Survivor's Manual for CIS 1210

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This is a course about Algorithms and Data Structures using the JAVA programming language. We introduce the basic concepts about complexity of an algorithm and methods on how to compute the running time of algorithms. Then, we describe data structures like stacks, queues, maps, trees, and graphs, and we construct efficient algorithms based on these representations. The course builds upon existing implementations of basic data structures in JAVA and extends them for the structures like trees, studying the performance of operations on such structures, and their efficiency when used in real-world applications. A large project introducing students to the challenges of software engineering concludes the course.

— *Description of CIS 1210 in course catalog*

Contents

§1 Introduction

§1.1 How to Use This Guide

Like the prerequisites state, you must have taken both CIS 1200 and CIS 1600 before taking this course. This course combines the programming aspect of CIS 1200 with the conceptual knowledge of CIS 1600. Most of this guide will go over the conceptual aspect and break it down (especially the math heavy parts) in Layman's terms and a relatable, informal tone. As for the coding aspect for homeworks, go do that on your own once you understand the conceptual knowledge.

For each section of content, I will have the long version and then the summary "TL;DR" version. The long version is meant for when you want to inform yourself of the material ahead of time, or the content is new for you and things don't fully make sense yet. The summary version is meant for review or to get the core ideas in the midst of the sea of content.

Be on the look out for these boxes:

Warning 1.1. These usually will contain an important caveat regarding the concept, like an oversight you can make if you're not careful. Pay attention to these when I use it.

Review 1.2. Concepts very often build off one another in this course with some from CIS 1600 and CIS 1200. So I will put these boxes when I think it would be wise to review a concept if you forgot it.

Advice 1.3 — Additional clues on how to use a particular concept, especially for homework problems or on an exam.

Lemma 1.4

Lemmas are generally claims we have to prove in order to make progress and help us better understand why a concept may work.

Example 1.5

A problem (generally one from class or recitation) that will illustrate the concept in action.

§1.2 What is an algorithm?

Imagine you need to get something done according to some rules. Like you have a physical dictionary and need to look up a word, say the word "computer." You know it's in alphabetical order. That's an essential aspect to making a process to finding your word. Maybe you flip to a random page and see words beginning with 'd.' You know you're too far to the right because 'd' comes after 'c.' So you need to start flipping to the left. But now, you end up at words starting with 'b,' which comes before 'c.' So you're too far to the left. From there, you can slowly but surely narrow down where the word is in the dictionary until you find it. This is an algorithm at play: you use a set rules to accomplish a task.

But efficiency is a key component. An inefficient algorithm that works with a lot of data could literally take decades to complete. What good is that if you have to wait that long for the result when there could be a much faster algorithm? But also, what good is an algorithm if your computer doesn't have enough memory for it to execute?

§2 GCD

Here, we'll get a first taste of what algorithm efficiency is all about. First, we define the GCD or greatest common divisor of two integers. The GCD of two integers a and b is the largest positive integer d such that d divides both a and b.

Review 2.1. Recall from CIS 1600 that an integer m divides n if and only if $n = km$ for some integer k.

§2.1 Naive Algorithm

In general, a "naive algorithm" is usually a simple algorithm that will accomplish the task. However, it doesn't leverage any shortcuts to make the work efficient. When working with larger numbers, this can be a massive problem.

We know the gcd of a and b is essentially the same as the gcd of b and a. So we can without loss of generality, assume $a \geq b$ (because if $a < b$, we can just swap a and b without issue). We know anything that divides some integer n cannot be greater than n. So it follows that any common divisor of a and b cannot be greater than b.

So the naive way is to check each integer from 1 to b, see which ones divide both a and b, and output the largest that divides both.

This gets the job done with something like $\gcd(160, 120)$ without taking too long, since the numbers are small enough. But what about $\gcd(33554435, 33554432)$? Or when working with even bigger numbers? Is there a more efficient way?

§2.2 Euclid's Algorithm and Its Proof

The notation $x \pmod y$ is essentially saying, the remainder when x is divided by y.

Lemma 2.2 (Euclid's Algorithm)

For positive integers a and b such that $a \geq b$, $\gcd(a, b) = \gcd(b, a \mod b)$

Proof. Let's prove this.

We know mod is basically remainder. Think about division back in elementary school where we have a quotient and remainder. So we can write $a = bq + r$ for integers q and r with $0 \leq r < b$. Essentially, q and r are the quotient and remainder, respectively, when a is divided by b.

Take a look at the equation $a = bq + r$. It's pretty clear intuitively that if some integer divides both b and r, then it must divide a. So any common divisor of b and r also divides a. You can prove it mathematically using the formal definition of divisibility. Anyway, that result we got means that $\gcd(b, r)$ (which is a common divisor of b and r) divides both a and b. So $\gcd(b, r) \leq \gcd(a, b)$ because $\gcd(b, r)$ is a common divisor of a and b, but it is at most the literal largest common divisor of a and b.

We can also rearrange the equation to $a - bq = r$, where it becomes clear that any common divisor of a and b also divides r. Do the same logic to get $\gcd(a, b) \leq \gcd(b, r)$.

The only way for $\gcd(b, r) \leq \gcd(a, b)$ and $\gcd(a, b) \leq \gcd(b, r)$ to hold simultaneously is if they're equal. So $\gcd(a, b) = \gcd(b, r)$, which completes the proof. □

So basically, we can keep using this lemma to keep changing the gcd into something else, until it becomes a base case.

I'll just tell you that the base cases are $\gcd(x, 0) = x$ for any positive integer x and $\gcd(x, 1) = 1$ for any positive integer x.

It's unexpected that you would come up with this entire proof from scratch, having never seen it before. But do understand the steps because you can apply a similar process to similar problems. The idea was to consider the two gcds separately and extract information on what relevant variables they divided.

§2.3 How fast is Euclid's Algorithm?

First, we have to prove a lemma:

Lemma 2.3

If $r \equiv a \pmod b$ with $a \geq b$, then $r < \frac{a}{2}$.

The intuition is that when you divide a by b, the remainder is not going to be that big compared to b. And since $b \leq a$, it is going to be even smaller compared to a. Like imagine if $a = 94$ and $b = 10$, in which $r = 4$. So r is smaller than b, which in turn is smaller than a. But want to see the math in action? I've got that covered for you.

Proof. We have 2 cases to consider:
Case 1: $a \geq 2b$
Remember that r is the remainder when a is divided by b. So since r is a remainder, $r < b$ or $b > r$. Then, $a \geq 2b > 2r \implies a > 2r \implies r < \frac{a}{2}$.
Case 2: $a < 2b$
We know $a \geq b$, so $b \leq a < 2b$. Clearly, these bounds mean that when a is divided by b, the quotient will be 1. So $a = b + r$, which rearranges to $r = a - b$. But $a < 2b$ or $-b < -\frac{a}{2}$, meaning that $r = a - b < a - \frac{a}{2} = \frac{a}{2} \implies r < \frac{a}{2}$. □

So applying the Euclidean algorithm once on a and b means we transform $\gcd(a, b)$ to $\gcd(b, r)$, where $r \equiv a \pmod b$. By the lemma, $r < \frac{a}{2}$. Applying it a second time means we transform $\gcd(b, r)$ to $\gcd(r, s)$, where $s \equiv b \pmod r$. By the lemma, $s < \frac{b}{2}$. So after applying Euclid's algorithm twice, we went from $\gcd(a, b)$ to $\gcd(r, s)$, where $r < \frac{a}{2}$ and $s < \frac{b}{2}$. Essentially, we halved both inputs in 2 steps.

§2.4 Comparing Runtimes

Definition 2.4 (Log function (informal definition))**.** For an integer n, the log function $\log_2(n)$ denotes the number of times you half to halve n until you get a number less than 2.

For example, $\log_2(16) = 4$ because $16 \to 8 \to 4 \to 2 \to 1$, so we have to halve 16 a total of 4 times until it becomes less than 2.

This function is extremely important throughout the course, but we'll get to that later.

Anyway, we end once we hit a base case. We could get lucky in the process and at some point, it becomes computing $\gcd(c, 0)$ for some integer c. If this happens, we're done because as stated earlier, $\gcd(c, 0) = c$. But what if we're not so lucky and have to keep halving? Well, even in the worst case scenario where we have to keep halving, if we halve the inputs enough times, it will eventually get to less than 2, which means it gets to 1, and that's a base case.

How many times do we have to do this? Well, we do 2 steps to halve both inputs. By the definition of the log, this means we have to do this a total of $2\lg(b)$ times, worst case scenario.

Now, let's just use a concrete example just to show how much of a difference the two algorithms make.

Suppose we needed to calculate $\gcd(33554435, 33554432)$. In the naive way, we'd have to test all the way up to 33554432 for both inputs, so that's $2 \cdot 33554432 \approx 67$ million times. Yikes! And that only gets worse the higher the numbers are. I'll tell you that $\log(33554432) = 25$. So we only need to do at most $2 \cdot 25 = 50$ steps with Euclid's, because the inputs halve each time, which allow us to more quickly reach a base case. Much better!

We say that Euclid's algorithm is $O(\log b)$, while the bad method is $O(b)$. What does the big O mean? We'll get to that later.

§2.5 Summary

We used some divisibility tricks in order to prove a useful lemma about gcd and then make a recursive algorithm out of it. We also saw how much of a difference we can make in the number of steps we have to do by implementing a more efficient algorithm.

§3 Crash Course to Runtime and Its Notation

Runtime will be a concept that will follow you around this course from start to finish. Essentially, with an algorithm and input of size n, we define a function $T(n)$ that models the algorithm's runtime in terms of n. However, in this course, we don't care too much about $T(n)$ exactly but rather, bounds on it and the rate of T's growth as n grows. For example, if T is constant regardless of n, we don't care about what constant it is equal to; just the property that the time is constant for all n.

