is stored internally in the `Set`, the `first()` and `next()` functions couldn't be `const`. Thus, we couldn't print any data structure that was passed as `const`, even though in actuality, printing doesn't change the contents of a data structure.

For both reasons, the more "standard" solution is to define a separate class, whose objects have the ability of traversing the elements of the data structure.

27.2 Iterators

Such a class is traditionally called an *iterator*, so we will use that term instead of "marker" from now on. Since an iterator is a class/object encompassing one marker, it must provide functionality to advance, to dereference (i.e., read the data), and compare for equality or inequality, in order to terminate a loop. For readability (by analogy with traditional `for` loops), these functions are usually implemented with operator overloading.

The class which is being iterated over must have the following functionality:

- Return an iterator initialized to the beginning. This method is usually called `begin()`, and returns an iterator.
- Return an iterator initialized to the end, so that we can test when we are done. This method is usually called `end()`, and returns an iterator.

Suppose that for our `Set<T>` class, implemented, say, using a linked list internally, we want to define an iterator `Set<T>::Iteratator` (we'll see momentarily how to do that). Then, in the `main()` function, our use of an iterator may look as follows:

```
int main()
{
    Set<int> LLS;
    for (int i=2; i<10; i++)
        LLS.add(i*i);
    LLS.remove(49);

    for (Set<int>::Iterator si = LLS.begin(); si != LLB.end(); ++si)
    {
        cout << *si << " ";
    }
    return 0;
}
```

Here, as you can see, we use comparison to the `end()` iterator to test whether we have passed the last element. To advance the iterator `si`, we use operator overloading, so that it looks as much as possible like a typical loop in which we would increment an integer. Similarly, we use `*si` to dereference the current value of the iterator, just like we do with pointers. So we're trying to make the code look as much as possible like the following:

```
int a[100];
for (int *x = a; x < a + 100; ++x)
   cout << (*x) << " ";
```

One important thing to keep in mind about iterators is that in general, we want to avoid modifying the underlying data structure while iterating over it. Most data structures do not guarantee what will happen if you try that, and it's always a bad idea to execute operations whose results are unpredictable. For instance, some implementations of an iterator may have copied all of the data from the data structure over (so they won't be affected by any change), while others may look at the data structure in real time (and will be affected).

27.3 Implementing an Iterator

Let us first see how we would implement an `Iterator` class for a `Set<T>`. First, we want to think about what data need to be stored internally. We need to have the marker; and since we are implementing the `Set<T>` using a linked list, that marker will be a pointer to an `Item<T>`. But we also need another field: we need to remember which data structure the marker is traversing. For instance, two markers both of which point to element 7 may not be the same if they are pointing to element 7 of *different arrays* (for implementations using arrays instead of linked lists). So we also need to store a pointer to the data structure being traversed. The signature thus has two private fields for data, and a few methods discussed below:

```
template<class T>

class Set {
  public:

  class Iterator {
    private:
      const Set<T> *whoIBelongTo;
      Item<T> *current;

      Iterator(const Set<T> *s, Item<T> *p)
       {
          whoIBelongTo = s; current = p;
       }

    public: // functions listed below
```

```
        friend class Set<T>;

        T & operator* () const
           {  return current->value; }

        bool operator== (const Set<T>::Iterator &other) const
        {    return (current == other.current && whoIBelongTo == other.whoIBelongTo); }

        bool operator!= (const Set<T>::Iterator &other) const
        {    return (!this->operator== (other)); }

        Set<T>::Iterator operator++ () const
        {
            current = current->next;
            return *this;
        }
    }
}
```

A few notes are in order about the implementation:

- Notice that we implemented the class as a nested class inside `Set<T>`, which means it will be referenced by `Set<T>::Iterator`. There's really nothing difficult about nested classes, and they make sense particularly for things such as iterators, where one class only is useful for another.

- Why did we make the constructor `private`? The reason is that we don't want just anybody to generate iterators for a given set and pass weird pointers. The only class to be allowed to generate a new iterator should be the set itself. By making the `Set<T>` a `friend`, we've made it possible for the `begin()` and `end()` functions of `Set<T>` to call the constructor.

- For the `==` operator, we compare the pointers (`current` vs. `other.current`), rather than their data (`current->data` vs. `other.current->data`). This makes sense because we might have a list that contains the same number multiple times; just because it does does not make a marker on the 5th element equal to a marker on the 8th. Also notice that we are comparing to make sure that both iterators are traversing the same data structure.

- For the `!=` operator, we took the easy way out. Instead, we could have implemented it from scratch (using DeMorgan's Theorem).

- For the increment operator, we not only want to move the marker, but also have to declare it of type `Set<T>::Iterator` (rather than, say `void`). The reason is that people may want to write something like `cout << *(++bi)`, where the iterator is moved and immediately dereferenced. While some people think that this is not good coding style, you should still support it.

Now that we have implemented the `Set<T>::Iterator` class, we can augment our `Set<T>` with two functions to return a start and end iterator:

```
Set<T>::Iterator Set<T>::begin()
{    return Set<T>::Iterator(this, head); }

Set<T>::Iterator Set<T>::end()
{    return Set<T>::Iterator(this, NULL); }
```

Again, a few notes on what we did here:

- Remember that the C++ keyword this is determined at runtime and always contains a pointer to the object from which it is called. In other words, an object can use the word this to find out where in memory it resides.

  In our case, this is used to tell the iterator the identity of the object it is traversing. The other argument is just the head, i.e., where the traversal should start.

- For the end() function, we give the NULL pointer as the current element of the iterator. The reason is that the end() iterator should encode the case when the for loop has reached the end of the linked list, which happens when the pointer is a NULL pointer. If instead, we wrote return Set<T>::Iterator(this, tail);, then by looking at what happens in our main() function above, you'll notice that the last element of the set wouldn't be processed.

Again, notice how iterators let us go through all elements of a container without knowing any internal details about it. Only the Set<T> and the Set<T>::Iterator need to know how Set is actually implemented.

The implementation of an iterator for a Set<T> based on a linked list was pretty straightforward. If we think about how we would implement an iterator for a Set<T> built using an internal array, we would quickly discover that the iterator will store internally a pointer to the set, as well as an integer to be used as an array index. Let's say that internally, our ArraySet<T> stores its data in a private array T *a. Now, the dereferencing would have to be of the form

```
T operator* () const
{    return whoIBelongTo->a[current]; }
```

This means that at the moment we want to return an item, we need access to a private variable in the data structure. Typically, we need to use friend access to ensure this, but when a class is defined within another (such as here Set<T>::Iterator inside Set<T>), it automatically is considered part of the parent class, and has full access to all the private and protected fields.

In our implementation, we only wrote a pre-increment operator. You may wonder how one would overload the post-increment one? After all, by writing

```
Iterator operator++ () { ... }
```

we'd be overloading the pre-increment one. How does C++ tell them apart? The answer is basically a hack. To implement the post-increment operator, you write

```
Iterator operator++ (int dummy) { ... }
```

dummy is just a placeholder variable. You don't actually pass any integers into your operator++. It's just a way you tell C++ *which* operator you are overloading.

Also, notice that if T were a struct, we may want to access its fields, so we may end up writing (*it).field1 when dereferencing the iterator. Typically, we'd like to write instead it->field1. You can in fact do that if you overload the -> iterator. What we gave here is the minimum functionality you should implement for your iterator, but if you at all think that you'll use it again later, or that other people may use it, you should implement a few more operators to make it look as much as possible as an actual pointer as you can.

27.4 The Bigger Picture

27.4.1 Design Patterns

So far in this class, we had seen pretty standard ways for objects of different types to interact: inheritance, one class containing fields of another class's type, one class throwing a member of an exception class and that's about it. This is our first example of classes interacting in more complex ways: we have one class whose "job" it is to traverse another class and provide some functionality (access to elements) that is not naturally handled within the original class. In other words, we have abstracted one particular functionality out of one class into another.

Once we absorb the ideas of object-oriented programming more fully, it becomes really fun to think about objects as each having their own identity, filling a role in a larger system of components, and interacting with each other in particular ways. Since the idea of an Iterator is fairly useful generally, it has been identified as one of many *Design Patterns*. Design patterns are an important way of identifying frequently occurring ways in which objects interact, and they help in designing well-structured larger software systems that can be extended easily later. As such, they are an important part of the field of *Software Engineering*. We will discuss them in a bit more detail in Chapter 33.

27.4.2 Foreach, Map, Functional Programming, and Parallelization

We have seen that for essentially all data structures (e.g., ones in STL), we will now want to use iterators and write loops of the following form:

```
for (Iterator it = structure.begin(); it != structure.end(); ++it)
   {
      // process *it
   }
```

Since the code will always have the exact same form, except for different ways of processing the elements, we could try to shortcut it even more. By implementing the processing of `*it` into a function `f`, we could implement a function:

```
void for_each (Iterator start, Iterator end, Function f)
{
  for (Iterator current = start; current != end; ++current)
     f(*current);
}
```

In fact, C++ implements an almost identical function that has only a few small differences. To use C++'s function, your iterator has to inherit from the abstract class `iterator` (for which you `#include<iterator>`). You'll have to implement your function, and pass it in. You have already seen this basic idea of passing a function pointer in an earlier homework — this is the first time we see it as a more general idea.

While using the `for_each` function would only save us a little bit of typing, it has a conceptual advantage: it clarifies what is going on in your code. For instance, by using this function, you are making it clear that you are simply applying the same function to each element, and there is no state transferred from one iteration to the next. In fact, this (and a few similar) types of structure appears so often that it comes pre-implemented like this in STL.

This kind of construction, where you pass a function as a parameter to another function and then apply it inside, is one of the key constructs of *functional programming*. The particular case in which one function is applied to each element of a collection is called the *map* paradigm. In other words, `for_each` implements the map paradigm in C++.

Thinking a little further, the map paradigm is half of the *map-reduce* paradigm of parallel processing. This is one of the really popular techniques for massively parallelizing Big Data computations over large numbers (hundreds of thousands) of machines, at the heart of what Google and other companies do. The idea is to farm out a lot of parallel computation on individual elements to machines (via map), and then combine the results into the final output (called *reduce*). If you use constructs such as `for_each`, then you make it much easier for your code to be transferred into map-reduce code, and thus parallelized later. Notice that this is where it comes in handy that the different iterations of the loop do not interact with each other, and we instead have each element processed by itself; by doing this, we ensure that the different parallel machines do not need to communicate with each other. (Network usage is slow.)

In addition to the `for_each` loop, if you use iterators, you also have some other standard functionality available: you can add up all elements, find the maximum, and a few others, simply by passing iterators into some pre-programmed functions. Check the textbook for some examples, in the context of the discussions of iterators and STL.

Chapter 28

Hashtables

[Note: this chapter covers material of about 2.5 lectures.]

28.1 Introduction and Motivation

We have started looking at efficient implementations of the `map` ADT. Balanced Search Trees (such as 2-3 trees or Red-Black trees) work quite well. But the choice most often used in practice is Hash Tables. Their analysis isn't as "beautiful" or "clean", but on the other hand, they tend to work better in practice. And understanding them fully raises a lot of interesting questions about the nature of computing.

To motivate the definition of Hash Tables, let's think about how we would implement a map if we *knew for certain* that all keys would be integers between 0 and 999999. In that case, there wouldn't be any need for all the work with balanced trees just to get $O(\log n)$ time. Instead, we could just define an array `ValueType a[1000000]`. All elements are initialized to some specific value $\perp$ to mean "unused." Whenever we are to add a pair (key, value), we simply set `a[key] = value`, which works because we assumed that `key` is always an integer between 0 and 999999. Looking things up is just as easy, as is removing elements. All of these operations take $O(1)$, so it's pretty much the perfect implementation of maps, when it works.

Of course, the problem with this is that it only works when the set of possible keys is small — here, there were just 1000000 possible keys. If the keys are 10 digit numbers (think USC IDs), then this would take an array of size 10^{10}, which would push what can be done with a normal computer. And if we move to a few more digits, or have the key be a string of length up to 80, the array we would need would be way too large.

If we follow the train of thought of the USC student IDs for a while, we notice the following: true, there are 10^{10} different IDs, but of those, only about 50000 or so are in use at any given time, between all the current students, faculty, and staff. So if we declared an array of size 10^{10} (even assuming we had the space), we would actually have almost all of it empty, using only very few positions. Instead, it feels like 50000 items should fit nicely into an array of size 100000. The only problem? We don't know which element should go into which array position. After all, that's exactly what our ADT map is supposed to do in the first place.

But what this suggests is the following approach. We define an array `a` that's reasonably large, say, 300000 in our USC ID example. Then, we have a function $h : \text{key} \mapsto \{0, 1, \ldots, 299999\}$ that maps keys to integers in the array's range. When we add/remove/query a key k, we look in the position $h(k)$ in the array, i.e., we read/write the position `a[h(k)]`. This is exactly the idea of a Hash Table.

28.2 Hash Tables Defined

To speak about any kind of map, we need to have a space of keys and values. Let's denote the space of all possible keys by K (think all 10-digit IDs in our USC ID example, or the set of all strings of at most 80 characters), and the space of all values by V (think all USC student/employee records). The possible number of distinct keys is an important quantity — we will denote it by $n = |K|$.

At its most basic (we will see some more elaborate variations later), a Hash Table is an array a of a chosen size m, with each entry $a[i]$ containing a pair (k, v) of a key $k \in K$ and value $v \in V$. The most important thing about hashing is how to map a given key to a location in the hash table. This is done by the *hash function* $h : K \to \{0, \ldots, m-1\}$. Theoretically, any such function h can be used as a hash functions; however, we will see very soon that some hash functions are better than others. Figure 28.1 illustrates the very basics of hashing pictorially, for the hash function $h(k) = k \bmod 13$ and a hash table of size $m = 13$.

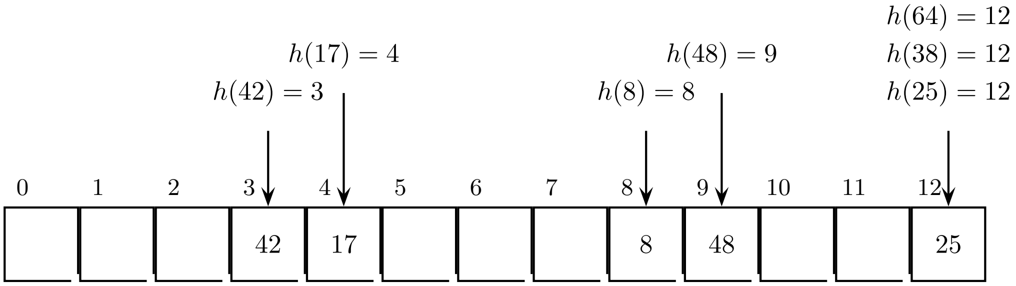


Figure 28.1: Basic hashing illustrated with the hash function $h(k) = k \bmod 13$, for a hash table of size $m = 13$. For readability, the figure omits the values stored along with the keys, even though they would of course be in the hash table. More illustrative figures can be found in the textbook.

In our most basic version of a Hash Table, we would implement the three map operations as follows:

`add(k,v)` : Write the pair (k, v) into the array location $h(k)$, i.e., set `a[h(k)] = (k,v)`.

`remove(k)` : Overwrite the position $h(k)$ with some element indicating that the position is unused, i.e., set `a[h(k)] =` $\perp$.

`get(k)` : Return the value stored in position $h(k)$ (and thus associated with k), i.e., `return a[h(k)].v`.

Of course, we can see an immediate problem with this basic implementation: if two keys k, k' map to the same array position $h(k) = h(k')$, then whenever k' is added after k, it will overwrite the entry for k, and our basic implementation loses everything it had stored about k. When $h(k) = h(k')$, that's called a *collision* in the hash function. In our basic implementation, a collision would be completely devastating. In Figure 28.1, notice that we have a collision of three keys (25, 38, and 64) in position $i = 12$.