Obviously, the smaller the runtime, the better because that means the algorithm is faster.

§3.1 Definitions and Seeing Them in Use

This section is unavoidably math heavy, but I will do my best in using Layman's terms. We need to get some important definitions over with though.

Definition 3.1 (Big O notation)**.** A function $f(n)$ is $O(g(n))$ (for some function $g(n)$) if and only if there exist positive constants c and n_0 such that $f(n) \leq cg(n)$ for all integers $n \geq n_0$.

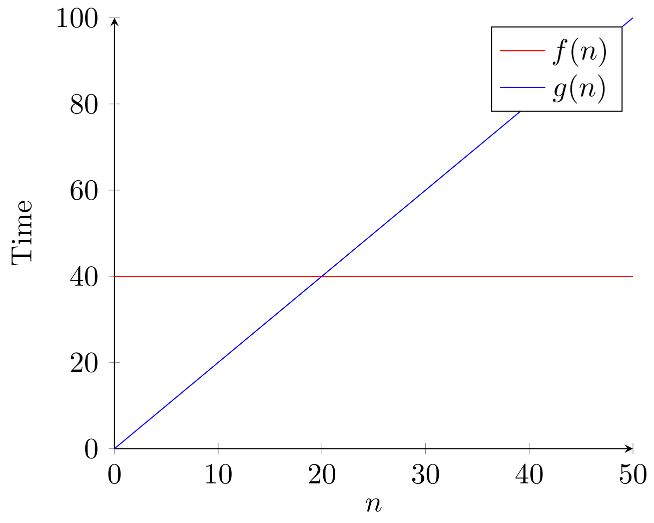
For example, the function n is $O(n^2)$ because $n \leq n^2$ for all integers $n \geq 1$. Also, $2n$ is $O(n)$ because if $c = 2$, then $2n \leq cn$ for all $n \geq 1$. Essentially, when we say $f(n)$ is $O(g(n))$, we're saying the rate of growth of f in the long run is equally as ideal or more ideal than the rate of growth of g in the long run. In other words, the growth rate of g poses as an upper bound for the growth rate of f.

Here's the intuition behind the constant c. Basically, multiplying any function by a constant doesn't change the general pattern in its rate of growth. Multiply a constant function by a constant? Still a constant function. Multiply a linear function (a function in the form $f(x) = ax$ for a constant a) by a constant? It will still be a linear function and grow like one. When we analyze runtimes, we don't care about these constants, just how increasing n effects the behavior of the growth of the runtime. For example, if an algorithm's runtime is linear we don't care if it's $4n$ or $9n$ or $7128n$, just that it's linear. So having the c with $f(n) \leq cg(n)$ is essential to allow us to say constants in front of f don't matter because we could choose c appropriately to counter out any effects those constants may have on the left hand side. We saw this in our $2n$ vs n example earlier where we used a c to counter the 2 constant on the left.

Here's the intuition behind the constant n_0. When we analyze function runtimes, we want to look at the big picture, or which will be better/worse in the long run rather than a few small inputs. Take the set of functions $f(n) = 40$ and $g(n) = 2n$. Consider this table with a few small inputs for n:

n	1	5	10	15
$f(n)$	40	40	40	40
$g(n)$	2	10	20	30

If this is all we looked at regarding f and g, we would see f has worse time and foolishly conclude g is the better function. But we don't care about some cherry picked, small inputs. We care about looking at f and g in the long run. In fact, let's graph the two functions:



It looks like $g(n)$ only starts to become worse than $f(n)$ after a certain point. In fact, if g simply had a worse growth rate than f in general, g would always have to show its "true colors" as the worse function after n becomes large enough. The only reason g didn't show its true colors right away is because it had a headstart in less time over f with the small inputs but no longer had that later.

That's why we define a cutoff point n_0 and only care about $n \geq n_0$. This gets around these headstarts and allow us to focus more on a function's true colors and how it behaves in the long run.

Now, let's return to the original definition of big-O notation with the $f(n) = 40$ and $g(n) = 2n$ example above. So g's linear behavior is going to be worse than f's constant behavior in the long run, so we expect $f(n)$ to be $O(g(n))$. In fact, for all $n \geq 20$, we can see that $f(n) \leq g(n)$. So our choice of constants is $c = 1$ and $n_0 = 20$ to conclude that $f(n)$ fits the definition of $O(g(n))$.

Now, for definitions involving similar language and variables, but with crucial distinctions:

Definition 3.2 (Big Omega notation)**.** A function $f(n)$ is $\Omega(g(n))$ (for some function $g(n)$) if and only if there exist positive constants c and n_0 such that $f(n) \geq cg(n)$ for all integers $n \geq n_0$.

Essentially, if $f(n)$ is $\Omega(g(n))$, the growth rate of g poses as a lower bound (instead of upper) for the growth rate of f. For example, $2n$ is $\Omega(n)$ and is also $\Omega(40)$.

Definition 3.3 (Big Theta notation)**.** A function $f(n)$ is $\Theta(g(n))$ (for some function $g(n)$) if and only if $f(n)$ is both $O(g(n))$ and $\Omega(g(n))$

Essentially, if $f(n)$ is $\Theta(g(n))$, the growth rate of f and g are more or less the same. For example, $2n$ is $\Theta(n)$ (because it is $O(n)$ and $\Omega(n)$).

Warning 3.4. Once you get the hang of these notations, it should become easy to simplify O(some expression) without much justification. But be warned that on homework or midterms, they may ask you to explicitly find constants c and n_0.

We should practice with problems involving explicitly finding c and n_0.

Example 3.5

Prove that $\frac{n^2}{5} + 500n + 1000$ is $\Theta(n^2)$, while finding constants c and n_0.

So we need to prove $\frac{n^2}{5} + 500n + 1000$ is both $O(n^2)$ and $\Omega(n^2)$, by definition of big Theta. Note that the values of the constants we choose for O can be different from those we choose for Ω, as long as they work in both individual cases.

First, let's do $O(n^2)$. We need to find a c and n_0 such that

$$\frac{n^2}{5} + 500n + 1000 \leq cn^2$$

for all $n \geq n_0$. One thing we do know is, for all positive integers n, we have $n \leq n^2$ and $1 \leq n^2$. So $500n \leq 500n^2$ and $1000 \leq 1000n^2$ for all $n \geq 1$. So in fact, for all $n \geq 1$,

$$\frac{n^2}{5} + 500n + 1000 \leq \frac{n^2}{5} + 500n^2 + 1000n^2 \leq 1500.2 \cdot n^2.$$

Then, c and n_0 natural come out: we have $c = 1500.2$ and $n_0 = 1$.

Now, we do $\Omega(n^2)$. This is even easier, since $500n + 1000$ is always positive for all $n \geq 1$, we know $500n + 1000 \geq 0$. Thus,

$$\frac{n^2}{5} + 500n + 1000 \geq \frac{n^2}{5}.$$

So our constants are $c = \frac{1}{5}$ and $n_0 = 1$.

This proves $\frac{n^2}{5} + 500n + 1000$ is both $O(n^2)$ and $\Omega(n^2)$, so it is $\Theta(n^2)$. ■

Let's try a harder example, but this will necessitate induction.

Example 3.6

Prove that $\log_2(n)$ is $O(n)$, while finding constants c and n_0.

Before we get into the proof, let me just say, this result will be extremely useful for you from now until the end of the course. DON'T FORGET IT.

Anyway, this one looks harder. Before proving the function with an n^2 was $O(n^2)$ and $\Omega(n^2)$ wasn't too hard because both $\frac{n^2}{5} + 500n + 1000$ and n^2 were sort of, in the same "family." But not here.

Irrespective, we want to find positive constants c and n_0 such that $\log_2(n) \leq cn$ for all $n \geq n_0$.

Here's a key observation: we can cherry pick a value of c and n_0 to our liking in making things work out, like we did last example. But once we pick c and n_0, we have to stick to our choice. We can't keep changing it to try to get the inequality to always hold.

I gave a hint towards induction, but in trying to work stuff out, let's try to do the inductive step and pick c that makes it convenient.

So the inductive step would involve proving

$$\log_2(k) \leq ck \implies \log_2(k+1) \leq c(k+1)$$

for some arbitrary k greater than the base case (which we'll get to later). We're assuming $\log_2(k) \leq ck$ is true, so let's make it look more like what we want to prove by adding $\log_2(k+1) - \log_2(k)$ to both sides to get:

$$\log_2(k+1) \leq ck + \log_2(k+1) - \log_2(k).$$

Take my word on this that $\log_2(x) - \log_2(y) = \log_2(\frac{x}{y})$ for any positive real numbers x and y (we'll get to log rules later). So we have

$$\log_2(k+1) \leq ck + \log_2\left(1 + \frac{1}{k}\right).$$

Now, if we can prove that $ck + \log_2\left(1 + \frac{1}{k}\right) \leq c(k+1)$, we'd be done with the inductive step because then,

$$\log_2(k+1) \leq ck + \log_2\left(1 + \frac{1}{k}\right) \leq c(k+1) \implies \log_2(k+1) \leq c(k+1).$$

So we work with

$$ck + \log_2\left(1 + \frac{1}{k}\right) \leq c(k+1) \implies \log_2\left(1 + \frac{1}{k}\right) \leq c.$$

We know k is an arbitrary integer larger than the base case, so k could be ridiculously big. However, $\frac{1}{k}$ gets smaller as k gets bigger. In fact, for $k \geq 1$, it's easy to see that $1 + \frac{1}{k} \leq 2$ (because equality holds at $k = 1$, but the left hand side keeps getting smaller and smaller after that). You halve something that's less than or equal to 2, and you're guaranteed to get something less than 2 after that one halve, so by the informal definition of a log, we have $\log_2(1 + \frac{1}{k}) \leq 1$ for $k \geq 1$. So we can choose $c = 1$ with the caveat that $k \geq 1$ for the inductive step to work.

That's the induction step covered and now, we need to make sure the base case holds, which will be $n = n_0$ (basically the "cutoff" point where we want to start examining the functions). So we would need $\log_2(n_0) \leq n_0$, since we chose $c = 1$. The good thing is n_0 doesn't have to be optimal; it just has to satisfy the base case and work with the prior caveat that $k \geq 1$ for the inductive step to work (imagine if our prior caveat was $k \geq 101$ for the inductive step to work. Then, we couldn't just choose $n_0 = 97$ for example because then the inductive step fails for $k = 98$). Anyway, we know $\log_2(2) = 1$ (halve it once to get it under 2). So $n_0 = 2$ works as a base case. And when we do the inductive step for an arbitrary integer $k \geq n_0 = 2$, we don't violate the caveat so we're good.

Now that we found convenient constants to work with, we can rewrite the induction proof into something more familiar:

Solution:

Let $c = 1$ and $n_0 = 2$. I will show that $\log_2(n) \leq n$ for all integers $n \geq 2$.

Base Case:

Since $\log_2(2) = 1$, we have $\log_2(2) \leq 2$. Check.

Inductive Step:

Assume that $\log_2(k) \leq k$ holds for an arbitrary integer $k \geq 2$. I will show this implies that $\log_2(k+1) \leq k+1$. If $\log_2(k) \leq k$ holds, then

$$\log_2(k) + (\log_2(k+1) - \log_2(k)) \leq k + (\log_2(k+1) - \log_2(k))$$

$$\implies \log_2(k+1) \leq k + \log_2\left(1 + \frac{1}{k}\right).$$

We know for $k \geq 1$ (which will always hold for $k \geq 2$), we have $1 + \frac{1}{k} \leq 2$. Then, $\log_2(1 + \frac{1}{k}) \leq 1$. Thus,

$$\log_2(k+1) \leq k + \log_2\left(1 + \frac{1}{k}\right) \leq k + 1,$$

completing the induction.

Advice 3.7 — When given a homework problem where you have to find the constants, this thought process will help where you try to do the inductive step and choose a c that makes it work out. Then, you choose n_0 so that the base case works. You do have to go back and write it up like a normal induction proof, but at least you know the constants that work.

Example 3.8

True or false: 3^n is $O(2^n)$.

Let's go about this trying to find c and n_0 until we either find it, or we reach a contradiction. So we need $3^n \leq c \cdot 2^n$ for all $n \geq n_0$. This rearranges to $(\frac{3}{2})^n \leq c$ for all $n \geq n_0$.

Here's the thing: we can choose c to be whatever we want, but once we choose it, we cannot change it to fit the inequality. For example, suppose we chose $c = 400$. It turns out the inequality holds for $n = 1, 2, 3, ..., 14$, but for all $n \geq 15$, it no longer holds. So there is no n_0 for which it will hold for all $n \geq n_0$ because the n it fails for are limitless.

The issue here is that, take my word on this, the function $(\frac{3}{2})^n$ can always get as big as it wants if n is large enough. So even if we choose c to be 250 million or whatever, it is still a fixed value at the end of the day, since we can't just change it. And guess what! The function $(\frac{3}{2})^n$ will eventually catch up to c, even if it is 250 million and then the inequality no longer holds for n after that.

So we reached a contradiction, where we try to choose c but by doing so, we learn there is no n_0 (or cutoff point, essentially) where the inequality will hold for all future n past some n_0. This is because the left hand side will always catch up to c.

Thus, 3^n is NOT $O(2^n)$. In fact, 3^n is $\Omega(2^n)$.

§3.2 General Facts about Runtime

Now that we have the hang of runtime, I'll give you some useful facts that will be helpful to eyeball bounds on certain functions.

- For a degree d polynomial in n, meaning a function in the form $f(n) = a_d n^d + a_{d-1} n^{d-1} + ... + a_1 n + a_0$ for constants a_d, a_{d-1}, ..., a_1, a_0 with $a_d > 0$, we have $f(n)$ is $\Theta(n^d)$.
- Any nth degree polynomial is always $O(m^n)$, when $m > 1$
- Logs are always $O(n)$

So we have this hierachy where logs are better than polynomials, but polynomials are better than exponential functions.

§3.3 Constant Time Operations

Here are some examples of constant time operations (meaning these run in $\Theta(1)$):

- Checking if two primitive data types are equal to the same value
- Accessing an element at a certain position in an array
- Adding two numbers (adding n numbers is NOT $\Theta(1)$ though)
- Comparisons like "is $x > y$?"

These will be useful for you to know when you need to analyze runtime of your algorithm. Just take my word on these; don't try to seek out an explanation.

§3.4 Summary

- We learned about runtime and how we define different notation to signify upper bound, lower bound, or same ballpark in growth.
- c is used in these definitions to dilute the effects of constants in front of the functions because we don't care about them when measuring growth.
- n_0 is used so we can see a function's true colors in the long run and not make faulty assumptions based on a couple of small inputs.
- Sometimes there are cases where you don't have to do too much work to get c and n_0. Other times, you have to do the math or even induction. But with induction, you can try to choose c and n_0 to make the process convenient.

§4 Log Rules

I taught you an informal definition of logs, specifically $\log_2$. Now, here's the formal definition:

Definition 4.1 (Log function (formal definition))**.** The inverse of an exponential function: for a base b and positive real number x, we have that $\log_b(x)$ is equal to the real number r such that $b^r = x$.

The base can be any positive real number besides 1. Most commonly in this course, you'll see $b = 2$. An example with another base, we know that $3^4 = 81$, so we can say $\log_3(81) = 4$.

Here are some properties of logarithms:

- $\log_b(b^x) = x$, essentially the fundamental definition of logarithms
- $\log_b(x) + \log_b(y) = \log_b(xy)$ (DO NOT USE THIS IF THE BASES ARE NOT THE SAME) Very useful for combining logarithms.
- $\log_b(x) - \log_b(y) = \log_b(\frac{x}{y})$
- Change of base formula from base b to a new base c: $\log_b(x) = \frac{\log_c(x)}{\log_c(b)}$. Since $\log_c(b)$ is essentially a constant for a fixed b and c, this means changing the base of a log is just multiplying by some constant.
- $\log_b(x) = \frac{1}{\log_x(b)}$, uses the above formula by changing from base b to base x
- $b^{\log_b(x)} = x$, useful for getting rid of logarithm terms in the exponent
- $\log_b(c^x) = x \cdot \log_b(c)$, useful for getting rid of exponents inside log terms or putting them inside to later combine log terms.
- $x^{\log_b(y)} = y^{\log_b(x)}$, occasionally useful if y and x are better off with switched places
- If $b > 1$ is fixed, while x is changing, the value of $\log_b(x)$ increases as x increases.
- $\log_b(1)$ is always 0. Using the above point, this means that $\log_b(x) > 0$ when $x > 1$ (so long as $b > 1$).

While there is no shame in referring to these from time to time, you should ideally try to memorize them, especially for the closed notes midterms. To make it easier to memorize, it helps to memorize the intuition. With the addition property, it comes from the fact that we add exponents when multiplying, like $2^3 \cdot 2^2 = 2^5$, so $\log_2(2^3) + \log_2(2^2) = \log_2(2^5)$, which becomes $3 + 2 = 5$.

Also, the base tends to be irrelevant with logs in this course, as long as it is a fixed number for all terms you're using it with. So really, there's no difference between using $\log_2$ or $\log_3$, as long as all relevant terms are assumed to be all base 2 for example, and you don't try to combine $\log_2$ and $\log_3$ terms.

Example 4.2 (Recitation Problem)

Prove that $\lg(n!) = \Theta(n \lg n)$, while finding constants c and n_0. Assume base 2 for all the logarithms.

We know $n! = n \cdot (n-1)!$ and $1! = 1$ from CIS 1600. Let's use our trusty log rules, specifically that addition property one. Using this, we know $\lg(n!) = \lg(n) + \lg((n-1)!)$. Taking this a step further, $\lg(n!) = \lg(n) + \lg(n-1) + \lg((n-2)!)$. Do this enough times until we get to the base case for factorial, and we get

$$\lg(n!) = \lg(n) + \lg(n-1) + \lg(n-2) + \cdots + \lg(2) + \lg(1)$$

for an arbitrary positive integer n. Now we'll get both upper and lower bounds on this.

First, an upper bound. We know lg increases as its input increases by a given property I listed. So for the sake of upper bound, we can bump all terms up to n:

$$\lg(n!) = \lg(n) + \lg(n-1) + \lg(n-2) + \cdots + \lg(2) + \lg(1)$$

$$\leq \underbrace{\lg(n) + \lg(n) + \lg(n) + \cdots + \lg(n) + \lg(n)}_{n \text{ of these}} = n \cdot \lg(n).$$

Since n is an arbitrary positive integer, the above holds for all such n. So we showed $\lg(n!)$ is $O(n \lg n)$ with $c = 1$ and $n_0 = 1$.