Collisions are really the central aspect of hash tables, in that all of our work will go into (1) how to avoid them as much as possible, and (2) dealing with them when they do appear. We will talk more about those in Sections 28.3 and 28.4.

One other important concept about hash tables is what's called the *load factor*. Our hash table has size m, which means that there is room for up to m items in it. But we also care about how many elements we are *actually* storing in the array right now — we denote this number by s. The ratio $\alpha = \frac{s}{m}$ is called the *load factor* of the hash table. When it is small, there is a lot of room in the table. If it ever exceeds 1, we are guaranteed that a collision must have occurred. Going back to Figure 28.1, assuming we found a way around overwriting elements in the case of collisions and placed the elements elsewhere, the load factor would be 7/13.

28.3 Avoiding Collisions, and Choices of Hash Functions

Our first hope in dealing with collisions would be to avoid them altogether. Then, we could use our nice and simple implementation. Alas, there is no hope for that. If $n > m$, i.e., there are more keys than positions in the hash table, then by the Pigeonhole Principle[1], there must be at least two keys k, k' with $h(k) = h(k')$, so we are guaranteed that there is a possible collision. Any data set that contains k and k' will then have a collision. Thus, avoiding a collision is possible only when $n \leq m$, and that case is much less interesting in practice. The textbook and other sources call a completely collision-free hash function a *perfect* hash function; while it would be nice to have one, and the idea of a perfect hash function is appealing and illuminating, a perfect hash function is unattainable for all practical purposes.

Now we know that collisions cannot be avoided in the *worst case* if $n > m$. But how soon do we expect collisions to actually occur? If we do worst-case analysis, i.e., analyze things as though the world is out to get us, then of course we need to assume that the world "deliberately" picked out k, k' to create a collision as the first two keys we see. But for reasons that we will see in a moment, for hash tables, we often like to perform the analysis under an assumption of *random* keys. So how many random keys do we need to draw until we expect to see our first collision? There are m possible indices of $h(k)$ we can draw, and if any two draws have the same index, then we have a collision. This is exactly an instance of the Birthday Paradox[2], so we would expect our first collision to occur around key number $\Theta(\sqrt{m})$. In other words, even if we think that the keys are drawn randomly (which should be pretty friendly to the hash table), the first collisions should occur around load factor $\alpha = \Theta(1/\sqrt{m})$. This is all the more reason why we will need to deal with collisions below.

28.3.1 Theory behind Choices of Hash Functions

So what makes a good hash function? Well, first of all, h itself should be easy enough to compute fast. Also, it should spread out keys as much as possible, in order to avoid collisions. So clearly, the following, while fast to compute, is the absolute worst hash function: $\forall k : h(k) = 0$.

Modulo Arithmetic

Assuming that the keys are integers, a function that *does* nicely spread out keys would be the function $h(k) = k \bmod m$, which wraps keys around the array.

Is this a good hash function? For starters, it's easy to compute. As far as using it in practice, it's not too bad, but there are some potential problems with it. Let's return to our USC ID example to see what problems may occur. Suppose that for each USC student and employee, the last 4 digits always captured the year that the person joined USC. And suppose also that our hash table has size $m = 10000$. Then, taking $k \bmod m$ will exactly shave off the last 4 digits. But now, all the values of $h(k)$ will be between 1920–2013. So only 94 entries in our large array will be used, leading to lots of (unnecessary) collisions.

It is quite common for keys to have similar patterns, where particular bits of a string encode particular information, and that information will be the same for many of the items. Then, we get very clustered key items in particular digits, and if the hash function does not break up these clusters, they will end up leading to lots of collisions in the hash table. This is definitely true for the function $h(k) = k \bmod m$ when m is a power of 2 or 10. The best choice of m is a number that will not have such patterns, and for that, prime numbers are the best choice.

The reason is that a prime number is, by definition, relatively prime to any other number. In particular, suppose that your keys had a pattern where many keys have the same trailing sequence of digits (base 2, 10, or other). That means that there are many keys $k \in K$ with the same value of ($k \bmod 2^d$) or ($k \bmod 10^d$). Let S be the set of all those keys, having the same value. (For concreteness, let's say we are doing this in binary, so all future references will be to 2^d instead of 10^d.) If we take two such keys $k, k' \in S$, their difference $k - k'$ will be a multiple of 2^d. This means that the difference will only be divisible by m if it is

[1] Students taking CS170 should have learned about this by now. If not, check out the textbook on Discrete Mathematics, or Google the term.

[2] This is another standard concept from CS170. The basic version says that if you have 365 days in the year, then around the time when you have 23 people in the room, there is a reasonable probability (more than $\frac{1}{2}$) that some pair of them have the same birthday. More generally, when you have n items, and you select repeatedly uniformly randomly from them (such as choosing a birthday among n days of the year), around $\Theta(\sqrt{n})$ is when you expect to see the first selected pair with the same selected item. Again, more information can be found in textbooks on Discrete Math or on probability, or by Googling.

a multiple of $m \cdot 2^d$. (This is where we use primality of m.) But if the difference is not divisible by m, then $(k \bmod m) \neq (k' \bmod m)$, so k and k' cannot be mapped to the same location unless $k - k'$ is a multiple of $m \cdot 2^d$. This in turn means that each key $k \in S$ can collide only with a $1/m$ fraction of the other keys in S, meaning that the hash function spreads around the keys in S as much as possible.

So the advantage of using a prime number for the array size m is that it spreads a certain set S (or multiple sets) of keys around the array. But why should we focus only on those specific sets S? In other words, why is it more important to spread out keys that share some postfix in whatever natural representation (base 2 or base 10)? In practice, those patterns are probably more likely to occur than other, more abstruse, patterns. But if we want to explore the underlying math a little more, we should dig deeper.

Mapping Randomly

What would be the best way to break up *all* patterns? One way to make sure to break up all patterns would be to map each key k to an independently and uniformly random index $i \in \{0, \ldots, m-1\}$. This would be great in that it would certainly break up all patterns. It would nicely spread out keys. The only problem? It would make it completely impossible to find an item again, since we put it in a random location. Apart from this (unfortunately fatal) problem, a random mapping would be a fantastic hash function.

So mapping items to random locations obviously does not make sense. But the intuition does help out with our analysis. In a sense, random mapping sets the “gold standard” that we should strive for, minus the randomness. When analyzing how well hashing will do in practice, we rarely look at all the specifics of the hash function anyway. Therefore, when we have a good hash function, we will normally pretend that it creates something close enough to an actual random mapping that we can pretend it is actually random (for the purpose of analysis). Then, we can pretend that keys are actually drawn randomly from K, which will drastically simplify our analysis. Remember how earlier, in talking about the Birthday Paradox, we said that we can analyze hashing as though the keys are random? Retroactively, this is the justification.

Actually, there is one way in which we can map items randomly, and it’s a standard technique, at least in terms of theory. We have a whole bunch of hash functions. When we initialize our hash table, we choose one at random from the set. Because it’s a fixed function, we know how to compute it and find stuff. But because it was chosen randomly, it shares many of the nice properties of random mapping. This technique is called *universal hashing*.

What we haven’t said yet is why *any* non-random function h should be allowed to be analyzed as though it were random. If we are not flipping coins or rolling dice or measuring radioactive decay (which is a great source of randomness in practice), what makes something non-random “random-like?” There is a huge and active research area within CS complexity theory on *pseudo-randomness*, and it connects quite closely with hashing. Let’s explore this a little more.

The Complexity Theory Lens

Which keys exactly should we spread out, and why? Going back to the Pigeonhole Principle, the stronger version of it says that if you map n pigeons to m pigeonholes, then there must be at least one pigeonhole with at least $\lceil n/m \rceil$ pigeons. So if n is much larger than m (think $n = 10^{20}$ and $m = 10^8$), then there is some array entry i such that at least 10^{12} keys k all have $h(k) = i$. Let’s call this set of keys S. Those keys in S sure aren’t spread out, since they were designed specifically with the goal of being terrible for our chosen hash function h. If nature were really nasty to us, it would only give us keys from S, and never mind how we deal with collisions, the hash table would get really inefficient.

So here is the key insight: while the Pigeonhole Principle guarantees the *existence* of a set S of keys that all collide in the same place, the proof of the Pigeonhole Principle is inherently non-constructive, so it doesn’t tell us how to *find* such a set, short of exhaustively searching through all n keys. If finding the set S were actually very difficult, then we could put some faith in the fact that nature would not have been able to perform all the computations necessary to feed us a nasty input. Or at the very least, humans won’t accidentally perform those computations in their choice of what data items to enter into our map (such as their choice of USC ID numbers).

Let's formalize this a little more. For any array index i, let $h^{-1}(i) = \{k \in K \mid h(k) = i\}$ denote the set of all keys k with $h(k) = i$, i.e., all keys mapped to array position i. We say that h is a *one-way hash function* if given i, it is hard to compute $h^{-1}(i)$. Or, stated differently, given a target location i, it is hard to find at least one hash key k that is mapped to i. (Of course, remember that given the key k, computing $h(k)$ should always be easy — the important thing is that inverting the computation is supposed to be difficult.) If it is hard to compute on purpose a key to map to i, then we would expect that we wouldn't *accidentally compute a whole bunch* of keys all mapping to the same location.

If this was a little difficult to understand and wrap your head around, then go back and read it a couple more times. This concept of defining *patterns* as "something that is easy to compute" is quite powerful, and lies at the heart of a lot of CS theory, and fully understanding it will probably expand your view of computing quite a bit.

Now, if you understand the idea, you may ask: what does it mean for something to be "hard to compute?" It turns out that there is a lot of work in computational complexity theory on different notions for this question. At the center is a notion called NP-hardness, which you will learn about in CS270. It would be really nice if there were natural hash functions h for which in a provable sense, the problem of computing $h^{-1}(i)$ were NP-hard. The unfortunate truth is that this is an open question. The existence (or lack thereof) of one-way hash functions is an incredibly important research topic, and would have profound implications for computational complexity theory and even more for cryptography and security.[3]

Returning to the connection with randomness, if nature cannot (efficiently) tell apart whether our hash function h is *actually* random, or just a one-way hash function, then this makes our hash function "almost as good" as random, which is a natural definition of *pseudo-randomness*: if no patterns can be discovered *fast*, then a function is pseudo-random.

Again, Section 28.3.1 is probably a little more complicated to understand during a first and second reading, so make sure to spend enough time digesting it.

28.3.2 Practice of Hash Functions

As we said above, in practice, a hash function h should be fast to compute, and it should spread out items well across the table.

The first part of computing a hash function is to map items to integers, since that's where they should eventually end up. Perhaps the simplest way would be to write down the sequence of characters describing the item (e.g., a string, or something more complicated translated into a string), then look at it written in binary. In practice, if we only use certain characters (e.g., only lowercase letters), we may choose another translation (e.g., 'a': 1, 'b': 2, ..., 'z': 26). This would avoid some extra zeroes.

Once we have obtained a number k, one way or another, we can do a number of things to it. In the end, we definitely want to take the number modulo m, so that it stays within array bounds. Some other standard methods are to *fold* the number, by adding all digits (this makes sense mostly when your hash table is very small), or adding a weighted combination of digits. For instance, the hash function implemented in Java basically reads the number/string in base 31, in order to break up patterns. (Having weights as powers of primes is also a good idea.) If you look around on Google and Wikipedia, you'll find a large number of hash functions, most of them not too difficult to compute.

28.3.3 Another Application of Hash Functions

Returning a bit to our complexity-theoretic view of hashing and randomness, you may have noticed a completely different application. Consider the issue of storing a user's password. If you store it in plaintext in a file, then your users are in serious trouble if a person breaks into the central computer — the attacker can now read all of your users' passwords, and since they are probably reusing passwords on other sites, also break into their accounts there. Believe it or not, some big companies had exactly this problem, having stored passwords in plain text.

[3] If you would like to learn more about this topic, check out the undergraduate cryptography class.

What you should do instead is store the passwords as a hash. In other words, when the user signs up with a password p, you store $h(p)$ in your file instead. When the user tries to log in and enters a password p', you compute $h(p')$ and test whether $h(p') = h(p)$. If so, you let the user log in; otherwise, the password was clearly wrong. Notice that you didn't need to store p itself. True, there is a chance that the user entered a password p' that collided with p. But if you had a good hash function, and m is large enough, then this is very unlikely. And the advantage is that even someone with access to your database cannot figure out p, so they cannot log in to the user's account, because the hash function is hard to invert.

In order to make this work, a simple heuristic for a hash function (something like modulo arithmetic and weighted combinations of digits) will not work any more. We now need functions that actually come close to being hard to invert. Such hash functions are called *cryptographic hash functions*. Two of the most well-known (and widely used) ones are MD5 and SHA. We will not go into their definition in this class, but you can readily find them by Googling. They are not all that difficult to implement, though a bit slower than the simple heuristics. So you probably wouldn't want to use them to implement hash tables.

If you ever implement a user database for your own company, please do remember to follow this practice — passwords should never be stored unencrypted anywhere. (There are also other ways to make them more secure, including a technique called "salting.")

28.4 Dealing with Collisions: Chaining and Probing

We have now explored in quite some depth the question of what makes a good hash function. But as we said from the beginning, never mind how great the hash function, you will run into collisions, most likely when the load factor reaches $\alpha = \Theta(1/\sqrt{m})$, i.e., quite early. For instance, if you have a hash table with 1000000 elements, you will get your first collision around element 1500, with 998500 elements of the hash table unused. So we need to deal with collisions.

28.4.1 Chaining

While most textbooks start with probing, chaining is really the easier to understand and implement method of dealing with collisions. The core idea is to replace each array entry i of `a` with an array or linked list in which to store all elements that are mapped to $a[i]$. So instead of overwriting $a[i]$ when another key k' maps to i, we append the entry (k', v') to the list at $a[i]$. When we are looking for a key k, we do a linear search of the list at $a[h(k)]$, and similarly when we remove k. A linked list (or possibly expanding array) is probably a better choice here than a fixed-size array.[4] Chaining is illustrated in Figure 28.2 below, for our initial example:

Runtime Analysis

The efficiency will depend on how long the lists in particular positions i are. If they are short (constant length), then all operations will be really fast. As they get longer, the running time will get dominated by the linear searches through the lists at $a[i]$.

So we would like to figure out how long the lists will be. If the load factor is α, then the *average* list length will be exactly α. But of course, that doesn't mean that the longest list would have length α, even if the hash function were perfectly random. And if the list lengths are very uneven, then most of the queries will probably be for elements that are in long lists. If we write $\ell_0, \ell_1, \ldots, \ell_{m-1}$ for the list lengths at indices $0, 1, \ldots, m-1$ (remember that $s = \sum_i \ell_i$ is the total number of elements in the hash table), then the average query time is $\Theta(\frac{1}{s} \sum_i \ell_i^2)$: the reason is that with probability ℓ_i/s, we pick an element from $a[i]$ to look for, and it will take $\Theta(\ell_i)$ to find it. So large lists will have a large impact on the average query time.

(This example is a bit similar to a "mistake" often made by colleges in reporting average class size. If you offer 10 classes, and class 1 has 910 students in it, while the other classes have 10 students each, the

[4] In principle, we could get fancy and actually have little sub-hashtables, or balanced search trees, for each entry $a[i]$. This may actually work reasonably well in practice, but it's not clear whether it'll do much better than just using a larger array in the first place and picking a good hash function.