Now, a lower bound. We know each term in the sum is nonnegative because $\lg(1) = 0$ and increasing the input will result in the log being a positive value. So deleting some terms from the sum is only going to decrease its value for a lower bound. Thus, let's delete everything less than $\lg(n/2)$:

$$\lg(n!) = \lg(n) + \lg(n-1) + \lg(n-2) + \cdots + \lg(2) + \lg(1)$$

$$\geq \lg(n) + \lg(n-1) + \lg(n-2) + \cdots + \lg(n/2+1) + \lg(n/2).$$

Similar to what we did previously, we can bump down the values in each log term for a lower bound:

$$\lg(n!) \geq \lg(n) + \lg(n-1) + \lg(n-2) + \cdots + \lg(n/2+1) + \lg(n/2)$$

$$\geq \underbrace{\lg(n/2) + \lg(n/2) + \lg(n/2) + \cdots + \lg(n/2) + \lg(n/2)}_{n/2 \text{ of these}} = \frac{n}{2} \cdot \lg(n/2).$$

Since we're using base 2, using that division/subtraction log property:

$$\lg(n!) \geq \frac{n}{2} \cdot \lg(n/2) = \frac{n}{2} \cdot (\lg(n) - \lg(2)) = \frac{n}{2} \cdot (\lg(n) - 1).$$

Note that $\lg(4) = 2$. Since we know about lg's increasing properties, we know $\lg(n) \geq 2$, when $n \geq 4$. So assume $n \geq 4$. Then, $\frac{\lg(n)}{2} \geq 1$. This becomes $\lg(n) - 1 \geq \frac{\lg(n)}{2}$. Back to our work,

$$\lg(n!) \geq \frac{n}{2} \cdot (\lg(n) - 1) \geq \frac{n}{2} \cdot \frac{\lg(n)}{2}.$$

But this works only when $n \geq 4$. So we can set $n_0 = 4$ and $c = \frac{1}{4}$ to say $\lg(n!)$ is $\Omega(n \lg n)$.

Thus, we can conclude that $\lg(n!)$ is $\Theta(n \lg n)$, since we showed both O and Ω. Side note, remember how we worked in base 2, but one of those properties said changing the base is essentially multiplying by a constant? That means the Θ holds, even if chose some other base besides 2, since we don't care about constants in Θ analysis.

Extra side note, you know how we deleted everything less than the $n/2$ term when doing the Ω bound? That technique is helpful in general with these bounds because you can try to get stuff in the desired behavior you want for that bound. We'll see something later where we will want to use this technique.

§5 Binary Search (and the real start of algorithm learning)

§5.1 Introduction

You may have heard of this algorithm before, but I'll go over it, so we're all on the same page. Now that we have some of the basics down on runtime, we can get into the structure of how algorithms are taught. There are three key components they look for with algorithms, particularly on the homeworks:

- The algorithm itself. They usually want you to write it in plain English and no psuedocode. There is psuedocode in the lecture notes, but my guide will dumb it down so it is easy to understand and follow along.
- A proof of correctness. This is basically showing why the algorithm returns what we want it to do. There is some nuance to how they may want you to do it, but we can get in to that later.
- Runtime. Basically justifying that the algorithms runs in the given runtime. At the point they start making you do this on homework, you don't need to be super precise on details. For example, you don't need in-depth justification on why $O(2n)$ is $O(n)$, but it never hurts to ask on the class board privately.

Anyway, let's get in to a simple example of an algorithm. Say we have an array of size n that we know is sorted. How do we check if a particular number is in the array?

Well, we could go through each of the n cells in the array. Worst case, we go through the entire array and don't find our target at all. Each cell requires constant time work (checking if the number there is equal to the one we're looking for) and we do this n times. So our runtime is cn for some constant c, meaning this naive algorithm is $O(n)$.

But we can do better than this, especially with leveraging the fact that the array is sorted.

Review 5.1. If you're rusty on recursion from CIS 1200, review it now. A number of algorithms here on out will rely on it. Remember the idea is, it's a function that calls itself to solve a similar problem but of smaller size to make it easier to work out the final task.

§5.2 The Algorithm

So we have two inputs: our array and a target element, which is the element we're searching for in the array. Here's the algorithm:

Base Case: If the array is of size 1, check if the lone element is equal to our target element. If it is, return true. Otherwise, return false.

Otherwise, we have an array of size greater than 1. Check the element in the very middle of the array. Then, we do one of the three things:

- If this middle element is equal to our target element, we found it, so we return true.
- If the middle element is less than the target, recursively call the algorithm on the portion of the array to the RIGHT of the middle.
- If the middle element is greater than the target, recursively call the algorithm on the portion of the array to the LEFT of the middle.

§5.3 In Action

Let's suppose we have this sorted array and we want to search for 7:

0	1	2	3	4	5	6
1	3	4	5	7	11	15

Okay, so at the middle of the array is 5. This is less than our target, so we consider the right half of the array (positions 4-6) and recurse there. So it boils down to this:

4	5	6
7	11	15

Check the middle, it is 11, bigger than our target. So we recurse on the left half (position 4).

4
7

We're at a base case (1 element). So we just check this lone element. Yes, it is 7, our target, so we found true.

§5.4 Proof of Correctness (and intro to PoC via Induction)

Review 5.2. Review induction and strong induction if you're rusty on those. Recursive algorithms rely on them.

So here's the informal way to think about it, considering the example we just did. The middle element is 5. We know the array is sorted. So we know everything to the left of 5 (in the middle) is smaller than 5 because the array is sorted. So anything to the left of the middle is smaller than 5, which is smaller than 7, so we don't care about it.

Now, 7 could be in the right half. We don't know yet. But we essentially boiled it down to checking whether it is in the right half, which is why we recurse on that right half.

Similar logic holds if it turned out the middle was larger than the target, in which the right half is irrelevant and we only care about the left half.

It also shouldn't be too hard to see why the base case works (if it's 1 element, either the target is that lone element or it's not). Same with when we get lucky and the middle just so happens to be the target.

How THEY want you to prove a recursive algorithm though is through induction. I'm not going to go through all the ideas but just enough of the idea. First, we check the base case for our proof by induction, which should usually be the base case of the recursive algorithm.

Then, we need to do the inductive step in showing it works for an array of size n. We'll use strong induction. So we justify why we search a specific half of the array in the cases as we did and not do something crazy like randomly pick the half. But here's the inductive part: when we make the recursion, it boils down to the inductive hypothesis holding for a smaller n because we're essentially doing the same problem with a smaller size. We know this is true by the inductive hypothesis, so it holds. We used strong induction here because the smaller array isn't necessarily $n-1$, more like $n/2$, so we need to use strong induction to make the proof work.

Also, with this example, you now more clearly see the parallels between induction and recursion.

Advice 5.3 — When saying to work with an array of size $n/2$, don't worry about n being odd (where $n/2$ won't be an integer).

§5.5 Runtime

So we can agree that before we do the recursive call, everything is of constant work, right? We check if we're at a base case, then we check the middle element, and compare it to the target. All constant work. We could end early if we're lucky and find the target in the middle, but worst case, we'll have to recurse on one half of the array (in other words, solve a subproblem of size $n/2$). So if $T(n)$ is a time function for worst case scenario, we can say $T(n) = c + T(n/2)$. We know the base case is when we have size 1 and that's clearly of constant time, so $T(1) = d$ for some constant.

Anyway, with the recurrence $T(n) = c + T(n/2)$, we can substitute n with $n/2$ so we get $T(n/2) = c + T(n/4)$. Plugging this back in means $T(n) = c + (c + T(n/4)) = 2c + T(n/4)$. But we can plug in $n/4$ into the original recurrence to get $T(n/4) = c + T(n/8)$, so we have $T(n) = 2c + T(n/4) = 2c + (c + T(n/8)) = 3c + T(n/8)$.

Again, if we get lucky and find it in the middle in any of the recursive calls, we finish early. But to simulate the worst case scenario, we assume it has to go all the way to base case, which is when it becomes $T(1)$. Notice that we keep halving the input, like going from $n/2$ to $n/4$ to $n/8$ and we add c each time. So at worst, we add c as many times as it takes, to halve n until it gets to 1. This is $\log_2(n)$ times. So we can say $T(n)$ is roughly $c \log_2(n)$ meaning $T(n)$ is $O(\log n)$. Better than $O(n)$, for sure, so we didn't have to check everything in the array.

This subsection was not rigorously and formal, but we'll have techniques later to more formally solve recurrence relations. Hopefully, you get the general idea.

However, remember Binary Search only works for sorted arrays. And an array may not always be sorted. Well, in the next section, we'll learn how to sort an array.

§5.6 Summary

- We saw how recursion is used in a simple algorithm to find a specific element in an array.
- We basically use the middle element to determine which half of the array our target has to be in, should it be present in the array.
- We got a taste of a Proof of Correctness, where we have to reason through our steps.
- We saw how induction is the primary tool for proving a recursive algorithm because it naturally has to deal with a similar situation but a smaller size.
- We saw how binary search is $O(\log n)$, which is better than checking every element one by one.

§6 Insertion Sort

§6.1 Introduction

So we need a sorted array to use binary search. And how do we sort an array, since not all of them will be that way? Well, let's see one such example of a sorting algorithm!

§6.2 The Algorithm

Suppose the array is of size n. Suppose the positions of the array are labeled 1 to n (so it doesn't start at 0).

Run this loop for j from 2 to n, incrementing j by 1 each time:

- Consider the jth element in the array.
- If it's smaller than the element to the left of it, have it switch places with the element on its left.
- If it's still smaller than the element to the left of it, make a switch again. Keep making switches with the element on the left, until we reach a point where it is bigger than the element to the left of it, or it reaches the left end of the array.

§6.3 In Action

Let's sort this array with insertion sort:

1	2	3	4	5	6
5	2	4	6	1	3

So first, we start at $j = 2$, so we go to position 2 and see the 2 there. Then, we compare it with 5 on its left. Since 2 is smaller than 5, we make the switch. Now, 2 is at the left end of the array, so we don't make any more switches. Here's what the array looks like now:

1	2	3	4	5	6
2	5	4	6	1	3

So now, we move on and increment j, so $j = 3$. We see 4 at position 3, which is less than 5. So we swap 4 and 5. But 4 is greater than 2, so we don't make another swap. Here's what the array looks like now:

1	2	3	4	5	6
2	4	5	6	1	3

Now, $j = 4$. 6 is greater than 5, so we don't make any swaps. The array didn't change.

You can see where this is going, so here's what it looks like after $j = 5$:

1	2	3	4	5	6
1	2	4	5	6	3

And $j = 6$:

1	2	3	4	5	6
1	2	3	4	5	6

The array is sorted. Do you see why it's called insertion sort after this example? We basically take each element one by one and find the appropriate place in our line so far to insert it, so stuff is in the correct order.

We could also implement this recursively, where the base case is when $n = 1$ and we just do nothing, since it's already sorted. Otherwise, we recursively sort the first $n - 1$ elements and figure out how to insert the nth element.

§6.4 Proof of Correctness (and intro to Loop Invariants)

Take a good look at the array again after $j = 2$:

1	2	3	4	5	6
2	5	4	6	1	3

Notice those 2 shaded cells and how 2, 5 are in order.

Now, look at what the array was after $j = 3$:

1	2	3	4	5	6
2	4	5	6	1	3

Notice those 3 shaded cells and how 2, 4, 5 are in order.

Is this a coincidence? No. Think of it sort of like induction.

Our base case is before we do anything, the first element on its own is already sorted.

The inductive step comes from the fact that, if the first i elements are already sorted and we're working on $j = i + 1$, the first $i + 1$ elements will be sorted after. This is because the "inductive hypothesis" implies that the first i elements are sorted. We find the appropriate place to insert the new element (which is when the first time when the left element is less than the new element after the swaps). The swaps cause everything bigger to be on the right of the new element without destroying the relative order of the original elements. Everything on the left is in order, too. Thus, the $i + 1$ elements are in order. So this acts like induction where we show how one step being true implies the next step is true.

Basically, we showed there is this invariant where the first i elements are sorted after the iteration for $j = i$ is over. To formalize a loop proof in this class, they want to see a loop invariant, which has 3 main things:

- Initialization: Show that the invariant is true before the loop even starts. This is sort of like the base case. For insertion sort, this is when we showed the 1st element is already sorted.
- Maintenance: Show that if the invariant is true when the ith iteration ends, it still holds true after the $(i + 1)$th iteration ends. This is like the inductive step. For insertion sort, this is when we showed inserting the new element in the way we did keeps everything in order.
- Termination: That the loop gives us what we want at the end. For insertion sort, the initialization and maintenance steps ensure the new element we add maintains order. We end with the nth iteration where we have n elements in order. In other words, we have the sorted array, which is what we want.

§6.5 Runtime

Okay, so we can agree that the source of the work done in insertion sort is through checking whether we need to make swaps and actually doing swaps, right? Making a single check is constant work, just compare two variables. Making a single swap is also constant work, just make a temporary variable to save the values being swapped and then do it. So now, it boils down to how many checks and swaps we actually do.

To organize it, let's count the number of checks and swaps separately, by iteration. So how many happen during the jth iteration? Guess what. It depends on the original array! Say like we had 2, 3, 4, 5 sorted so far. If we wanted to insert 6, we don't have to make any swaps. But if we wanted to insert 1, we would have to make multiple swaps. Okay, so even for arrays of the same size, there could be very different runtimes! So instead, let's consider bounds on the number of checks and swaps total.

Let's define C_j and S_j to be the number of checks and swaps, respectively, in the jth iteration. Let's let a and b be the constants for one check and one swap, respectively. The runtime of insertion sort will be $T(n) = \sum_{j=2}^{n}(a \cdot C_j + b \cdot S_j)$. This is because in the jth iteration, we do C_j checks, which take a time each, so that's $a \cdot C_j$ time total. Similar thing goes for $b \cdot S_j$. And then of course, we sum over all iterations.

Let's suppose it's the jth iteration, where the first $j - 1$ elements are sorted and we're inserting a jth element. No matter what, it has to be checked with the element on the left. So $C_j \geq 1$ always. But if it's greater than that element, no swaps occur. So $S_j \geq 0$ always.

Now, let's consider worst case scenarios. Remember we keep making swaps until we either hit the left end, or we check the left element and it is less than the current element. If the latter happens, the iteration ends early. But in the worst case, we keep having to make swaps until we hit the left end. So we have $S_j \leq j - 1$ because we make $j - 1$ swaps in the case we have to do it until we hit the left end. Also, $C_j \leq j$ when that happens because we keep checking with the element on the left, with the last check realizing we're on the left end of the array.

So we have our formula $T(n) = \sum_{j=2}^{n}(a \cdot C_j + b \cdot S_j)$. If we assume the best case scenario, which is when C_j and S_j are as low as they can be, we get

$$T(n) = \sum_{j=2}^{n}(a \cdot 1 + b \cdot 0) = \sum_{j=2}^{n}(a) = n - 1.$$

So the best case is $\Theta(n)$, which would occur when we don't have to make swaps, so something like $1, 2, 3, 4, 5, 6$.

If we assume C_j and S_j are as high as they can be, it becomes

$$T(n) = \sum_{j=2}^{n} (a \cdot j + b \cdot (j-1)) = a \cdot (2 + 3 + 4 + \cdots + n) + b \cdot (1 + 2 + 3 + \cdots + (n-1)).$$

Remember the sum of the first i positive integers is $\frac{i(i+1)}{2}$ from CIS 1600. So

$$T(n) = a \cdot \left(\frac{n(n+1)}{2} - 1\right) + b \cdot \frac{(n-1)n}{2}.$$

This is $\Theta(n^2)$, which would occur when we have to keep making swaps until they reach the end, so something like $6, 5, 4, 3, 2, 1$.

As you can see, there's no one size that fits all with the runtime of insertion sort, not when there's this disparity in the best and worst cases. And yes, that means for an arbitrary array we need to sort, sometimes it's close to the best case, other times it's close to the worst case. All we did is just find bounds.

§6.6 Summary

- We saw our first sorting algorithm, which is done by appropriately inserting numbers in an already sorted portion of the array
- We saw how a loop invariant is used to show how the first j elements are sorted every step of the way
- It turned out there was no one runtime to describe all cases of insertion sort. The best case is $\Theta(n)$ but the worst case is $\Theta(n^2)$.

§7 Runtime of Recurrences

§7.1 Introduction

So we saw binary search earlier, a recursive algorithm. Well, we need to learn how to algorithms in the same family but have different variations on their recursive equations. First things first, here's some important formula:

$$\sum_{i=1}^{n} i = \frac{n(n+1)}{2}$$

$$\sum_{i=1}^{n} i^2 = \frac{n(n+1)(2n+1)}{6}$$

$$1 + r + r^2 + \cdots + r^n = \frac{r^{n+1} - 1}{r - 1}$$

$$1 + 2 + 2^2 + \cdots + 2^n = 2^{n+1} - 1 \quad \text{(A result of the formula above by using } r = 2\text{)}$$

These are usually provided for you on a test, but helpful to remember they exist so you know to go and reference it when need be.

§7.2 Expansion Method

Let's go back to the recurrence for the worst case for binary search, meaning we don't get lucky ever and find what we want when checking the middle. We don't care about how we derived the recurrence right now, just what it is.

$$T(n) = \begin{cases} T(n/2) + c, & n > 1 \\ k, & n = 1 \end{cases}$$

where c and k are some constants. If you recall, what I did was I kept plugging the recurrence into itself. To refresh your memory, we have this equation,

$$T(n) = T(n/2) + c \quad (1)$$

But we can plug $n/2$ for n in (1) to get

$$T(n/2) = T(n/4) + c \quad (2)$$

Plug this back in to (1) to get

$$T(n) = (T(n/4) + c) + c = T(n/4) + c + c \quad (3)$$

We plug $n/4$ for n in (1) to get $T(n/4) = T(n/8) + c$. Plugging this in to (3) implies

$$T(n) = (T(n/8) + c) + c + c \quad (4)$$

Monitoring our progress,

$$\begin{aligned} T(n) &= T(n/2) + c \\ &= T(n/4) + c + c \\ &= T(n/8) + c + c + c \end{aligned}$$

As you can see, we're expanding the equation out by feeding the recurrence in to itself, hence, the colloquial name for the technique. We can pretty easily see that the general form will be $T(n) = T(n/2^i) + i \cdot c$ at this point.

Advice 7.1 — You can use induction here to prove this, but they don't require it. The pattern could easily start to emerge if you expand enough times.

Anyway, we know this recursion has a base case. With the $n/2$ going to $n/4$ then $n/8$, it gets smaller each time. So if we were to, in theory, expand it enough times, we would reach the base case. And that base case occurs when the input is 1. So we want to set $n/2^i = 1$ because that's when the expansions reach the base case. Solving for i,

$$n/2^i = 1 \implies n = 2^i \implies i = \log_2(n).$$

So plugging this in to the general form means

$$T(n) = T(n/2^i) + i \cdot c = T(1) + \log_2(n) \cdot c = k + c \cdot \log_2(n).$$

So $T(n)$ is $\Theta(\log n)$.