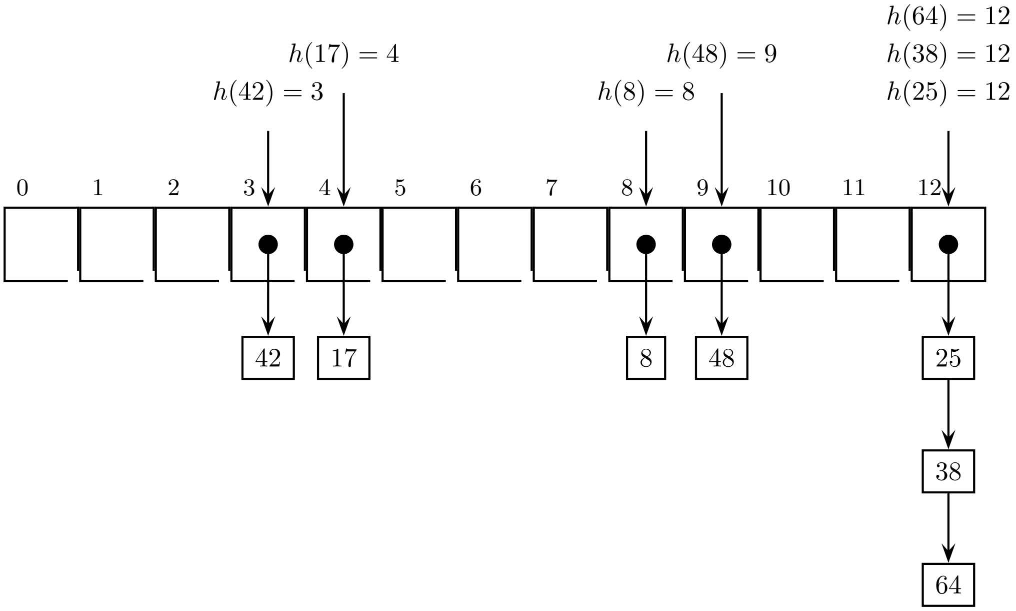


Figure 28.2: Illustration of chaining, still with the hash function $f(k) = k \bmod 13$, for a hash table of size $m = 13$. All `null` pointers are omitted. Notice that all the colliding elements in bucket 12 are chained as a linked list.

"average" class size is 100, namely $\frac{1}{10} \cdot (910 + 9 \cdot 10)$. On the other hand, most students really experience a massive class size, so the average experienced class size is $\frac{1}{1000} \cdot (910^2 + 9 \cdot 10^2) = 829$.)

So how large do we think the largest list in a hash table will be? To analyze this, we'll assume a random distribution of keys. Then, we are looking at distributing s keys randomly into n hash buckets. This type of analysis is typically called "balls in bins," since we can think of the items as "balls," which are thrown randomly into "bins;" we then want to know facts about statistics of the bins. Using standard probability calculations you should have seen in CS170 (Binomials and Union Bounds), it is not hard to analyze this. The most interesting regime is when $s = \Theta(m)$, i.e., when the number of items is a constant fraction of the number of hash buckets. Then, the largest hash bucket will have size at most $O(\log m)$ with high probability. On the other hand, one can also show that it will end up being $\Omega(\log m)$ with high probability.[5] So we should expect to spend about time $\Theta(\log s)$ in the worst case when searching for one of s items in a moderately loaded hash table. So, interestingly, while many searches in hash tables take only constant time (if the lists are short), the logarithmic time we saw in search trees does make a comeback.

The thought of overloaded hash buckets we talked about just now brings up another important idea: when your hash table gets too overloaded (and thus too inefficient), it's usually a good idea to make the array larger. When expanding the array, of course, it will become necessary to rehash all the items to their new positions, as in general their current position (let's say $k \bmod m$) will not be the same as their new position ($k \bmod m'$), for the new array size m'. As we will see, this applies even more strongly for probing. As a rule of thumb, the load factor of your hash table should usually be kept under 1/2.

28.4.2 Probing

An alternative to the "chaining" idea is called *probing* or *open addressing*. Here, we only have our one array `a` of pairs, and no lists or buckets or subarrays. So when a collision occurs, we need to find a new location

[5] When $s \geq m \log(m)$, i.e., the hash table is overloaded by a factor $\alpha = \Omega(\log m)$, the same type of analysis shows that the largest load in any bucket will become $\Theta(\alpha)$ with high probability. In other words, the law of large numbers kicks in, and the buckets will be more evenly (over-)loaded.

to place the key. Say that we are trying to insert a key k into location $i = h(k)$, but $a[i]$ is already occupied by some other pair. So k needs to go somewhere else, into some position i', where we can find it later. The difference between different probing rules is in how they search for i'.

Linear Probing

Probably the simplest probing rule is *linear probing*: if position i is occupied, next try $i+1, i+2, i+3, \ldots$, until there is a free position. Linear probing is a very bad idea in practice, and in theory. Suppose that we have reached a state in which half the items are in positions $0, \ldots, m/2$, while the remaining positions are empty. Now, under our useful randomness assumption, the probability that the next key k belongs in a position $i \in \{0, \ldots, m/2\}$ is $\frac{1}{2}$. For all such position i, linear probing will put k in position $m/2+1$. In other words, with probability $\frac{1}{2}$, the next item will be placed at $m/2+1$, usually after a long linear probing search. So large clusters have a tendency to grow even larger.

More formally, if you look at the current clusters (sequences of 1 or more consecutive occupied array positions), and c_j is the size of cluster j, then the probability that cluster j will grow by 1 is c_j/m. Whenever you have quantities whose rate of growth (or probability of growth) is proportional to their current size (as is the case here), you have a "rich-get-richer" dynamic, which will lead to a heavy tail in the size distribution. In other words, we would expect — mathematically — some very large clusters, and this is indeed borne out in practice.[6] So linear probing is a bad idea.

Quadratic Probing and Double Hashing

Quadratic probing works as follows: When the key k is supposed to be mapped to $i = h(k)$, but position i is already occupied, you check the array positions $i+1, i+4, i+9, \ldots, i+j^2, \ldots$ in order. The advantage is that the sequences starting from i and $i-1$ are very different looking, so you won't get all that clustering from lots of keys mapped to different locations, but in the same block. For instance, suppose that key k is eventually stored at $i+9$, because $i+1$ and $i+4$ were also already in use. Now, key k' comes along, which belongs in $h(k') = i+1$. Position $i+1$ is already taken, but fortunately, k' now tries positions $i+2, i+5, i+10, \ldots$, so it won't run through the unsuccessful sequence $i+4, i+9$. The only clustering we could get will be from actual collisions, i.e., item pairs k, k' with $h(k) = h(k')$, and there will be a lot fewer of those. Quadratic probing is illustrated in Figure 28.3 below.

To deal with those types of collisions as well, we can use *Double Hashing*. Here, the sequence of positions explored for a key k depends not only on the position i where it originally belonged, but also on the actual key k itself, so that different keys, even if colliding under h, will be probing different sequences. More formally, in addition to h, we have a secondary hash function h'. Then, if $i = h(k)$ is taken, k next probes the positions $i + h'(k), i + 2h'(k), i + 3h'(k), \ldots$. This way, we spread out the probe positions much better across elements. If you do intend to implement hashing with probing, this would be the way to go.

28.4.3 Implementing Hash Tables with Probing

We just talked in depth about how to implement the `add` function: we compute $i = h(k)$. If $a[i]$ is unused, we place k there. Otherwise, we probe a sequence of positions, and place k (and the corresponding value) in the first empty position among them.

Of course, with probing, it is absolutely crucial to expand the hash table sufficiently proactively. For chaining, when the load factor gets high, we end up having to search through many longer lists. For probing, if we reach $\alpha \geq 1$, the table is full, and we simply cannot add any new elements.

To search for a key k (i.e., to implement `get`), we do basically the same thing. We start at $i = h(k)$. If the key k is stored at position i, we found it, and return the corresponding value. Otherwise, we follow the same probing sequence. As soon as we probe a position containing k, we have found it, and return the

[6] If it amuses you, you can try to write a quick simulator and verify this yourself, by putting 300000 elements into a hash table of 1000000 elements, then drawing the occupied array positions.

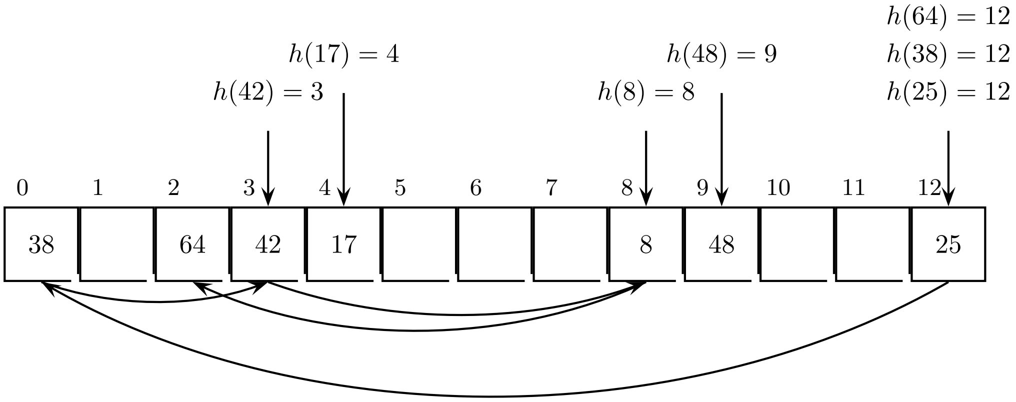


Figure 28.3: Quadratic probing illustrated with the hash function $h(k) = k \bmod 13$, for a hash table of size $m = 13$. When 38 is inserted, because $h(38) = 12$ is full, the next position that is probed is $12 + 1 \equiv 0 \pmod{13}$, which is available, so 38 is placed there. When 64 is inserted, because $h(38) = 12$ is full, the next position probed is $12 + 1 \equiv 0 \pmod{13}$, which is also full. After that, $12 + 4 \equiv 3 \pmod{13}$ is probed, but also full. Next is $12 + 9 \equiv 8 \pmod{13}$, which is also full. Finally, $12 + 16 \equiv 2 \pmod{13}$ is available, so 64 is placed there.

value. If in the probing sequence, we hit an empty position, that's a sign that k is not in the array, and we can terminate.

That leaves removing a key k. Of course, to remove k, we need to first find its position, the same way we just described for `get`. Then, we mark the position as unused, so it becomes available again. So far so good.

But there is now a big problem. Suppose that we remove a key k that was stored at i. There is another key k' with $h(k') = h(k)$ that was added at some point when position i was occupied. Let's say we stored it in $i + 1$. After we delete k from position i, we receive a `get` request for k'. We look in position i, and see that it's empty. So we infer that k' is not in the array. In other words, we have removed the link that let us continue probing for k', and k' cannot be found any more.

This is a serious problem, and in fact, removing items from a hash table is quite non-trivial when probing is used. One solution is to completely rearrange the hash table (e.g., rehash everything) after each removal, but this is clearly inefficient. Most textbooks (ours included) usually just ignore the question altogether, or write something like "Removal of items is quite challenging." One solution which is at least correct is to have a special marker "Deleted" for table cells that were once occupied, and then deleted. This is different from the $\perp$ marker used to denote entirely empty cells. This way, when we later do probing, we know to continue probing when hitting a "Deleted" cell.

The downside of this approach is that after a while, most cells in the table may be marked "Deleted", making search very slow (in particular, when the key searched for is not in the table). It's probably best to keep track how many elements have been deleted, and rehash the entire hash table every now and then when there have been enough deletions. But frankly, in practice, if you really implement hash tables, it's probably a better idea to just use chaining.

28.5 Bloom Filters

We have mentioned before that maps and sets are quite similar in nature. Remember that sets implement the following three functions on a set K of keys:

- `add (KeyType k)`: adds the key to the set.
- `remove (KeyType k)`: removes the key from the set.

- `bool contains (KeyType k)`: returns whether the set contains the particular key.

Sets can be considered a special case of maps, when we don't store any value (or a dummy value). When we use a hashtable to store a set, we still have to store the full key k in position $h(k)$; otherwise, when there is a collision, we wouldn't be able to answer correctly whether the set contains the particular key, because we wouldn't know whether the position $h(k)$ is occupied by k, or by another key k' with $h(k') = h(k)$. Storing the keys could take quite a lot of space. For instance, if keys are 100-character strings, each key will take up about 200 bytes of storage in our hashtable. In this section, we will develop a data structure called *Bloom Filters* which will store sets "approximately," in the sense that some queries will be answered incorrectly. In return, it will be much more space efficient.

In Bloom Filters, removal of keys is typically not implemented, so we will ignore it, too. Let's return to our reason for storing the key: to avoid disastrous effects of collisions. Suppose, though, that we were willing to put up with that risk. Then, we could make our hashtable an array of individual bits a. When we add the key k, we set $a[h(k)]$ to true. To check whether the key k is in the set, we return $a[h(k)]$.

Remark 28.1 As an aside, when you want to store an array of bits, an array of `bool` is not ideal. While a `bool` only encodes a single bit, it takes up more memory in your computer. The way to store a bit array is to declare an array of `int` and access the bits individually. You can do this by *masking*: to get the j^{th} bit of the number x, you compute `x & (1 << j)` (bitwise "and" with a string that has zeroes except in position j). To access the j^{th} bit overall, you access `a[j / 32] & (1 << (j % 32))`.

What's the problem with that? When there is a collision between k and k', and key k' has been put in the table (so $a[h(k')]$ has been set to `true`), we will return `true` also for the question of whether k is in the table. This is called a *false positive*: the data structure says "Yes," even though the correct answer is "No." Notice, however, that this approach gives no false negatives: when the data structure answers "No," the key really isn't in the set.

The way we defined it so far, the likelihood of false positives is quite high. To bring the likelihood of false positives down, what Bloom Filters do is mark not one but multiple positions for each key, and check those same positions. Specifically, Bloom Filters have j different hash functions $h_1, h_2, \ldots, h_j$. The two functions are now implemented as follows:

- To add a key k, we set $a[h_i(k)] = \text{true}$ for $i = 1, 2, \ldots, j$.
- To check whether key k is present, we check whether each of $a[h_i(k)]$ is true, for $i = 1, 2, \ldots, j$.

First, it's clear that we still don't get false negatives. Since we set all positions to `true` when adding a key, if one of them is `false`, then we cannot have added the key, so it's not there. But it's still possible that we have false positives: the different positions may have been set to `true` by multiple different keys, so when we check, they are all `true`.

Let's analyze how likely this is. To do so, as we discussed earlier, we'll assume that we have good hash functions, so that we can treat them as essentially random. Suppose that we are checking the position x. What's the probability that bit x has been set to `true`?

Let's first look at just one key k and one hash function h_i. The probability that $h_i(k) = x$ is $1/m$, so the probability that $h_i(k) \neq x$ is $1 - 1/m$. Therefore, the probability that all of the $h_i(k)$ are different from x is $(1 - 1/m)^j$.[7]

Now, if we have inserted s keys into our hash table, the probability that all s of them have completely missed position x (i.e., that $h_i(k) \neq x$ for all i and all k) is $((1 - 1/m)^j)^s = (1 - 1/m)^{js}$. Therefore, the probability that at least one key has already set position x to true is $1 - (1 - 1/m)^{js}$. To make this expression a bit easier to deal with, we can use the fact that for small values y, we have that $e^y \approx 1 + y$, and apply that with $y = -1/m$. Then, the previous probability is roughly $1 - e^{-js/m}$.

[7] Here, we are treating the hash functions as independent. That's a somewhat more subtle issue that researchers have been studying, but for our purposes, independence is a reasonable assumption, and dealing with how to generate independent random hash functions would be a bit too far afield for an intro class.

Therefore, the probability that all j positions that we are checking for a key k are set to `true` (even though we haven't added k to the set) is $(1 - e^{-js/m})^j$.

Let's assume that the load factor is $\alpha = s/m$. What's the optimum number of hash functions now? With a bit of calculus, we can arrive at $j = \frac{1}{\alpha} \cdot \ln(2)$, which we can plug into our expression to get a probability of

$$(1 - e^{-js/m})^j \;=\; (1 - e^{-j\alpha})^j \;=\; (1 - e^{-\ln(2)})^j \;=\; 2^{-\frac{1}{\alpha}\cdot\ln(2)}.$$

Next, we want to figure out how large we need to make our Bloom Filter in order to get a false positive probability of at most p, while accommodating at least s elements in our set. So we want to solve $2^{-\frac{m}{s}\cdot\ln(2)} \leq p$ for m. We first change this to $2^{\frac{m}{s}\cdot\ln(2)} \geq 1/p$, and then take logs on both sides and solve for m, which gives us that $m \geq \frac{s\ln(1/p)}{(\ln 2)^2} \approx 2s\ln(1/p)$ (because $(\ln 2)^2 \approx 0.48 \approx \frac{1}{2}$).

What does this mean? Suppose that you want a false positive rate of at most 0.1%, so $p = 1/1000$. Because $\ln(1000) \approx 7$, you get that your table needs to have size about $14s$. In other words, to get a false positive rate of 1/1000, you need to store about 14 bits per key. If you wanted a false positive rate of 1%, then about 9.2 bits per key would be enough. The number of hash functions you should be using is about $\ln(2) \approx 0.7$ divided by the load factor, so it would be about 10 hash functions for false positive rate 0.1%, and about 7 hash functions for false positive rate 1%. Both of these are values commonly used in practice — generally, the range is between 2–20 hash functions for practical Bloom Filters.

Bloom Filters have become quite a hot topic the last few years, in particular in the context of "Big Data" (e.g., Google's Big Table, some parts of Chrome, as well as in Bitcoin). Typically, you wouldn't use them to store a set in a critical application. Instead, you would use them as a simple pre-filter. If the Bloom Filter says "No," then you can also respond "No." When it says "Yes," you start a more expensive post-processing step to make sure you don't mess up. This works well when you have somewhat smaller sets, and most answers are actually "No."

Chapter 29

Log-Structured Merge Trees

[Note: this chapter covers material of about 0.5 lectures.]

In this chapter, we will look at another implementation of maps called *Log-Structured Merge Trees (LSMs).*[1] They were introduced in Google's now-famous "Big Table" paper, laying out an architecture for massive maps that are optimized for sequential interaction with hard disks. They are now implemented in a number of real-world database systems. The exact architecture motivations for this data structure are beyond what we can cover in this class, but you are welcome to search for more information online and read up on why certain design choices are made.

For our purposes, they serve the twin purposes of (1) showing you a neat, easy-to-implement, and perhaps unexpected implementation of maps with somewhat different running times for the operations, and (2) giving a good illustration of amortized analysis. The simple LSM implementation we consider here will implement `add` in amortized $O(\log n)$ per operation, and `get` in amortized $O((\log n)^2)$ per operation. (We will not implement `remove`, as that would break our nice amortized analysis.) Notice the somewhat counterintuitive fact that insertion is *faster* than lookups.

In our simple LSMs, we have a linked list of sorted arrays of sizes $1, 2, 4, 8, \ldots$. To be more precise, for each k, we will either have one sorted array of size exactly 2^k, or no sorted array of that size (and, say, a `NULL` pointer instead). These arrays are chained together in a linked list. Each array is sorted individually, but there is no sorting across arrays. Figure 29.1 shows an example of what you might get.

Because each array is sorted, we can perform Binary Search in it, which takes at most $\Theta(\log(2^k)) = \Theta(k)$ in the k^{th} array. Since we don't know which array to search in for a given key, in the worst case, we have to try each of the arrays (for k ranging from 0 to $\log_2 n$), giving us a time of $\sum_{k=0}^{\log n} \Theta(k) = \Theta((\log n)^2)$ for the `get` operation.

To add a new key, we create a new array of size 1 for it, and try to insert it as the first array ($k = 0$). Of course, this does not work if there is already an array of size 1. In that case, we merge those two arrays into a sorted array of size 2, and try to insert that at $k = 1$. If there is already an array of size 2, we again merge the two arrays of size 2 each into a new array of size 4, and try to insert that. And so on. In each step, if the k^{th} position is already taken, we merge the two current arrays of size 2^k (using the `merge` function (Algorithm 17.5) from MergeSort — see Chapter 17) into an array of size 2^{k+1} and continue with that one, replacing the array of size 2^k with `NULL`. For example, if we insert the key 3 into the structure of Figure 29.1, we will first produce the array $[3]$, and merge it with $[5]$, to produce $[3, 5]$. This is merged with $[2, 4]$, to produce $[2, 3, 4, 5]$, which is then put in position $k = 2$. The final state will look as shown in Figure 29.2:

29.1 Amortized Analysis of Insertion

First, notice that in the worst case (when all the positions in the linked list are already taken by arrays), we will be performing a sequence of merges ending with an array of size n. We recall from our analysis

[1] For once in this class, the word "log" does not refer to a logarithm, but to a list of items written down in order.

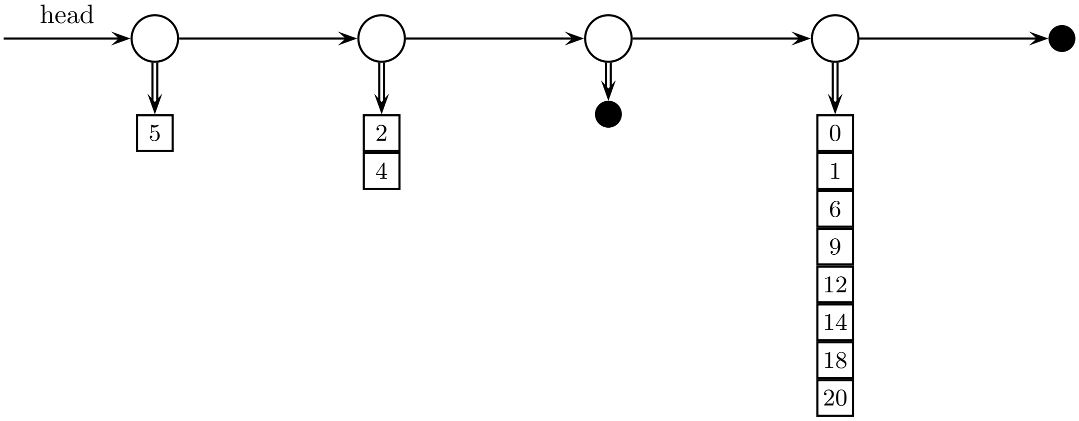


Figure 29.1: An LSM with 11 elements. Little black circles denote `NULL` pointers. Double lines denote pointers to arrays, while single lines are the overall linked list of arrays. We currently have arrays of sizes 1, 2, 8, but no array of size 4.

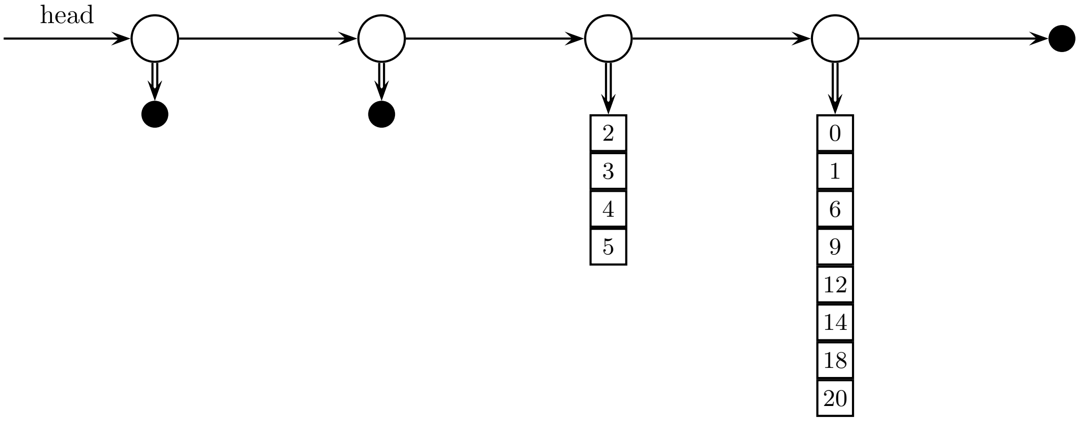


Figure 29.2: The list of arrays after inserting the key 3.

of MergeSort that the `merge` function takes linear time. Thus, the time to get an array of size n was $\Theta(1+2+4+\ldots+n) = \Theta(n)$. Thus, the worst-case time of the `add` function is $\Theta(n)$. But we also see that this worst case should not happen often. In fact, half the time, when we insert an element, the array in position 0 is empty, so we can just insert the element. Of the remaining cases, half the time (so a quarter total), the next position (the array of size 2) is empty. More generally, in a 2^{-k} fraction of the cases, the first $k-1$ arrays were taken, but the k^{th} array is available. (In this way, this data structure resembles the binary counter from Chapter 10.)

When the merging stops in the k^{th} array, we have an array of size 2^k, and have spent time $O(1)+O(2)+O(4)+\ldots+O(2^k) = O(2^k)$ to produce it. (Notice that this is where the data structure differs from the binary counter — there, when we finish in digit k, we only spent k time total.) So the total time for a sequence of n insertions (resulting in a data structure with n items in it) is

$$\sum_{k=0}^{\log_2 n} \frac{n}{2^k} \cdot O(2^k) \;=\; O(\sum_{k=0}^{\log_2 n} n) \;=\; O(n \log n).$$

Hence, the amortized cost per insertion is $O(\log n)$.

Now, to practice credit schemes, let's try that approach. Here, the idea is that costs are incurred any time an array is merged. We will give each element its own little credit account, so that it can pay for its share of the merge. When does an element need to pay? Every time it moves from some array k to the next one $k+1$. If each element that is being merged can chip in one dollar then, we get a linear number of dollars for a linear merge cost, so the merge is all paid for. So when we first put a new element into the structure, we should give it enough credit to pay for all its future moves.

But how many times will it move in the future? We don't know that at the time of insertion, so how much credit do we give the element? At this point, it is useful to remember that the whole "credit" idea is only a part of the analysis; the implementation of the data structure knows nothing about credits given to any elements. And at the point we are analyzing a sequence of insertions, we know how long the sequence is (say, n insertions, for a final size of n), and hence, we know how many times the element will be moved ($\log n$ times). So we endow the element with $\log n$ credits initially. Then, we maintain the invariant that each element sitting in the array at level k has $\log n - k$ credits left. Elements then use one of their credits for each merge, which maintains the invariant.

So in summary, we have shown in a second way that insertions into the list of arrays structure take $O(\log n)$ steps amortized in the worst case.

29.2 Some Remarks on Efficient Implementation

Here are a few thoughts on the implementation in real "big data" systems, which also motivate the name "Log-Structured Merge Trees". Each individual array is like a "log" of some sorted data. Typically, the smallest array (which in practical implementations will not have size 1, but a "small" size like 10^8 that fits in main memory easily) will be kept in main memory, and all the larger ones on disk. In fact, the small array in main memory is not kept in an array, but in an efficient data structure like a balanced search tree.

When the "small array" (or search tree) gets too big, it is written out into its own sorted file on disk. Thus, over time, more and more files accumulate. Every now and then, the system cleans up those files by merging files of the same size repeatedly, just as we discussed. This doesn't necessarily have to happen as soon as there are two files of the same size; as you saw in the analysis, the `get` function gets slower as there are more arrays/files, so we need to merge them before the number of files becomes too large, but the exact time does not matter too much.

The important thing is that the files on disk can be merged (and the new file written) with linear scans through them, making access much more effecient. On the other hand, searching in any one array/file only takes logarithmically many steps, and thus is also still fairly efficient.

At this point, let us also briefly revisit that funky $\log^2 n$ cost for the `get` operation. It arose basically because we have $\Theta(\log n)$ arrays, and in each of them, we perform a binary search costing essentially $\Theta(\log n)$. (In some of them, the cost is less, but there are enough arrays for which the cost is $\Theta(\log n)$.) If only there were a way to diagnose without binary search whether an element is in the array; then, we could just skip the arrays known not to contain the element, and binary search only in the right one. Do we know of any data structure that answers the query "Is this element present?"

In fact, we do. Sets are designed exactly for this purpose. Of course, since we are trying to build a map in the first place, assuming that we have a set implementation feels a bit like cheating. But notice that our set implementation does not have to be perfect. It's o.k. if it sometimes claims that an element is in an array when it really isn't. The only result will be that we do an unnecessary binary search, slowing us down a bit. But nothing breaks. So an approximate set implementation will be just fine. And we just saw how to do that: In Section 28.5, we learned about Bloom Filters, which are a lightweight use of hash functions to build an approximate set implementation. So we can use a Bloom Filter for each of the arrays/logs to save ourselves 99% of the binary searches, and drastically speed up the `get` operation. And this is one of the main reasons why Bloom Filters have seen so much interest recently.

Chapter 30

Splay Trees

[Note: this chapter covers material of about 1 lecture.]

Returning to Search Trees, we will now learn about a different way to keep them balanced, sort of. Splay Trees are interesting, in that they do not explicitly balance the tree or limit its height (like B trees, Red-Black Trees, or AVL Trees). Instead, they perform an operation called "splaying" ("to splay" means "to spread") with each `add`, `remove`, or `get` operation. The goal of splaying is to move the most recently accessed key to the root of the tree, by performing a sequence of rotations. In the process, almost as a side effect, the tree "tends to" get more balanced. This is not always guaranteed, but instead, what happens is that when one operation is really expensive, it tends to improve the tree a lot, and must have been preceded by a lot of cheaper operations. In other words, we will be able to establish a good *amortized* time of $O(\log n)$ per operation, even though the *worst-case* time is actually $\Theta(n)$.

30.1 Self-organizing Data Structures

Why would we set an explicit goal of moving the most recently accessed key to the root? It's so that if we search for the same key again in the near future, it will still be at (or near) the root, and thus found much faster than the "typical" time. The justification for doing this is that memory accesses are often "local:" if a particular item was recently accessed, it is much more likely that the same item will be accessed again in the near future. Similarly, if a memory location was recently accessed, it is much more likely that a *nearby* memory location will be accessed next. Why is this? Think about pieces of code like the following:

```
mymap[key].field1 = value1;
mymap[key].field2 = value2;
mymap[key].field3 = value3;

for (i = 0; i < n; i ++) a[i] = a[i]*2;
```

In the first three lines, we update three fields of the value stored in `mymap` associated with `key`. This is perfectly normal code, and it will access the same `key` three times. In the final line, we do what we do very often: go through an array one by one. So we will access consecutive memory locations.

Researchers have done extensive studies and found that normal programs have a lot of such locality. Thus, it makes sense to design data structures that make use of this locality to give better access times in practice than in the worst case. Data structures that get reorganized in response to *queries* (as opposed to just insertions or deletions) are called *self-organizing data structures*. There are a number of examples, and Splay Trees are among the most important.

Another classic example is a linked list in which the most recently accessed element is always brought to the head of the list next. One can show (the proof is not completely trivial, and often covered in graduate algorithms classes) that for any sequence of operations, following this procedure uses at most twice as many computation steps as the best one could do with a linked list if one were given the whole future sequence of element accesses in advance.[1] As such, this is a classic example of the analysis of *online algorithms*.

Perhaps the most important and prominent "data structure" for dealing with locality is the cache. The motivation for using a cache (which all computers nowadays do) is that really fast memory is expensive, while slower memory is much cheaper. So we would like to keep in that fast memory the data items that we need to access frequently, or in the near future. Of course, we don't know which items will be accessed in the future. But locality tells us that items that were accessed recently, and items that are close to ones that were accessed recently, are more likely to be accessed in the near future. There are a number of cache replacement strategies to exploit this general idea, and you can learn more about them in computer architecture classes.