Example 7.2 (Class)

Find a Θ bound for $T(n)$ given the recurrence relation

$$T(n) = \begin{cases} 3T(n/2) + kn, & n > 1 \\ c, & n = 1 \end{cases}$$

Okay, I'll let you know this one is not as pretty and is math heavy, but bear with me. Let's again, do our technique where we plug the recurrence in to itself. Multiplying stuff out is fine, but let's refrain from adding.

$$\begin{aligned} T(n) &= 3T(n/2) + kn \qquad (1) \\ &= 3\left(3T(n/4) + \frac{kn}{2}\right) + kn \\ &= 9T(n/4) + \frac{3kn}{2} + kn \qquad (2) \end{aligned}$$

$$
\begin{aligned}
&= 9\left(3T(n/8) + \frac{kn}{4}\right) + \frac{3kn}{2} + kn \\
&= 27T(n/8) + \frac{9kn}{4} + \frac{3kn}{2} + kn \qquad (3)
\end{aligned}
$$

From (1), (2), and (3), we can guess the pattern:

$$
\begin{aligned}
T(n) &= 3^iT(n/2^i) + \left(kn + \frac{3kn}{2} + \frac{9kn}{4} + \cdots + \left(\frac{3}{2}\right)^{i-1} kn\right) \\
&= 3^iT(n/2^i) + kn\left(1 + \frac{3}{2} + \left(\frac{3}{2}\right)^2 + \cdots + \left(\frac{3}{2}\right)^{i-1}\right)
\end{aligned}
$$

We want to see when we expanded enough times that we can stop because we hit a base case. So we want $n/2^i = 1$ or $i = \log_2(n)$, once again. So let's do some simplification, first using one of the formula I provided earlier in the section to sum up the powers of $\frac{3}{2}$:

$$
\begin{aligned}
T(n) &= 3^iT(n/2^i) + kn\left(1 + \frac{3}{2} + \left(\frac{3}{2}\right)^2 + \cdots + \left(\frac{3}{2}\right)^{i-1}\right) \\
&= 3^{\log_2(n)} \cdot T(1) + kn\left(\frac{(3/2)^i - 1}{3/2 - 1}\right) \\
&= 3^{\log_2(n)} \cdot c + 2kn\left(\left(\frac{3}{2}\right)^i - 1\right) \\
&= 3^{\log_2(n)} \cdot c + 2kn\left(\frac{3^{\log_2(n)}}{2^{\log_2(n)}} - 1\right) \\
&= 3^{\log_2(n)} \cdot c + 2kn\left(\frac{3^{\log_2(n)}}{n} - 1\right)
\end{aligned}
$$

Recall one of our log identities: $x^{\log_b(y)} = y^{\log_b(x)}$. This means $3^{\log_2(n)} = n^{\log_2(3)}$, which means the n can be swapped to a more convenient place.

$$
\begin{aligned}
T(n) &= 3^{\log_2(n)} \cdot c + 2kn\left(\frac{3^{\log_2(n)}}{n} - 1\right) \\
&= n^{\log_2(3)} \cdot c + 2kn\left(\frac{n^{\log_2(3)}}{n} - 1\right) \\
&= n^{\log_2(3)} \cdot c + 2k \cdot n^{\log_2(3)} - 2kn \\
&= (c + 2k) \cdot n^{\log_2(3)} - 2k \cdot n
\end{aligned}
$$

Since $\log_2(3) > 1$, the $n^{\log_2(3)}$ is the dominant term over n because of a larger exponent. So this is $\Theta(n^{\log_2(3)})$. This one was a doozy.

Advice 7.3 — I would always try to write down at least 2 or 3 expansions when I need to show my work. Don't always try to combine terms because a pattern like c, then $c + 2c$, then $c + 2c + 4c$, then $c + 2c + 4c + 8c$ would be much easier to see if you don't combine terms than if you did and got c, $3c$, $7c$, $15c$.

§7.3 Master Theorem

Theorem 7.4

Suppose a recursive algorithm had a time function $T(n)$ and $T(1)$ is a constant. If the recurrence is

$$T(n) = aT\left(\frac{n}{b}\right) + \Theta(n^k)$$

for some constants a, b, and k, then we have three cases:

- If $a > b^k$, then $T(n)$ is $\Theta(n^{\log_b a})$
- If $a = b^k$, then $T(n)$ is $\Theta(n^k \log_b n)$
- If $a < b^k$, then $T(n)$ is $\Theta(n^k)$

You will not be expected to memorize this and you will given this on tests. The proof? Not until CIS 3200.

Warning 7.5. On the homeworks and tests, you may get recurrence relation problems where they want you to use expansion and not Master Theorem. In that case, expand and DO NOT CITE THIS THEOREM AT ALL (or you may get 0 credit). Doesn't hurt to check in with the TAs and professors when in doubt.

Advice 7.6 — However, when trying to do an algorithm problem, this theorem is incredibly useful for checking the runtime of a recursive algorithm without having to use expansion. You may be able to cite it when doing a runtime analysis for designing an algorithm. Even in cases where you they force you to use expansion, you can use the theorem to check your work.

§7.4 Summary

- We basically repeatedly substitute the recurrence in to itself and expand out the terms each step of the way.
- After enough times, we notice a general pattern of what the equation looks like the ith time we plug it in to itself.
- At that point, we can set i so that it reaches a base case, which is something we know the runtime of.
- Then, we unavoidably have to do some algebra. We do have formulas related to summations, should we need them.
- Master Theorem can help check our work or be useful later when we need to justify the runtime of a recursive algorithm but don't need to go through the trouble of expansion.

§8 Iterative Code Analysis

§8.1 Introduction

For loops are incredibly common in programming, so we ought to know how to analyze their runtime.

Let's look at a simple example:

```
for (int i = 1; i <= n; i++) {
    print("1210");
}
```

Well this just prints "1210" n times. Remember that printing is constant time. So this is $\Theta(n)$.

But here's a not so simple example:

```
for (int i = 1; i <= n; i++) {
    for (int j = i; j <= n; j++) {
        print("1210");
    }
}
```

Well, this is annoying. Not only do we have an extra inner loop, but the loop with j starts at a different value, depending on i.

Also, who says i has to only be increasing by 1 each iteration? We can have something like this:

```
for (int i = 1; i <= n; i = 2*i) {
    for (int j = i; j <= n; j++) {
        print("1210");
    }
}
```

This time i doubles each iteration instead of increasing by 1, so that's even nastier to deal with.

Well, we're going to learn some techniques for these iterative snippets of code.

§8.2 Superset-Subset Method

Let's get right in to an example where I explain the thought process.

Example 8.1 (Class)

Find a Θ bound on the runtime of this code snippet:

```
for i <- 1 to n (incrementing i by 1 each time)
    for j <- 1 to i*i (incrementing j by 1 each time)
        for k <- 1 to j (incrementing k by 1 each time)
            print("1210")
```

Yuckiness aside, let's think about this. So we're printing something (constant time) some number of times. So it boils down to how many times it runs. We know how nested for loops work: we keep incrementing inner loops until they reach their limit. Once that happens, we go back to the previous loop and increment there before restarting the inner loop.

First off, we'll have $i = 1$, $j = 1$, then $k = 1$ because that's the starting values for each variable. So with the given values, the j loop runs from 1 to 1^2. In other words, we only have $j = 1$ for now. Then, we have k running from 1 to j, which in this case, only runs from 1 to 1, since j is limited to 1. So the k loop reaches its limit immediately, but then going back, so does the j loop. So we only do $(i, j, k) = (1, 1, 1)$.

This is the end of the $i = 1$ iteration, so we increase i by 1, as stated in the for loop.

Now, $i = 2$ and we restart the j and k loops at their starting values. So we have j running from 1 to 4, and then k running from 1 to j. So we do $(i, j, k) = (2, 1, 1)$ then $(2, 2, 1)$, $(2, 2, 2)$, $(2, 3, 1)$, $(2, 3, 2)$, $(2, 3, 3)$, $(2, 4, 1)$, $(2, 4, 2)$, $(2, 4, 3)$, $(2, 4, 4)$. That marks the end of the $i = 2$ iteration.

You're starting to get the picture: every time we print, there's some triple (i, j, k) associated with it. So we want to count the number of triples.

How about not count the number of triples directly, and instead, get bounds on them?

Let's try to get a superset of the triples, which serves as an upper bound. So in the for loop, we know $1 \le i \le n$ and $1 \le j \le i^2$ and $1 \le k \le j$.

Let's think about the j loop. When $i = 1$, we have j going from 1 to 1. When $i = 5$, we have j going from 1 to 25. When $i = n$, we have j going from 1 to n^2 (which is as big as the bounds can be).

Here comes the trick: the largest the stopping point is for the j loop is n^2, for all i that we work with. So let's deliberately extend the upper bound to be n^2 for the j loop, regardless of i. So now, we have a new set of triples where $1 \le i \le n$ and $1 \le j \le n^2$ and $1 \le k \le j$. Already much nicer to work with since the j loop's upper bound doesn't depend on i (which we know, changes occasionally).

Warning 8.2. You have to make sure when you extend the bounds, it actually results in the duration of the loop increasing for every i we work with and not decreasing any of them. Otherwise, we wouldn't have a superset.

If we said the stopping point for the j loop is $n^2/2$ for all i, that's a problem. Because when $i = n$, the j loop goes from 1 to n^2. But the new stopping point decreases the j loop for $i = n$, so some of the original triples won't make it into the "superset," and this defeats the purpose of a superset.

Now, the k loop. When $j = 1$, we have k going from 1 to 1. When $j = 7$, we have k going from 1 to 7. When $j = n^2$ (the max), we have k going from 1 to n^2. Again, let's deliberately extend the upper bound for the k loop to be n^2, regardless of the value of j.