30.2 The Splay Tree Operations

The implementations of the standard operations `add`, `remove` and `get` are exactly the standard implementations of Binary Search Trees. The only difference is that after the standard operation is executed, the `splay` operation (defined below) is called. Spelled out in more detail, they are as follows:

`get(key)`: Find the key by comparing it to the key in the current node, and going left or right (or finding it right there), depending on whether it was smaller, larger, or equal to the node's key. If they search terminates at a `NULL` pointer, the key was not in the tree. Let x be the last non-`NULL` node visited by the search (i.e., either the node containing the key, or the parent of the `NULL` node). After the search terminates, call `splay(x)`.

`insert(key,value)`: Search for the key, inserting it in the place where the (unsuccessful) search terminated. (Or update the value associated with the key in the existing node.) Either way, let x be the node now containing the given key. Call `splay(x)`.

`remove(key)`: Search for the key. If the key was found, swap it with the successor key in the tree. Let x be the leaf node that contains the key (after the swap), and p its parent. Delete x from the tree, and call `splay(p)`.

The `splay` operation aims to move the given node x to the root of the tree by a sequence of rotations. There are three cases which are slightly different based on which child of its parent x is (and whether there is a grandparent). In the following, we let x be the node to be moved to the root, p its parent, and g its grandparent, if any.

1. x is the left child of p, and p is the left child of g. (Similarly if they are both right children.)

   In this case, the way to get x into g's position is to first make a right rotation of p and g, and then a right rotation of x and p. This looks as shown in Figure 30.1.

   After the two rotations, p will have moved up two levels in the tree. We now recursively (or iteratively) continue with `splay(x)`, moving x further up.

   Notice the perhaps mildly counter-intuitive fact that we first rotated x's parent and grandparent, rather than x itself. We could have done the rotation differently, rotating x and p first. In that case, we would end up with x at the root, with g as its right child, and then p as the left child of g. The way we described it is the way things are typically done for Splay Trees.

2. x is the right child of p, and p is the left child of g. (Similarly if x is the left child of p and p is the right child of g.)

   In this case, the way to get x into g's position is to first make a left rotation of x and p, and then a right rotation of x and g. This looks as shown in Figure 30.2.

   As before, after the two rotations, p will have moved up two levels in the tree. We now recursively (or iteratively) continue with `splay(x)`, moving x further up.

[1] Of course, you are still much better off using a better `map` data structure than linked lists.

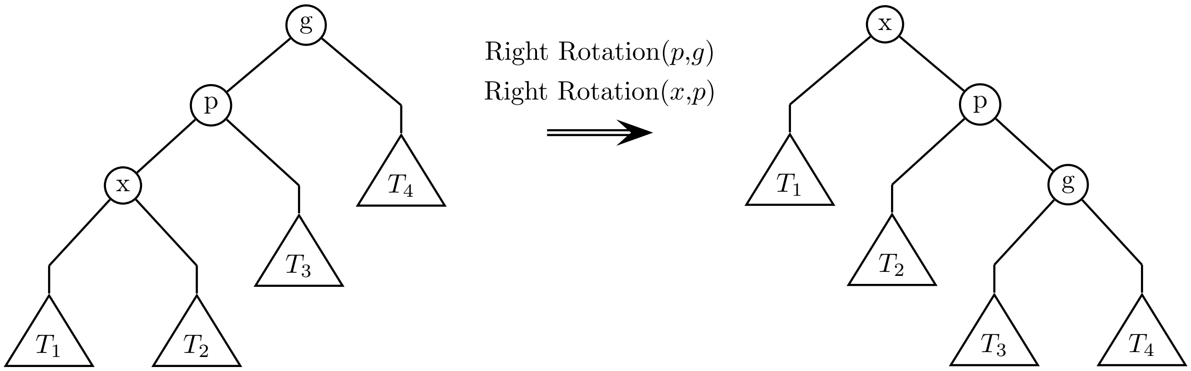


Figure 30.1: Case 1 of splaying: both x and p are left children.

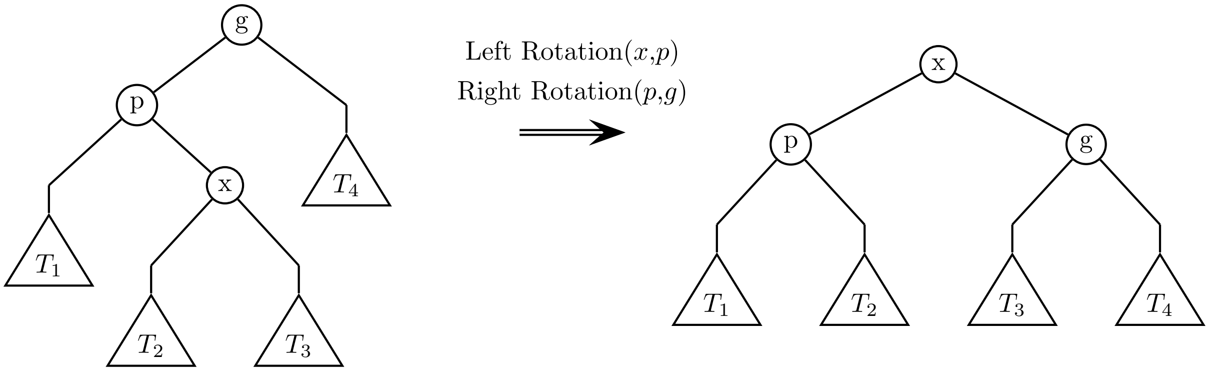


Figure 30.2: Case 2 of splaying: x is a right child of p, and p is a left child of g.

3. x's parent is the root of the tree.

   This is the easiest case: we simply rotate x with its parent, as follows:

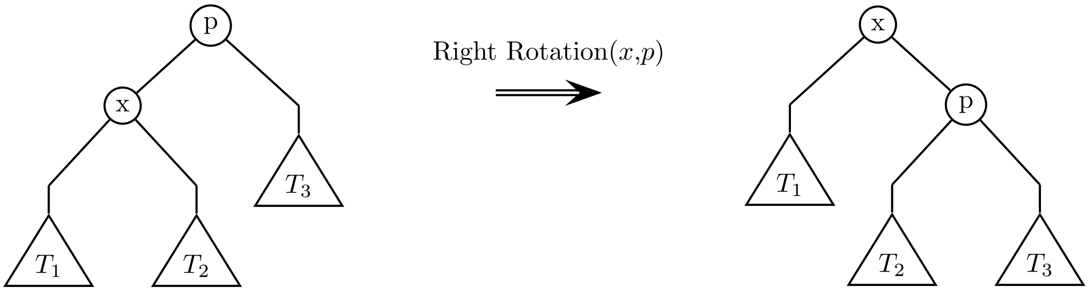


Figure 30.3: Case 3 of splaying: x's parent is the root.

In this case, no recursive or iterative calls are needed, as x has made it the root at the end.

Before moving on to an analysis of the amortized worst-case time per operation, let's think a bit about how we could make a Splay Tree really unbalanced and deep, ideally turning it into just a linked list. Consider inserting the keys in the order $1, 2, 3, \ldots, n$. Whenever key k is inserted, it is inserted as the right child of the root (which at that point contains the key $k - 1$), and then rotated into the root. This will eventually produce a linear structure with n at the root, a left child of $n - 1$, and so on, all the way down to 1. Then, searching for the key 1 will take n steps. However, notice that to get to this point, we had to perform n operations, each of which cost only $O(1)$, namely, insertions that were the right child of the root. We could have been a bit more careful in designing a bad case, so that the insertions were a bit more expensive. But as a general idea, producing an expensive operation requires a lot of preceding cheap operations.

30.3 An Example

To illustrate the splaying operation, consider the initial splay tree shown in Figure 30.4, and a `get(1)` operation:

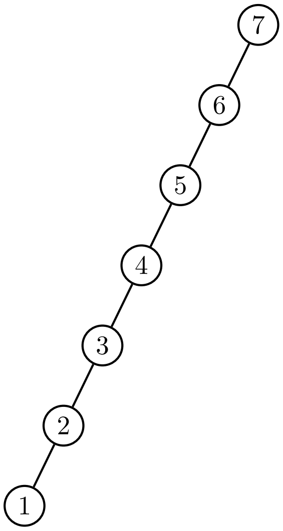


Figure 30.4: A degenerate example splay tree in which to look up key 1.

As we perform splay operations to move the key 1 up to the root, the tree will gradually look as shown in Figure 30.5.

Notice that while not perfectly balanced, this tree already looks much better than it did before. Next, in the resulting tree, we perform a `get(3)` operation, trying again to access the most expensive-to-access element. Then, the splay operations result in the sequence shown in Figure 30.6.

So after just two operations chosen to be as expensive as possible each, we arrive at a fairly nicely balanced search tree.

30.4 Analysis of the Amortized Running Time

For Splay Trees, the "simpler" type of analysis of just counting how many operations take how long will not work. We really do need the credit scheme here. To motivate the credit scheme we will use, we think a bit about what the really bad instances look like. They are characterized by being "mostly path-like," meaning that many nodes have almost as many nodes below them in the tree as their parents. In a nice and balanced binary tree, each node has roughly half as many descendants as its parent. In a pure path, each node has just one fewer descendant than its parent.

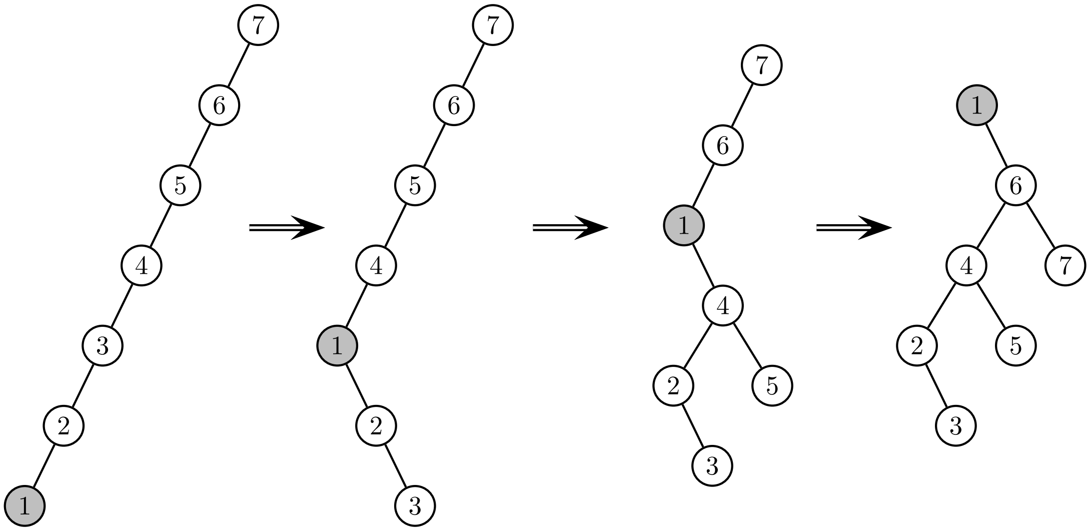


Figure 30.5: The tree after three splay steps, following a lookup of '1'.

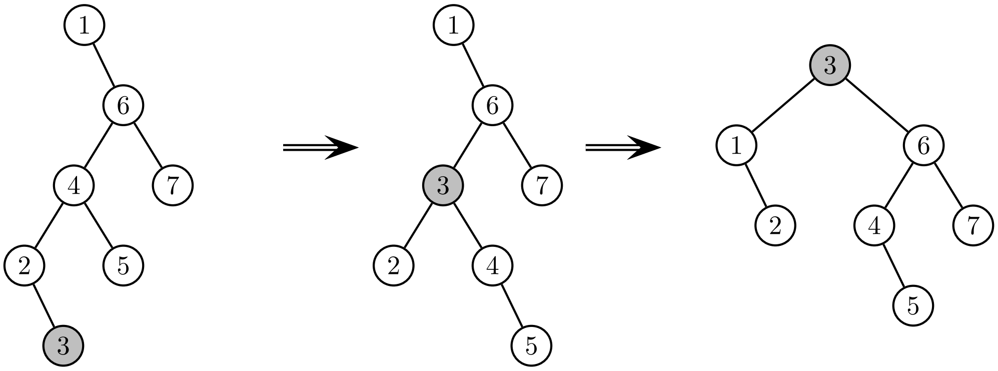


Figure 30.6: The tree after looking up the key '3', and splaying it up.

When the tree has become very path-like, this is a sign that in the future, there may be potentially very expensive $\Theta(n)$ operations coming. So in that case, we would like to have a lot of credits stored up in the tree to pay for those operations. On the other hand, if the tree is already very balanced, we don't so much mind having few credits, as there are no expensive operations to be feared for a while (until bad inputs have made the tree degenerate again).

There are of course many potential candidates of specific credit schemes that might capture this, and finding the right one that will work for a particular analysis is often an art form. For Splay Trees, here is one that works well. For each node v of the Splay Tree, let n_v be the total number of descendants that v has (i.e., children, grandchildren, and so on), including itself. We will maintain the invariant that at any time, each node v has exactly $c_v = \lfloor \log_2 n_v \rfloor$ credits.[2] (If at any point, a node has too many credits, we just throw them away.) So we need to think about what this means in terms of the cost of the operations, in terms of inserting credits into the system (where we have to pay extra), and in terms of using credits to pay for expensive operations.

First, let's think about the searching part. When the node v we terminate at is at height h in the tree, the cost of the searching is $\Theta(h)$, and then the splaying costs another $\Theta(h)$. This is true for each of `add`, `remove`, and `get`. We can lump the extra $\Theta(h)$ in with the cost for `splay`, which we analyze in detail below. This just shows that we can ignore the other costs.

The next thing we need to worry about is the fact that `add` and `remove` change the structure of the tree, and thus the values of n_v. This may change how many credits nodes need to have, and to maintain the credit invariant, we may have to pay extra with these operations. So let's look at these operations:

`remove:` When we remove a key, the only way the tree changes (until `splay` is called) is by taking away a node. Thus, for some nodes v, the value n_v decreases by one, while for the others, it stays exactly the same. Because the n_v values only decrease or stay the same, and all nodes had enough credits before, they certainly still have enough credits now. (In other words, `remove` operations really cannot hurt us.) We might have to throw away some credits, but that does not cost anything.

`add:` The situation is a bit more interesting when we add a key. Now, for some nodes v (all the ones on the path from the root to the new leaf), the number of descendants n_v has increased by one. For some of these nodes, this may also lead to an increase in the credit target $c_v = \lfloor \log_2 n_v \rfloor$, which means that we have to insert one more credit for each of those nodes v.

How many such nodes v could there be? First, notice that if you look at the sequence of n_v values as we traverse from the root to a leaf, this sequence will be strictly decreasing, starting from n, and ending at 1. An increase in $\lfloor \log_2 n_v \rfloor$ happens exactly for nodes v for which $n_v = 2^k - 1$ for some k. But there can be at most $\log n$ possible values of k (namely, $0, 1, \ldots, \lfloor \log_2 n \rfloor$) for which this is true, and for each such k, there is at most one node on the path having $n_v = 2^k - 1$, because the n_v decrease strictly. Thus, we have to insert at most a total of $\log_2 n$ credits, and can ascribe a cost of $O(\log n)$ to the `add` operation.

Looking at this argument, you can see a little bit why we chose $\log n_v$ rather than n_v or $\sqrt{n_v}$ as our credit target function. Otherwise, we might have to insert too many credits in the `add` step.