So now, we have a new set of triples where $1 \leq i \leq n$ and $1 \leq j \leq n^2$ and $1 \leq k \leq n^2$. With our method of deliberately extending the loop duration (and never shrinking it), each of the original triples is covered in this new set. So this new set is a superset of the original triples. And it isn't too hard to calculate the runtime of this. By multiplication rule, it is $n \cdot n^2 \cdot n^2 = n^5$. But this superset is only an upper bound on the original set, so we can say the original set is $O(n^5)$.

We need an Ω bound too though because we're trying to prove a Θ. Good news is, we can play a similar trick. This time, we take the original bounds and decrease them instead of extend them. Again, the original loops were $1 \leq i \leq n$ and $1 \leq j \leq i^2$ and $1 \leq k \leq j$.

Let's suppose we changed the i loop to $n/2 \leq i \leq n$. We're deliberately cutting off the triples involving $i = 1$, $i = 2$, $\cdots$, $i = n/2 - 1$, but that's okay when this new set we're making is going to be a subset of the original one that's easier to count.

So our new set involves $n/2 \leq i \leq n$ and $1 \leq j \leq i^2$ and $1 \leq k \leq j$. Let's see how the j loop works as we go through all values of i.

When $i = n/2$, we have j going from 1 to $n^2/4$. When $i = n/2+1$, we have j going from 1 to $(n/2+1)^2$. When $i = n$ (the largest it can be), we have j going from 1 to n^2. Let's deliberately shrink the j upper bound to always be $n^2/4$, since for every i, the j loop either stops at $n^2/4$ or goes past it. So now we have $n/2 \leq i \leq n$ and $1 \leq j \leq n^2/4$ and $1 \leq k \leq j$.

Let's work on the k loop. For $j = 1$, we have k going from 1 to 1. For $j = 2$, we have k going from 1 to 2. For $j = n^2/4$ (the highest j can be), we have k going from 1 to $n^2/4$. Let's deliberately shrink the k upper bound to 1, since for every j, the k loop either stops at 1 or goes past it. So now we have $n/2 \leq i \leq n$ and $1 \leq j \leq n^2/4$ and $1 \leq k \leq 1$. The length of the i loop is $n/2$, the j loop is $n^2/4$ and the k loop is 1. So this is $n^3/8$ overall and since this is a subset serving as a low bound for the original code, this means the original code is $\Omega(n^3)$.

But combined with $O(n^5)$, this isn't very informative. We ideally wish we could get $\Omega(n^5)$ instead. Did we mess up? Well, let's look at our bounds again for the subset. We had $n/2 \leq i \leq n$ and $1 \leq j \leq n^2/4$ and $1 \leq k \leq 1$. Remember how in our superset we had $\Theta(n^2)$ for the k loop, but here, we have $\Theta(1)$ for the k loop? That seems to be a discrepancy we should address.

But why did we have our k bound in the subset be so awful? Well, in because the smallest j could be forced us that. Because $j = 1$ was a possibility, we have to deal with k going from 1 to 1, which is not much room to work with. And we couldn't extend this bound in a subset, only decrease it. So when we made the subset, the $j = 1$ pulling this k loop down meant all the others like $j = n^2/4$'s k loop had to be pulled down to 1 with it.

Well, we could cut off small j from the lower bound to give more breathing room in the k loop. Let's go back to the step where we determine the j loop: $n/2 \leq i \leq n$ and $1 \leq j \leq n^2/4$ and $1 \leq k \leq j$. Well, how about changing j's bounds so that it is $n/2 \leq i \leq n$ and $n^2/8 \leq j \leq n^2/4$ and $1 \leq k \leq j$. This is still a subset, but we increased the lower bound on j to give more breathing room on the k loop. Now, let's see how the k loop works.

For $j = n^2/8$, we have k going from 1 to $n^2/8$. For $j = n^2/8 + 1$, we have k going from 1 to $n^2/8 + 1$. For $j = n^2/4$, we have k going from 1 to $n^2/4$. Now, we can make the cutoff for the upper bound on k be $n^2/8$, since for each j we work with, the k loop either stops at $n^2/8$ or goes past it. So now we have $n/2 \leq i \leq n$ and $n^2/8 \leq j \leq n^2/4$ and $1 \leq k \leq n^2/8$. When computing this, it comes out to $n/2 \cdot n^2/8 \cdot n^2/8 = n^5/128$. This is a subset of the original, so we know the original is $\Omega(n^5)$. Much better!

Warning 8.3. Similar to my warning for superset, for subset, make sure you're never increasing the duration of any iteration, or you'll be including triples in the "subset" that aren't original ones. That would defeat the purpose of a subset.

So the Ω and O helps us conclude that the original code is $\Theta(n^5)$.

Advice 8.4 — I think the hardest superset-subset problem is the first one you see. Once you've seen one, others will start to feel natural but can still be tricky.

Superset is usually easy because you just have each upper bound be the highest it can be.

Subset is tricky, but you'll want to pay attention to the runtimes of each individual loop and use them to model the runtimes of your subset. For example, we have k be $\Theta(n^2)$ in the superset, so we ideally wanted k to be $\Theta(n^2)$ in the subset, too. Hence, why we wanted the length of the k loop to be something like $\frac{n^2}{2}$ or $\frac{n^2}{5}$. Also, we had to carefully position the i and j loops so the k loop works out. This comes with practice and seeing examples.

Here's a practice example that will be easier to reason with now that you have seen one example:

Example 8.5 (Recitation)

Find a Θ bound on the runtime of this code snippet:

```
for i <- 1 to n (incrementing i by 1 each time)
    for j <- i to n (incrementing j by 1 each time)
        for k <- i to j (incrementing k by 1 each time)
            print("1210")
```

Superset is easy: make each loop run the largest it can be. Have i go from 1 to n. Then j goes from 1 to n. Then, k goes from 1 to n. So that's n^3, meaning the original code is $O(n^3)$.

Subset is tricky, but let's think about this carefully. So we have the j loop starting at some value after i and going to n. Then, the k loop runs for values between i and j. We want each loop length to be $\Theta(n)$, just like our superset.

We want the j range to be values all after i, but the k range to be values between i and j. So let's have i go from 1 to $n/3$, then j go from $2n/3$ to n, then k go from $n/3$ to $2n/3$. Convince yourself this is actually a subset with the intuition of decreasing loop bounds. This works out to $\Omega(n^3)$.

So then the original code is $\Theta(n^3)$.

§8.3 Table and Summation Method

Well, in that example before, we had each loop incrementing by 1 each time. But that won't always be the case, as we'll see in an example.

Example 8.6 (Recitation)

Find a Θ bound on the runtime of this code snippet:

```
for (int i = 4; i < n; i = i*i) {
    for (int j = 2; j < sqrt(i); j = 2j) {
        print("1210");
    }
}
```

I'm just going to tell you: the superset-subset method isn't going to work well here when the loop's iteration method isn't increasing by 1 each time but doing wacky stuff instead. So we're going to have to do some math! But before that, let's consider what is going on here.

So we start at $i = 4$. Let's suppose some time passes and the j loop completes, so we need to change i. We change it to $4 \cdot 4$ or $i = 16$, as instructed by the for loop. Then, run the j loop again with this new value of i. Suppose some time passes and the j loop completes again. Then, we change i to $16 \cdot 16 = 256$.

So we keep doing this process of running the j loop with a value of i and modifying i with the condition provided. But we stop when $i < n$.

But let's examine the value of i at each iteration number. First iteration, i is $4 = 2^{2^1}$. Second iteration, i is $16 = 2^{2^2}$. Third iteration, i is $256 = 2^{2^3}$. we notice a pattern: in general, the xth iteration of i, the value of i is 2^{2^x}. How would you notice this? By squaring i each time, we keep multiplying the exponent by 2, so the powers of 2 in the exponent accumulate. Let's make a table to organize our data:

iteration # of i	1	2	3	$\cdots$	x
Value of i	2^{2^1}	2^{2^2}	2^{2^3}	$\cdots$	2^{2^x}

We can also examine the j loop's values as it goes through iterations. First iteration, j is 2. Second iteration, it is $2 \cdot 2 = 4$. Third iteration, it is $2 \cdot 4 = 8$. So for the yth iteration of j, the value of j is 2^y.

iteration # of j	1	2	3	$\cdots$	y
Value of j	2^1	2^2	2^3	$\cdots$	2^y

Just like the last example, it boils down to how many times we print "1210." Print is of constant time, so let's just say it takes time 1. The intuition behind converting i and j to x and y is that, unlike i and j, we have x and y incrementing by 1 each time. So we can write the runtime in the form

$$\sum_{x=1}^{U}\sum_{y=1}^{V} 1,$$

where U and V represent upper bounds for x and y, respectively. In particular, U happens when i reaches its upper bound and rememeber that the value of i depends on x. Similarly, V happens when j reaches its upper bound, with the value of j depending on y. This sum is something that is feasible to evaluate, most of the time.