This leaves us with the `splay` operation, which is the most interesting/challenging part of the analysis. We will consider any one of the `splay` steps, where a node x gets moved to the position formerly occupied by its grandparent g. Let c_v be the credits of the nodes before this `splay` operation, and c'_v the credits after the operation. What we will show is that the cost of one splay step, together with necessary credit rearrangements, can be paid for by spending some credits, with an additional cost of at most $3(c'_x - c_x)$ to be paid on top. (Here, c'_x is the credit after just one double-rotation.)

Now, when we sum up all of those extra costs, the $-c_x$ term in the next step always cancels out the c'_x from the previous step. (This is called "telescoping series.") Thus, we are left with an extra payment of $c_x^{\text{final}} - c_x$. At the end, the credit of the root is $\lfloor \log_2 n \rfloor$, while initially, $c_x = 0$. Thus, the total extra payment (beyond credit usage) is at most $O(\log n)$. Taking all of this together, once we have shown the claimed accounting for just one double-rotation, we have shown an upper bound of amortized $O(\log n)$ for all operations.

30.4.1 The Left-Left Case

So now, let's analyze what happens in the double-rotation steps. First, let's look at Figure 30.1. Let n_x, n_p, n_g be the number of descendants of the three nodes before the double-rotation, and n'_x, n'_p, n'_g after the double rotation. Similarly, let $c_x = \lfloor \log_2 n_x \rfloor, c'_x = \lfloor \log_2 n'_x \rfloor$, and the same for p, g.

[2] Why $\log_2 n_v$, and not n_v, or $\sqrt{n_v}$, or something else? Because when the inventors tried it, the log worked, and the others didn't. As we said before, the invention of credit schemes is a bit of an art form, or trial-and-error process. Though you will see a bit of evidence for this choice later in the analysis.

What do we know about the new values? Because x becomes the root, we know that $n'_x = n_g$, so $c'_x = c_g$. The total number of credits we have available before the double-rotation is $c_x + c_p + c_g$, and after the double-rotation, we need to have $c'_x + c'_p + c'_g$ credits. So we need to add

$$(c'_x + c'_p + c'_g) - (c_x + c_p + c_g) \;=\; c'_p + c'_g - (c_x + c_p) \;\leq\; 2 \cdot (c'_x - c_x), \tag{30.1}$$

because of the three nodes, x is at the root after the double-rotation, and at the bottom before. We now distinguish two cases:

1. If $c'_x > c_x$, then as discussed above, we are willing to incur an extra cost of $3(c'_x - c_x)$, of which $2(c'_x - c_x)$ pays for the credit insertion (and rearrangement), while the remaining $c'_x - c_x \geq 1$ is enough to pay for the constant cost of the actual double-rotation.

   This is the case in which we cannot say too much about whether the tree gets better or worse.

2. The more interesting case is that $c'_x = c_x$. In that case, because $c'_x = c_g \geq c_p \geq c_x$, we get that $c_x = c_p = c_g = c'_x$, while $c'_g, c'_p \leq c'_x$.

   In fact, we will see next that $c'_g < c'_x$. The reason is that x and its entire subtree (T_1, T_2) in the original tree, and g and its entire subtree in the final tree (T_3, T_4) are disjoint (as you can see in Figure 30.1). Thus, $n_x + n'_g \leq n'_x$. But because $\lfloor \log_2 n_x \rfloor = \lfloor \log_2 n'_x \rfloor$, we get that $n_x > \frac{1}{2} n'_x$, so $n'_g < \frac{1}{2} n'_x$, meaning that $c'_g < c'_x$. Thus, we get that

   $$(c'_p + c'_g) - (c_x + c_p) \;=\; (c'_p + c'_g) - (c'_x + c'_x) \;<\; (c'_x + c'_x) - (c'_x + c'_x) \;\leq\; 0.$$

   Thus, by performing the double-rotation, we actually free up at least one credit (without having to pay anything extra), which is enough to pay for the double-rotation right there. This is the case where the tree structurally becomes better: when $c'_x = c_x$, that tends to imply that most of g's initial subtree was actually below x, so the tree was unbalanced before, leaning heavily to x's side. The double-rotation fixes this partially, moving g further down and x further up.

30.4.2 The Right-Left Case

Next, we consider the case of Figure 30.2. We use the same notation as before. The calculation is exactly the same as before up to Equation (30.1), and the first case of the subsequent case distinction (where $c'_x > c_x$) is also exactly the same.

The only slightly different argument happens in the case when $c'_x = c_x$. We still have $c'_x = c_g \geq c_p \geq c_x$ and $c'_g, c'_p \leq c'_x$ in that case. Now, because p and g are the roots of disjoint subtrees of x (after the rotations), we get that $n'_x = 1 + n'_g + n'_p$, which means that at least one of n'_p, n'_g must be strictly smaller than $n'_x/2$. For that node (let's say p), $c'_p \leq c'_x - 1$. Then, we again get that

$$(c'_p + c'_g) - (c_x + c_p) \;<\; (c'_x + c'_x) - (c'_x + c'_x) \;\leq\; 0,$$

so the double-rotation again frees up at least one credit to pay for the operations. Again, this is the case where the tree structure improves.

30.4.3 Child of the Root

Finally, we are left with the easiest case: when x's parent was the root (see Figure 30.3). Now, the credits before the rotation are $c_x + c_p$, and after the rotation, they are $c'_x + c'_p$, where $c'_x = c_p$. The difference is

$$(c'_x + c'_p) - (c_x + c_p) \;=\; c'_p - c_x \;\leq c'_x - c_x.$$

So, similar to in the first case of each of the double-rotations discussed above, by inserting $3(c'_x - c_x) + 1$ credits, we can cover all the required credit changes, and still have at least 1 credit left for the actual constant-time rotation operation. (This applies even in the case $c'_x = c_x$, because of the added 1.[3])

[3] Why didn't we do this "add 1" trick for the other cases? Because there, we might have to add 1 for each step of the `splay`

operation, which would have cost too much. Here, we are at the root, so the 1 only needs to be added once, which we can afford for the analysis.

Chapter 31

Skip Lists

[Note: this chapter covers material of about 1 lecture.]

For another implementation of maps, we return to some of our early days, where we simply used an array or linked list to store the key-value pairs. At the time, we said that there was no reason to keep a linked list sorted, because to find the right position, we couldn't take shortcuts like jumping to the middle of the list, which is what we need to do for Binary Search. Once we have found the right position, insertion and removal are constant time, which is an advantage of linked lists over arrays.

While standard linked lists don't have any shortcuts to jump to the middle of the list or other places, there is no reason why we shouldn't be able to introduce such shortcuts. For instance, from the first position, maybe we want a shortcut to the middle, and to the elements roughly $1/4, 1/8, \ldots$ of the way. From the middle, maybe we'd want shortcuts to the elements $3/4, 5/8, 9/16, \ldots$ of the way. And so on. That way, we could basically simulate Binary Search in a linked list, reaping the benefits of the fast insertion and removal of linked lists while also getting $O(\log n)$ lookup time. This is the basic idea behind Skip Lists.

31.1 The Basics of a Skip List

In reality, to keep the structure a bit simpler, we don't have the shortcuts from 1 to $n/2^k$, but rather to multiples of 2^k, for each k. We can think of building $\log n$ linked lists, each representing a faster and faster lane of the "linked list highway." The slowest "lane" is the original sorted linked list. The next faster "lane" skips every other element. The next faster one then skips every other element of that lane. And so forth, until we get to the superhighway, which only contains the first and last element.

To simplify the presentation and implementation a bit, one typically inserts at the beginning of the list an element with key $-\infty$ (which is used as the head), and at the end an element with key ∞, used as the tail. This avoids having to deal with a number of checks for NULL, but otherwise does not really affect the implementation.

First, notice that in terms of implementation, to have all these shortcut links, each node now has an array of next pointers, rather than a single one. So the Node data structure changes as follows:

```
template <class KeyType, class ValueType>
struct Node {
  KeyType key;
  ValueType value;
  Node **next;  // array of next pointers
}
```

A diagram of what a Skip List would look like is given in Figure 31.1.

Now let's look for the key '17'. We start at the list element with $-\infty$, and see if the "fastest" link gets us somewhere useful. Because $\infty > 17$, it takes us too far, so we try the next lower link. That gets us to 21,

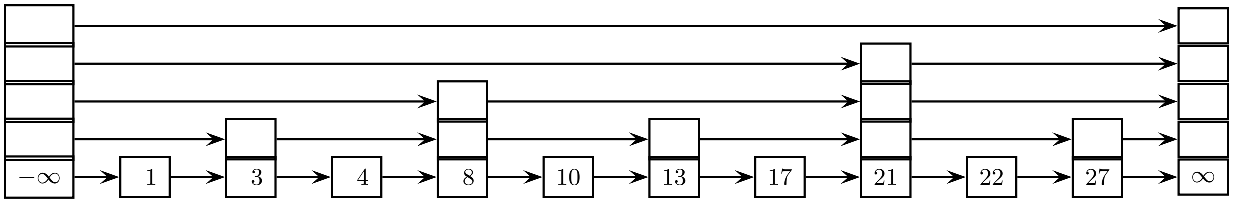


Figure 31.1: A skip list with 10 “real” keys and $-\infty, \infty$ keys.

which is still greater than 17, so we try the next lower one. That gets us to 8, which is less than 17, so we follow it. From 8, we try the next link at the same level, but that again takes us too far (21), so we go one level lower, and get to 13, which is less than 17, so we take it. Its next link at this level again takes us to 21, so we go down a level, and find 17. Generally, the search procedure looks as follows:

```
int level = maxlevel; // maxlevel is the number of links per node
curr[level] = head;
while (level > 0) {
   curr[level-1] = curr[level];
   level --;
   while (curr[level]->next[level]->key <= key)
         curr[level] = curr[level]->next[level];
}
```

We didn't really have to maintain a whole array of `curr` pointers, but it is not really extra work, and useful for insertions or deletions. The idea of the search procedure is to start with the “fastest” link, and follow it for as long as we can while staying smaller than (or equal to) the key. Then, we go down a level, and continue from there. When this procedure terminates, we have the useful property that for all levels, `curr[level]->key <= key < curr[level]->next[level]->key`. This means that we have found the element in `curr[0]`, or if we failed to find it, we know exactly where to insert it.

31.2 Analysis of Basic Skip Lists

Let's analyze how long the search procedure takes, and also how much extra memory we spend on all these extra pointers. (Remember that for Search Trees and Hash Tables, we used only a linear amount of space in the number of items in the map.)

First, the total number of levels traversed is equal to `maxlevel`. Typically, we will set `maxlevel` to $\log n$, or a reasonable upper bound on that value. At each level, we take at most one step. Why is that? Each step at level k moves 2^k positions forward in the list. If we took two steps, we would move forward $2 \cdot 2^k = 2^{k+1}$ steps. But that amount would have been available at level $k+1$. We switched down to level k, which means that stepping forward 2^{k+1} positions would have gotten us to a key that is too large. So the procedure performs at most one step (and thus constant work) at each level, for a total of $\Theta(\log n)$.

How much memory is used? It depends a bit on how careful we are. If we reserve room for $\log n$ links for every one of the n nodes, then the total memory is $\Theta(n \log n)$. But if we vary the amount of memory allocated in each node to reflect the actual number of links it has, we see that half the nodes have only one link, and a quarter of the nodes have two links, and 1/8 of the nodes have three links, and so on. Generally, a 2^{-k} fraction has k links. So the total number of links is $\sum_{k=1}^{\log n} k \cdot n/2^k$. We have computed this sum before, in Section 10.3, where we found out that it was $\Theta(n)$. So if we are careful with our implementation, the memory is in fact linear.

You may have noticed that so far, we have said very little about how to implement `add` or `remove`, besides saying that having all of the `curr[level]` is quite useful to implement them. If you look at Figure 31.1, you might get a little worried. What happens if we insert the key '2'? We would be able to do this quickly, but what happens to all of our nice pointers? The key '3' is now supposed to have an extra pointer, whereas '4' is not supposed to have one, and so on. We would need to update the pointer structure of *every* element of the linked list, meaning that the running time is $\Theta(n)$ for insertions, and similarly for removals.

For the "perfectly clean" version of Skip Lists we have seen so far, that is unavoidable: we couldn't hope to maintain all those perfectly arranged links without doing significant updating each time. Thus, as presented so far, Skip Lists would really only be useful if insertions and removals are exceedingly rare (say, they only happen during initialization), while we spend a lot of time searching for keys. If instead, we also want fast insertions and removals, we have to give up on the perfection of the Skip List structure, and settle for something that only closely resembles it. There are different ways to implement such Skip Lists, but the easiest is to use randomization, and we will discuss it next.

31.3 Randomized Skip Lists

If you squint at Figure 31.1 (rather than looking carefully), you may notice that the key property is really that the fraction of nodes that have k pointers be roughly 2^{-k}. We don't need them to be perfectly spaced, so long as there are no massive gaps, and they don't completely "bunch up" (e.g., all long-range pointers are in the left half of the linked list). In order to maintain such a property without a lot of effort, randomization is a very useful tool.

To illustrate, imagine that you are organizing an event, for which you give out blue wristbands. You would like to have roughly half of the visitors wear blue wristbands, and the other half no wristbands. The problem is that people arrive and depart as they please. If you were a control freak, you could constantly check all the exits, and as soon as you see two people with blue wristbands leave, you go into the room and ask someone else to put on a blue wristband to balance this out. That would be a lot of work.

If you only need to get it roughly right, then you could just flip a coin at the time of arrival for each person, to decide if they will get a wristband. This will not get the proportions perfectly right, but approximately. Of course, if the departures were correlated with whether a person has a wristband (e.g., people with wristbands are somehow unhappy and leave early), then this would not work. But if the wristband is uncorrelated with departure time, you would expect that the two groups would leave at roughly the same rate, so your populations would not deviate too far from half and half.

We can extend this idea further. If you want half of the blue wristband people to also have a green wristband, you can just flip a second coin for every blue wristband wearer. And if you want half of the blue-green people to also have a yellow wristband, you flip another coin. More generally, what we can do is keep flipping coins until we see the first tails. The number of flips that this took will be the number of wristbands that the person gets. Notice that the probability of seeing exactly k heads in a row, followed by tails, is $2^{-(k+1)}$. So that's the fraction of people with k wristbands. (This distribution of how many flips it took until we got tails is called the *geometric distribution.*)

We can directly apply this idea to Skip Lists. Whenever a new key is inserted, we generate its number of links according to the geometric distribution.[1] So far, we have described the geometric distribution with parameter $\frac{1}{2}$, but we could instead use any fixed parameter $p \in (0, 1)$: in our wristband example, we could give a p fraction of the guests a blue wristband, and a p fraction of those also a green wristband, and so on. That would correspond to the geometric distribution with parameter $1 - p$. (The parameter of a geometric distribution is the probability of *stopping* in each step, not of continuing.)

We call the number k (the number of heads we saw, i.e., the number of edges a node gets minus one) its *level.* Thus, in Figure 31.1, the keys 1 and 4 are at level 0 (having one edge), the key 3 is at level 1, and 21 is at level 3. Because our search procedure produces a whole array `curr` of predecessors, we can insert the new key as a new `next[i]` pointer for the right nodes at the right levels, and similarly give it the correct `next[i]` pointers. These are just standard insertions into a linked list.

[1] We could cap this distribution at some value we never want to exceed.

Any time an algorithm or data structure uses randomness, there is a chance that things will go wrong, e.g., we may end up putting all the nodes at the same level, thus producing just a standard linked list. While it is *possible* for this to happen, it is also exceedingly unlikely. We will show that, assuming that removals of keys happen independently of the number of links that a key has, finding a key still takes $O(\log n)$ steps in expectation. (In fact, one can show that this happens with high probability, not just on average, but we won't do that here.)

To analyze how many steps it takes to find the correct location for a key (to look up, remove, or insert), we consider the sequence of steps taken. Starting at the highest level L, at each point, we take the highest level step that is applicable. The level we can take will decrease over time, until we find the target key. To analyze the number of steps, we will look at the sequence *in reverse*. That is, we start at the target key, and gradually walk to the left until we hit the head of the Skip List. Whenever we reach a node at level k, we continue by using level-k edges until we reach a node of even higher level k', at which point we switch to those edges, and so on. Notice that this monotone increase of levels is possible: if we have a node at level k, and follow its level-k edge to the left, it must reach — by definition — another node at level k or higher.

Before analyzing the number of steps this takes, let's verify that the search path we produce backwards in this way is the same as what we produce searching for the key from the head in the standard search. Whenever we switch to level k for the first time in the backwards path, that means that this particular node is the rightmost level-k node to the left of the target. Why? Because otherwise, an earlier level-k node would have been available, and we would have used that node's level-k edge. So the points at which we switch up to level k are exactly the level-k predecessors of the target. But we saw earlier that those are exactly the nodes at which the real search switches *down* to the next level. So all those nodes are the same. In between level switches, in both searches, we follow the edges at the corresponding level, so overall, the search path is the same for both.

Next, let's figure out how many steps the search spends at each level, going from 0 to the maximum level L. Whenever the search reaches a node v in the list via a level-k edge, v must be at level at least k. The probability that its next coin flip came up heads, promoting it to level $k+1$ or higher, is p. Hence, in each step, the probability of going up a level is p. The expected number of steps to go up one level is therefore the expectation of a geometric random variable with parameter p. (Here, p is indeed the parameter that our quest to make it up a level ends; earlier, the $1-p$ was the parameter that a given node stops adding more links.) The expectation of a geometric random variable with parameter p is $1/p$. You might either just remember this fact, or we can quickly derive it here. Let T be the expected number of steps until we see heads. With probability p, this is equal to 1, and with probability $1-p$, the first coin flip was tails, so we have spent one flip and now have to start from scratch. This gives us that $T = p \cdot 1 + (1-p) \cdot (1+T)$. We can solve this as $pT = p + (1-p)$, which gives us $T = 1/p$.

Now, the total number of steps is the sum of steps to go from each level to the next. Because expectations are linear, we get that the expected number of steps in a search is $\sum_{k=0}^{L} \frac{1}{1-p} = \frac{L}{1-p}$. Then, once we are at the highest level, what's the maximum number of steps we have to take? Because in expectation, only $n/2^L$ nodes have made it to level L, this is the number of steps we have to take in addition. In particular, if we choose $L \geq \log_2 n$ (which we should), this extra number of steps is constant. Then, the total amount of time for the search is $O(\frac{L}{1-p} + 1) = O(\log n)$, so long as p is a constant. ($p = \frac{1}{2}$ is a perfectly fine choice here.)

So in summary, we get that the expected time for `get` is $O(\log n)$ in expectation. Importantly, notice that the expectation here is taken over the random choices that the data structure makes (which level to put nodes at), not over random inputs. That is, we do not need to assume anything about keys being random. Randomness is a very important part of computing. It often allows us to come up with much simpler and more elegant algorithms and data structures than if we had to make all structures deterministic. You will encounter some more examples in later classes, and most likely in the rest of your career as a computer scientist.

31.4 Comparison of Map Implementations

By now, we have seen four general-purpose implementations of maps: Balanced Search Trees (Red-Black or 2-3), Hash Tables, Splay Trees, and Skip Lists. (We've also seen Lists of Arrays, but those were mostly for illustrating concepts of amortized analysis. And Tries are specific to keys that are strings.) Let's compare a bit the guarantees that these different implementations give you, and where they have their advantages or disadvantages.

Balanced Trees: Gives you an ironclad worst-case guarantee of $O(\log n)$ for all operations. In addition, makes it very easy in linear time to iterate over all the elements in sorted order.

Hash Tables: Typical works in $O(1)$ time per operation. However, this depends on assuming that keys are mapped to random locations, or that the hash function ensures pseudo-random destinations. By Pigeon Hole Principle, there are inputs on which Hash Tables take $\Omega(n)$ per operation.

Splay Trees: Guarantees a worst-case amortized time of $O(\log n)$ per operation. Individual operations may take time $\Omega(n)$. Like Balanced Trees, allow easy iterating over all elements in sorted order. In addition, exploit locality, meaning that repeat accesses to recently accessed elements are $O(1)$.

Skip Lists: In expectation, all operations take $O(\log n)$, though with unlucky (very unlikely) choices of levels, they could take $\Omega(n)$. Fairly simple to implement, and allows iterating in sorted order in $O(n)$.

So which one should you use? It obviously depends. Do you need ironclad per-operation guarantees, or are a few slower operations acceptable? How worried are you about worst cases? Do you need the ability to iterate over all keys in order? How much locality do you expect?

In practice, most people use Hash Tables, as the $O(1)$ is really fast. But as you can see from the comparison, there are reasons to prefer the others in certain situations. If you can articulate the pros and cons for your *specific* application, that will be half the battle.

Chapter 32

Tries and Suffix Trees

[Note: this chapter covers material of about 1 lecture.]

We have now seen two good data structures for maps: Hashtables and Balanced Search Trees. As a general purpose technique, these work great. But in some cases, we know that our keys are of a specific type, and by using this information, we can design even more efficient maps. A case for which this has been explored in particular is when the keys are strings.

String keys are very frequent, and often part of large data sets. Consider the following applications:

Search Engines: You have a large text corpus (all web pages), and are looking for the occurrence of certain substrings in it. While you are allowed to spend a bit of time pre-processing, the lookup should be fast.

Text Editors: People often write long text documents, and one of the functionalities that is needed is to find (and maybe replace) occurrences of certain words in the text. Again, the `find` function should run nearly instantaneously, while the pre-processing may take a while (and will typically happen as the user is writing the text).

DNA and Protein Sequences: A lot of the important work in biology, and computational biology specifically, is concerned with finding strings in long strings. The long string may be either a genome sequence (written as millions of characters from the set $\{A, C, G, T\}$) or a protein sequence (written over a 20-letter alphabet).

Substrings in a genome sequence may be indicative of genomic predisposition for certain diseases. Common substrings between two genomes may tell us something about common ancestors of two species; or in the case of humans, if we look at several patients who developed the same type of cancer, and they have a substring that few other people have, we may investigate whether that subsequence codes for this particular cancer.

So the ability to find occurrences of a given key (in this context often called *pattern string*) in a given longer string is really essential; there are also quite a few related problems that we discuss later.

Let's start by thinking about balanced search trees as a solution. If we put n strings in a search tree as keys, and each string has length $\Theta(\ell)$, then in order to find a given key, we have to search over $\Theta(\log n)$ levels of the tree. So far, we have pretended that comparisons between keys take time $O(1)$, but when we are thinking about strings of length ℓ, we may have to revisit this assumption. It's more realistic that comparing two strings will take time $\Theta(\ell)$, so the total time for searching in a binary search tree with strings is $\Theta(\ell \log n)$. Our hope is that we can do better, and that's exactly what we'll explore in the next sections.

32.1 Tries

The name *trie* derives from the middle letters of the word "retrieval," because it is a data structure designed for use in the context of text retrieval. The inventor pronounced it like "tree," but this led to sufficiently much confusion that the accepted pronunciation nowadays is as in "try."

To explain how a trie works, let S be a set of strings we wish to store. The trie is organized as a tree, but not necessarily a binary one. Each edge of the tree is labeled by a letter. First, consider the first letter of each word in S, i.e., the set $L_0 = \{s[0] \mid s \in S\}$. We have exactly one edge out of the root for each letter in L_0. Each endpoint of an edge is labeled with the same letter $x \in L_0$ used to label the edge.

Now, for each letter $x \in L_0$, let $L_1^x = \{s[1] \mid s \in S, s[0] = x\}$ be the set of all letters that appear in the second position of some string in S that starts with the letter x. The node labeled x has one outgoing edge for each element of L_1^x, labeled with the corresponding letter. For each such edge, say, with label y, the endpoint is labeled xy.

More generally, suppose that we have a node labeled with a string s' which is a prefix of length k of a string $s \in S$; that is, s' consists of the first k characters of s. Then, for each character x such that there is a string in S whose prefix is the concatenation $s' \circ x$, we have an edge out of the node labeled s' to a node labeled $s' \circ x$, and the edge is labeled x.

When a string s in a node is actually in the set S, then we store that information, along with the corresponding value, at the node corresponding to s.

If this sounded a bit strange and abstract, an example will likely illustrate it. Figure 32.1 shows the trie for the words "heap", "hear", "hell", "help", "he", "in", "ink", "irk", "she".

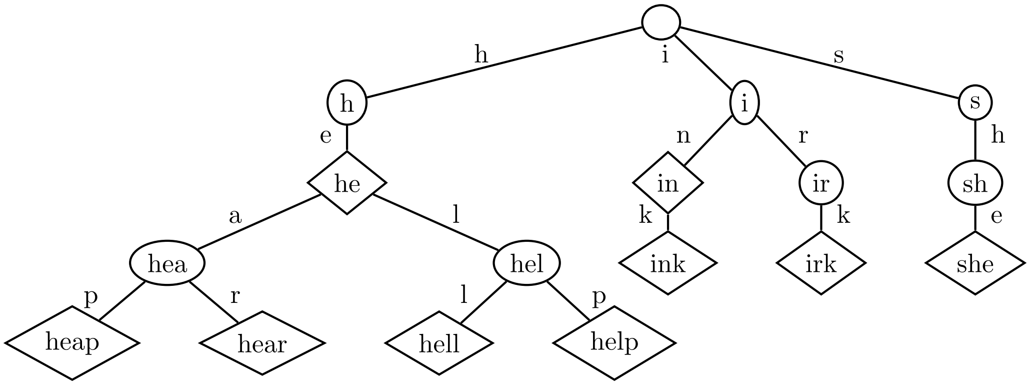


Figure 32.1: The trie for the given words. Oval nodes are just internal. Diamond-shaped nodes have key-value pairs associated with them. Reading the edge labels along any path gives you exactly the string for the node.

How to search in a trie should be pretty obvious. You start at the root. For the first step, you compare the first character of your key string t with the edges leaving the root. If there's no match, t is not in the map. If there is, you follow that edge, and continue (iteratively or recursively) from the new root node with the next character from t. When you have followed edges for all characters of t, you have reached the node corresponding to t.

Since each comparison of a single character takes only $\Theta(1)$ time, the entire search will take $\Theta(|t|)$, which is pretty much optimal, since surely, to search for a word, you must at least look at the entire word once.

Building a trie should also be pretty clear: you insert the words one by one, following existing edges for each word s as long as you can, and branching off when you have to.

Notice that a trie does not have to have edges for each possible character in each position. It only needs edges for those that actually occur in at least one string in that position, following these specific letters. Thus, the size of the trie is at most the sum of lengths of all the words in the string.

32.1.1 An Application: Routing and IP Addresses

When you contact another computer, such as a server for Google or another web site, or the host machine for an online multi-player game you are playing, how does your computer know where to send its requests, and how does the server know where to send the relevant data? The answer is that in order to communicate on the Internet, each computer must have an *IP address*, which is sort of its ID.[1]

In IP v4, still in use a lot today, this address comprises 32 bits. (IP v6 has longer addresses.) These 32 bits are typically written down as $x.y.z.w$, where each of the four numbers x, y, z, w has 8 bits and is thus between 0 and 255. The first 8 bits (x) define a subnetwork, roughly corresponding to a major provider or similar entity. Later numbers get more and more specific, and w is typically specific to your computer.

When you want to send a request to a host, say, `google.com`, you first need an IP address. To do so, your computer knows (often via its own subnetwork) about a domain name server (DNS), whose job it is to provide a mapping from names to IP addresses. So your computer first contacts its DNS, who tells it that the IP address is 64.233.180.175. (Google has a whole range of IP addresses, but this is one of them.) Then, your computer will try to send a message to 64.233.180.175.

You do not typically have a direct connection to the host you are trying to reach, so instead, your request is routed along a number of routers on the Internet. You can think of each router as a specialized piece of hardware whose job it is to figure out where to take the next step on a (hopefully relatively short) path to the destination.

Since routers are usually connected to a large number of other routers and machines, the router needs to know which of the many other routers to pass on a message with destination 64.233.180.175. This is where we need to implement a map: the key is the IP address, and the value is the outgoing link along which to route the message. This needs to run extremely fast, as routers have huge numbers of messages to deal with; in fact, most of these operations are implemented in hardware, rather than software, to make them faster.

The IP address of the destination can be considered a string of 4 characters, where each "character" is chosen among the 256 choices $0, \ldots, 255$. This view suggests that the right data structure (and the one used in practice) should be a trie. For instance, since all addresses starting with 64.233.180 belong to Google, the router doesn't need to look at the last character at all. In fact, it may be able to decide where to route the message even just looking at the 64 at the beginning, perhaps because all addresses starting with 64 are in the same area (of the Internet).

This idea of a tree structure in which some parts of the tree are much more finely subdivided (because you need more specific information) while others are not is actually very common all through computer science. For instance, many of the most important data structures for storing graphics objects (like quad-trees, oct-trees, KD-trees) are based on this idea, in some form or other. Tries are a good and easy way to learn about this idea first.

32.1.2 Path Compression

If you look back at our trie in Figure 32.1, you will notice that it is a little bit wasteful. We generate lots of intermediate nodes even though they have only one outgoing edge. We could save some memory, and perhaps also traversal time, by compressing these paths into a single edge. Of course, the downside will be that we may later have to split such an edge back up, when we are trying to insert a new word whose path branches off the current path at some point. But that may be worth it. In Figure 32.2, we have drawn the trie for the same set of words, but now in compressed form.

Notice that by definition, each internal node either contains a key itself, or it must have at least two outgoing edges; otherwise, we would have pruned this node away.

32.2 Suffix Trees

Now that you have understood tries and compressed tries, *suffix trees* will be pretty easy. Given a string s of length n, a suffix of s starting at i is the substring $s[i : n-1]$, i.e., it consists of the last characters of s

[1] "IP" stands for "Internet Protocol."

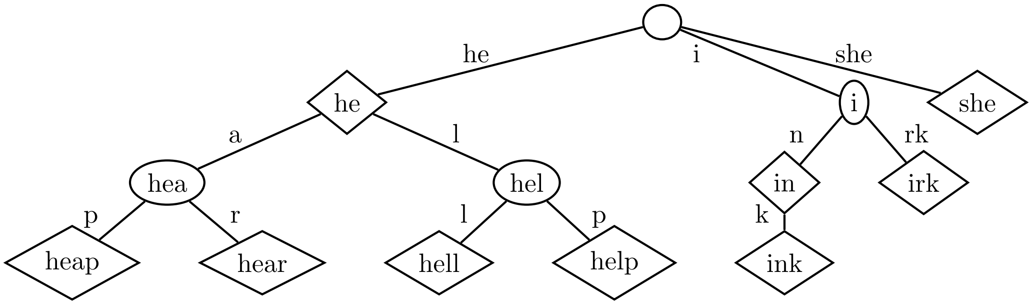


Figure 32.2: The compressed trie for the same words as above.

from position i until the end. The suffix starting at 0 is simply the entire string s. Now, the suffix tree of s is simply the compressed trie for all suffixes of s. In order to be a bit formal, we can also define it as follows: a suffix tree for the n-character string s is:

1. A tree with n leaves, labeled $0, \ldots, n-1$ (or equivalently, the n substrings $s[i : n-1]$ for all i).
2. Each non-leaf node has at least two children.
3. Each edge is labeled with a substring of s.
4. If e, e' are edges out of the same node, then the labels of e and e' must start with different characters.
5. For any root-leaf path (ending in the leaf labeled i), the concatenation of the labels on the path is equal to $s[i : n-1]$.

Before discussing in more detail why suffix trees are so useful, let's see an example, by drawing the suffix tree for the string MISSISSIPPI. It is a standard convention to always add a special character (for instance, '\$') at the end of the string; this helps ensure that we can draw the tree as described above. The outcome is shown in Figure 32.3.

To understand a bit better about how we constructed this suffix tree, first think of inserting each leaf directly under the root. That would almost work, except it violates the fourth property. So all suffixes starting with 'I' must share the same first step. Since the 'I' is followed by different letters, we have to have an edge labeled just 'I'. From there, the next character could be a 'P', an 'S', or a '\$'. If the next character is a 'P', we actually know all the next characters (there is only a single suffix starting with 'IP'), so we can just put the leaf right there. Similarly for the '\$'. If the next letter is an 'S', then there are two options, but they share the 'SSI' next, so we can label the edge with that entire substring. We can continue in this way.

We constructed the tree by hand here, and if you take the algorithm we probably would have used, it will likely be $\Theta(n^2)$. The really cool thing is that there is an algorithm — Ukkonen's algorithm — which constructs a suffix tree of s in time $\Theta(n)$. Also, notice that because we are compressing paths, the suffix tree always has $O(n)$ nodes: it has n leaves, and each internal node has degree at least 2. If we didn't do path compression, then you can see that the string "abcde. . .xyz" would have $\Omega(n^2)$ nodes, which means we can't construct it in time $O(n)$.

Ok, so why are suffix trees so useful that textbooks on strings devote hundreds of pages to them? Let's look at a few applications, and how to solve them easily:

- Find a pattern string t in s: Here, we can simply modify our original search algorithm for tries to use the multiple characters in tries. It therefore takes $O(m)$, and the total time — including building the suffix tree — is $O(n + m)$, i.e., just the time to look at each string once.

  Compare this to the "obvious" (brute force) algorithm for string search. You'd try each of $(n - m)$ positions as a start position, and then compare the m characters of t one by one with the corresponding

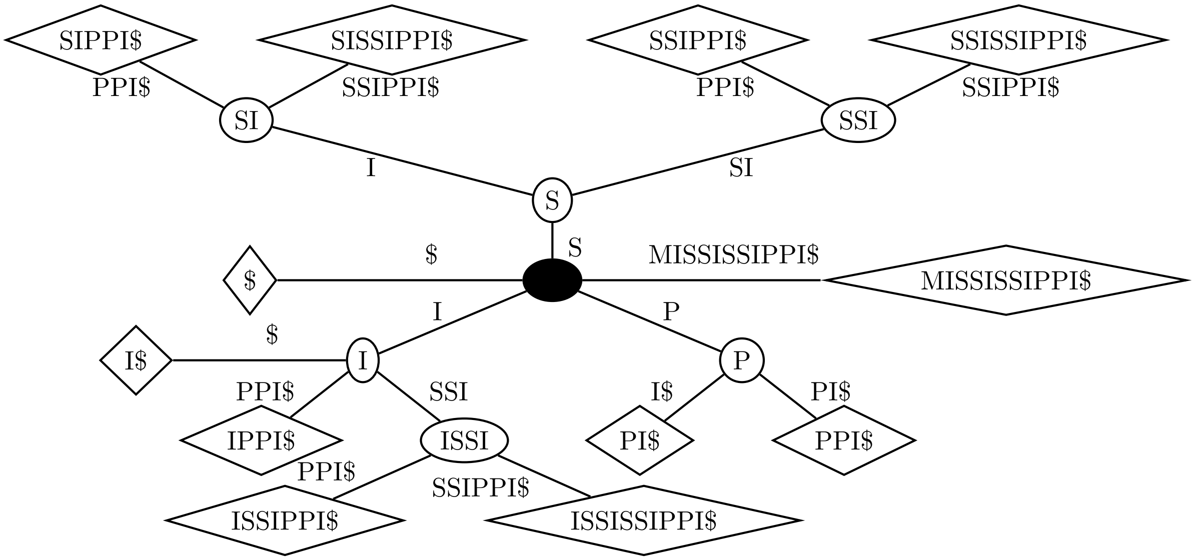


Figure 32.3: The suffix tree for MISSISSIPPI$. The root is shown in black, and in the middle of the diagram to maintain legibility.

characters of s. This would take $\Theta(m(n-m)) = \Theta(mn)$, i.e., the product of the string lengths. Going to $\Theta(n+m)$ is a huge improvement.

There are two classic algorithm for this string matching problem that run in time $O(n+m)$: Boyer-Moore and Knuth-Morris-Pratt. Traditionally, algorithms classes would devote significant time to these two algorithms, which are not exactly trivial (though not very hard, either). Once you know that you can build a suffix tree in linear time (which is not trivial, either), you don't need the specialized algorithms any more.

And of course, string matching is a really important task, as evidenced by the examples we looked at in the introduction to this chapter.

- Count the number of times that t occurs in s: This is very similar to the previous problem, but we would normally have to modify the Boyer-Moore or Knuth-Morris-Pratt algorithms in significant ways. Now, instead, we can find another very simple algorithm. Follow the suffix tree path for t to reach some node v. Now simply count the number of leaves in the subtree rooted at v. That's the number of times t occurs in s.

- Find the longest common substring of s and t, i.e., the longest string w that occurs both in s and in t. Again, this problem has applications in computational biology, where you may want to look for the longest genetic overlap between two species or individuals. (Typically, you'd be happy with approximate matches, i.e., a few mismatched characters would be ok. But this example still illustrates the importance of these types of problems.)

  There are several solutions based on suffix trees. One of the easiest ones is to build a suffix tree for the string $s\#t\$$, where both '#' and '$' are new special characters. For each node of the suffix tree, mark whether it corresponds to a string that occurs in s, in t, or in both. (This can be done with Ukkonen's algorithm.) Now, just look for the deepest node that is labeled with both s and t — this can be done easily in linear time by searching through all the nodes of the tree.

  So we get a linear time algorithm for this problem, which initially looks like even $O(nm)$ would be quite ambitious.

There are quite a few more similar applications of suffix trees. The nice thing is how they unify so many different string matching algorithms: practically all of the fastest algorithms can instead be implemented by building a suffix tree, then doing something really quite easy. So knowing about suffix trees can be an incredibly helpful tool for designing efficient algorithms.

Chapter 33

Design Patterns

[Note: this chapter covers material of about 0.5 lectures.]

Throughout the semester, as you have learned about object-oriented design, we have emphasized that its main benefit is the ability to cleanly reuse code later, by separating out functionalities and putting them where they belong, and by isolating interfaces (*what* functions a class provides) from implementations (*how* they are performed). Along the way, in addition to inheritance as a natural extension mechanism, we have also seen more interesting ways in which objects from different classes can interact, each taking specific roles and responsibilities within a larger task, and interacting with each other in pre-specified ways.

Perhaps the two most non-trivial ones were the *Iterator* paradigm (discussed in Chapter 27) and the interaction between slots and signals in Qt in Chapter 19. These are examples of *design patterns*: ways in which objects can interact with each other that occur with at least some regularity, and which — when considered in the design of your class structure — will make it easier later to extend and reuse your code. Design patterns are one of many important aspects of the broad field of Software Engineering, and you will learn about them a little more, and Software Engineering a lot more, whenever you take CSCI 201 and, more importantly, the Software Engineering class CSCI 310. For now, to show you a little more how to think about classes and their interactions, we will discuss a few common design patterns. Some of them are obvious, some are pretty clever, some are just workarounds for weaknesses in the C++ or Java programming languages. There are many more than we discuss here — this is just to give you a little taste. For the student interested in learning more, we recommend the classic book on "Design Patterns" by Gamma, Helm, Johnson, and Vlissides, as well as many online sources.

33.1 Observer

The *observer* paradigm is something that we already saw in action when we talked about Qt, and how slots in one class correspond to signals in another. More generally, the observer design pattern applies when you have one object that has some state (which may change, e.g., because the user enters values), and other objects which need to be kept informed about any changes in the first object, e.g., because they display the content of the object.

The classic example is something like a table of data as the first object, and several ways of displaying it. For instance, you may have a table of student grades, and display it as a histogram, pie chart, and in table format. How many and which kinds of displays are open will depend on the user's actions, so you can't predict ahead of time how many observers the object will have. In fact, you shouldn't hardwire too much what possible displays there are: perhaps in version 3 of your software, you'll also want to introduce 3-D charts and a display with a function plot. At that point, you'd like to simply say that there are now additional ways of displaying the data, without having to change the class for the actual table.

The way to separate out the functionality of storing the data and displaying it, and allow the easy creation of new ways of displaying, is by providing particular interfaces:

1. The class for your data table has a way for observers to register themselves, such as `void Table::register (Observer *obs)`. When this is called, the table adds `obs` to a list of registered observers.
2. The class for the displays has a way to be notified of changes, such as `void Observer::notify (Table *tab)`. Whenever anything changes in the table, it calls the `notify` function for all its observers, passing itself as an argument. Then, the observers will know how to update the way they display (or otherwise interact with) the data from the table. Of course, the `Table` class will have to provide an interface for the observer to actually get the data.

When this design pattern is followed, you can later add different ways to display the data, without ever changing a line of code in the `Table` class. You simply write a new class inheriting from `Observer`, and implementing the `notify` function accurately.

This paradigm is also called *publish-subscribe*: one object provides an interface for subscribing to updates, and the other has an interface for being notified of updates. When you subscribe to a mailing list that informs you of the upcoming concerts of your favorite band, you follow the same paradigm: the band doesn't need to know ahead of time who will be the subscribers: all it does is provide a way to put yourself on the mailing list. In turn, you provide an interface by giving an e-mail address, which is a standardized way for the band to update you on its status changes. The way you process those status updates (buy concert tickets, visit the web site, tell your friends, be disappointed because you can't go, etc.) is then up to you.

33.2 Visitor

Suppose that you have written a parser for mathematical formulas (as you did, for instance, on a homework). The best way to represent a parsed formula is via its *parse tree*. For instance, the parse tree for the formula "$2 * (x + 4)$" would be represented as in Figure 33.1.

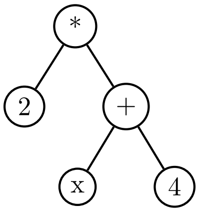


Figure 33.1: The parse tree for "$2 * (x + 4)$".

Once you have this tree representation, a lot of things can be done quite easily using DFS tree traversal (pre-order, in-order, or post-order), such as:

- Printing the expression in a nicely formatted way.
- Evaluating the expression at a particular value of x (which in turn could be used to plot the function).
- Substituting a different expression for x, e.g., $x = y^2 + 3$.

You can likely come up with quite a few others.

The question is where the functions `string prettyPrint ()`, `double evaluate (double x)` or `ParseTree *substitute (char variableName, ParseTree *expressionToSubstitute)` should reside. Clearly, the most natural fit is as member function of the class `ParseTree`. But that doesn't feel quite right. For starters, the tree should mostly store the data, but it's not really its job to print it. More severely, what if another user wants to print the tree in a different format? By now, you know that you wouldn't want that person to have to go in and change your code for printing.

The only other apparent solution is to give global access of all relevant internals in your ParseTree to the outside world, i.e., make almost everything global. But that is bad coding style, as it reveals too much about the implementation, and doesn't allow you to later rename variables or similar things.

Upon some reflection, this conundrum looks quite similar to what we solved by using the *Iterator* design pattern for container classes (Chapter 27). It allowed us to access the elements of the container in a structured and limited fashion. But upon further reflection, an iterator is not quite enough here. Iterators simply spit out the elements of the container in some pre-defined order. When we want to pretty-print the expression, we need to see elements in an in-order traversal. When we want to evaluate it, we need to traverse the tree post-order, and more importantly, know about the structure. And when substituting an expression, we actually need to change the tree structure.

So whatever we come up with needs to allow more access than an iterator. The *Visitor* paradigm provides a particular interface with which other objects can access the contents of nodes of the tree, such as following the left/right subtrees, or learning (and possibly replacing) what is stored at a node. This is like a compromise: the contents aren't really global, but rather, the way in which other objects can see what's in the tree and interact with it is carefully planned out.

One can conform to these interfaces and at the same time write a large number of different visitors which perform different functions. Importantly, one can later change what exactly visitors do, or write new ones, without changing the underlying ParseTree class.

33.3 Factory

Suppose that you are writing an office suite, which will comprise a text editor, spread sheet, database, graphics program, and a few others. You will want many of the user interface components to be the same, both because you want the look-and-feel to be integrated for your users, and because you want to reuse code and save some work. One of the dialogs that you'll surely want is to create a new document. Since this may entail quite a bit (asking the user, generating a default file, opening it, etc.), you may intend to put all of this into an object in charge of creating the document. The problem is that the generateDocument function may have to return different types of documents, based on what you are currently creating: a new TextDocument, SpreadsheetDocument, DatabaseDocument or GraphicsDocument. So there will definitely be differences between the classes you use for generating a document, yet perhaps 90% will be the same.

The solution is to use the *Factory* design pattern. You define an abstract class Document, from which all your types of document will inherit. You also define an abstract class Factory, which implements all of the common functions, and has a virtual function Document *generateDocument (). Then, you can inherit from Factory to produce new classes TextFactory, SpreadsheetFactory, DatabaseFactory, and GraphicsFactory. Each overwrites the virtual function generateDocument () to return the specific type of document you want in this instance. For instance, you can now write the following code:

```
Factory *factory = new TextFactory ();
Document *doc = factory->generateDocument ();
```

This will ensure that doc contains (or rather, points to) a TextDocument object afterwards. As you can see, you will need to change very little in order to make this generate SpreadsheetDocument objects instead.

So to summarize, the idea of the *Factory* design pattern is that you have an abstract Factory class, whose job it is to produce objects that your program needs. By inheriting from this abstract class, you produce different concrete factories, each of which produce the objects of the specific type you need. All of the specific types are subtypes of the abstract type that your abstract factory produces. This way, the factories can reuse a lot of code, even though they produce different types of objects. It also makes the code very extensible: if later on, you decide that your office suite will have a sound processing component, you can just define one new class of Factory, and leave almost everything else the same.

33.4 Adapter/Wrapper

Suppose that you were working on a project with a friend, and needed a Hashtable programmed from scratch. You asked your friend to have a function `insert(const KeyType & key, const ValueType & value)`, but unfortunately, he wasn't paying attention, and instead called the function `add (const Pair<KeyType, ValueType> & toAdd)`. In your code, you have a lot of references to `insert`, but your friend has also used his class extensively already, and has a lot of references to `add`. What to do?

Because there are many references to `add` in your friend's code, you can't just change the name of the function. And if you've written enough code (or there are other people on the team who were also relying on this specification), you shouldn't just replace all occurrences. A simple and obvious solution is to use an *adapter*: a class that provides the user interface you wanted, and internally just translates it to what you have. Here is how you could do that:

```
class HashtableAdapter : private FriendsHashtable {
   // use private/protected inheritance or member element of type FriendsHashtable

  void insert (const KeyType & key, const ValueType & value)
     { this->add (Pair (key, value)); }

  // identical copies of other functions
};
```

By doing this, you avoid having to rewrite everything, and can reuse your friend's code as though it were using the interface you actually need.

Remember that you saw the word *adapter* before? When we talked about C++ STL classes implementing standard data structures (Chapter 13), we mentioned that it has a few adapter classes, `Queue` and `Stack`. They are called that because they just put a different interface on the `vector` class. Instead of writing `v.insert (v.size(),item)`, you can write `v.push (item)`. So in that sense, STL considers `queue` and `stack` simply adapters put on top of the `vector` class. Of course, from a data structures viewpoint, they are very different, but in terms of implementation, they follow the *Adapter* design pattern.