So let's turn the for loops in to sums. Let's suppose we're at the xth iteration for i and then we're running the j loop until it hits its limit. So we stop when $j = \sqrt{i}$ roughly (the upper bound). Remember that $i = 2^{2^x}$, where x represents the iteration number for i. So we do the first iteration of j, then the second, then the next, until we stop. The stopping point is when 2^V (the value of j at the Vth iteration) hits $\sqrt{i} = \sqrt{2^{2^x}}$. We want to find this value of V as that is our upper bound. So $2^V = \sqrt{2^{2^x}}$ or

$$V = \log_2(\sqrt{2^{2^x}}) = \frac{1}{2}\log_2(2^{2^x}) = \frac{1}{2} \cdot 2^x = 2^{x-1}.$$

The inner loop basically prints as many times until the iteration number hits V, the upper bound, so we can represent this inner loop as

$$\sum_{y=1}^{V} 1 = \sum_{y=1}^{2^{x-1}} 1.$$

So given the value of x, the inner loop runs in that time. But the value of x goes from 1 to 2 to 3 and so on until it too reaches its limit. So we need to figure out when that is. Suppose U is the stopping point for x. Remember the stopping point for i here is when it gets to n. Then, we need 2^{2^U} (the value of i at the Uth iteration) to be equal to n. So

$$2^{2^U} = n \implies 2^U = \log_2(n) \implies U = \log_2(\log_2(n)).$$

So we run x from 1 to U. Combining the inner loop sum with these bounds on x implies the total runtime is

$$\sum_{x=1}^{U}\sum_{y=1}^{V} 1 = \sum_{x=1}^{\log_2(\log_2(n))}\sum_{y=1}^{2^{x-1}} 1.$$

No way around it now, we have to do the math. Inner sum is easy, just add up as many 1s as there are within the bounds for y:

$$\sum_{x=1}^{\log_2(\log_2(n))}\sum_{y=1}^{2^{x-1}} 1 = \sum_{x=1}^{\log_2(\log_2(n))} 2^{x-1}.$$

Now, we shift the index and use sum of powers of 2 formula to get

$$\sum_{x=1}^{\log_2(\log_2(n))} 2^{x-1} = \sum_{x=0}^{\log_2(\log_2(n))-1} 2^x = 2^{\log_2(\log_2(n))} - 1 = \log_2(n) - 1.$$

So the code is $\Theta(\log(n))$. Phew!

Advice 8.7 — Personally, I would always use superset-subset for when each loop is incrementing by 1 each iteration. If any of the loops are anything other than incrementing by 1 each time (like doubling), then do table and summation.

§8.4 Summary

This section was unavoidably tricky and it may take time to sink in. I explained stuff in detail so that you have more intuition on the steps and can be able to tackle similar problems.

- We saw how, for tricky nested for loops, we don't actually have to compute the exact number of how many times it runs. We can instead, find a superset by extending the duration of loops into something that's easy to calculate. Then, we similarly find a subset by diminishing the duration of loops.
- In times where the loops don't increment by 1 each time, we have to get in to some gritty math. But what we did though is figure out how the variables behave in each loop to get a general pattern of what their values will be at a certain iteration. Then, we change the sum to be in terms of iteration numbers.
- We also use the stop conditions on each loop to find upper bounds for the sums. In particular, the outer loop's upper bound depends on n. The inner loop's upper bound depends on the value of i, which depends on the value of x (the iteration number for the outer loop).
- Rewriting stuff in terms of x and y instead of i and j gets us something we can sum.

§9 Merge Sort

Warning 9.1. From here on out, my algorithm explanations, proof of correctness, and runtime will be less formal than before. Meaning, the purpose isn't for rigor: it's to get you to understand the idea of how it works. If I broke down every detail to the simplest level, we would be here for much longer than we need to when I can just spoonfeed you the intuition. But do go and try to read the formal proofs in the lecture notes when you have the intuition down as that will improve your understanding of the algorithms. It's just that those formal proofs feel unmotivated and convoluted without fundamental, intuition in Layman's terms first.

§9.1 Introduction

So insertion sort had a worst case time of $\Theta(n^2)$. Not ideal, so can we do better?

First, I need to introduce a sub algorithm called "Merge."

Given two sorted arrays, we want to combine them (merge) to form a single sorted array. Here's an algorithm to do that, where A and B are the original sorted arrays. Let C be the new sorted array that we want.

- If one of the two arrays are empty, take the leftmost element from the non-empty array and add it to the end of C.
- Otherwise, if both arrays are non-empty, compare the leftmost elements of A and B. Whichever is smaller, delete it from its respective array and add it to the end of C.
- Rinse and repeat until both A and B are empty.

Warning 9.2. In Java, you can't actually "delete" elements from the array as easily like I did. I only did so to make it easier to explain. How you would actually implement it is have some sort of pointer that moves to the right in the original arrays as you "delete" elements to know where you are in each array. Anything left of said pointers, you already added to the new array and no longer care about.

Let's do a quick demonstration with sorting these two sorted arrays:

1	2	3	4
8	11	17	30

1	2	3	4
1	2	18	19

We compare the leftmost elements of both. So 1 vs 8, 1 is smaller, so we add 1 to C and delete it from the second array. Compare leftmost elements again: 2 vs 8, 2 is smaller, so we add 2 to C and delete it from the second array. Now, 8 vs 18, 8 is smaller, so we add 8 to C and delete it from the first array. Repeat this process until we have all elements in C and it looks like this:

1	2	3	4	5	6	7	8
1	2	8	11	17	18	19	30

The proof of correctness for merge basically relies on the fact that both arrays are sorted. Anything to the right of the leftmost element is bigger than it. So the smallest element among both A and B has to be the leftmost element of either A and B; anything else is necessarily greater than the respective leftmost elements, so thus, is not a contender for smallest element among both arrays. So using this fact, we can make a loop invariant where every step of the way, we choose the smallest element among both arrays and maintain order in the progress for C. I don't need to spell out the full formal details but rather the full intuition.

Runtime? So transferring a single element from either of the two arrays to C is constant time; doing some comparison stuff, "deleting" it from the respective array, and moving it to C. We make as many transfers as there are elements in both arrays. So this is $\Theta(n+m)$, where n and m are size of A and B, respectively.

But merge only works for two sorted arrays! Well, what if we could recursively sort arrays and merge them into a sorted array? Let's see how that works in merge sort!

§9.2 The Algorithm

So we want to take an unsorted array as an input and the sorted version of it as an output.

Here's the algorithm:

Base Case: If the array is of size 1, we just return it.
Otherwise, divide the array in to two halves:

- Recursively call merge sort on the left half of the array
- Recursively call merge sort on the right half of the array
- Merge the two sorted halves

§9.3 In Action

I'll skip all the details involving merge, as my focus is more on the recursive action going on. Let's see how merge sort sorts this array:

1	2	3	4	5	6	7	8
8	10	3	7	1	2	11	4

- So we divide into two halves: $8, 10, 3, 7$ and $1, 2, 11, 4$. We recurse on the first half. We'll get to the second half later.
- So now, we divide the half into halves: $8, 10$ and $3, 7$. We recurse on the first half. Again, we'll get to the second half later.
- So now, we have 8 and 10, individually. We hit our base case for both. Now, we start working our way up. We merge 8 and 10, which gets us $8, 10$.
- When we broke $8, 10, 3, 7$ into two halves, we now have the recursive work done for the first half. We just need to do the second half: $3, 7$.
- We break $3, 7$ down, hit the base case, and merge them to $3, 7$.
- So now, we merge $8, 10$ and $3, 7$ (the two parts we got recursively). This comes to $3, 7, 8, 10$.
- When we broke the original array in half, we now have the recursive work done for the first half. Now, we have to do the recursive work for the second half. I'll spare you the details and say the second half works out to $1, 2, 4, 11$.
- So now, we did the recursive work on both halves of the original array and got $3, 7, 8, 10$ and $1, 2, 4, 11$. Now, we merge them to get $1, 2, 3, 4, 7, 8, 10, 11$.

§9.4 Proof of Correctness

This is basically the same strong induction idea back from binary search. To give the intuition, obviously an array of size 1 is sorted, so that's the base case.

The inductive step comes from dividing the array in to two halves and recursively sorting them (because the halves are arrays of size less than n, the strong inductive hypothesis means both will be sorted correctly). So the two halves are sorted after the recursive calls. We know merge works on two sorted arrays, so we get the array of size n sorted.

§9.5 Runtime

So let $T(n)$ be the time for merge sort. We first check if we're in the base case, which is of constant time. Otherwise, we recurse on both halves of the array, which means we solve two subproblems of size $\frac{n}{2}$. Then, we merge, which is of time $\Theta(n)$, as reasoned by our runtime analysis for merge. The constant time check for the base case doesn't matter too much when we have a $\Theta(n)$. So we say

$$T(n) = 2T(\tfrac{n}{2}) + \Theta(n).$$

By Master Theorem, this is $\Theta(n \log n)$. No need to go through the trouble of expanding it when they don't need us to. Since $\log n$ is better than n, this is better than $\Theta(n^2)$, which is insertion sort's worst case. So we found a more reliable sorting algorithm in terms of time!

Warning 9.3. Don't get the idea that insertion sort is obsolete just because merge sort has a better runtime than it. We'll see later that merge sort has flaws of its own.

§9.6 Summary

- We introduced a sub-algorithm called merge, which takes two sorted arrays and merges them into a single sorted array
- We use merge to create a recursive sorting algorithm. Here, the array is divided in to two halves which are recursively sorted. Then, the two halves are combined with merge into a single sorted array
- Merge sort's time of $n \log n$ is better than insertion sort's worst case time of n^2

§10 Divide and Conquer

§10.1 Introduction

So we know how merge sort works, right? We divide the problem in to two subproblems, then recursion solves the two subproblems, and then we combine the two solved subproblems. This is called a divide and conquer algorithm. It has 3 main steps:

1. Divide: This is dividing the problem into multiple subproblems (usually 2). In merge sort, this is when we divided the array in to halves
2. Conquer: This is recursively solving each subproblem. In merge sort, this is when we made recursive calls to both halves of the array.
3. Combine: This is combining the solved parts. In merge sort, this is merging the two sorted arrays.

Note that not all divide and conquer algorithms have a combine step. For example, with binary search, after some work, the recursive call was simply going to one of the two halves of the array, completely disregarding the other half.

Advice 10.1 — In that regard, whenever you have a problem involving find an instance of something in an array and they want $O(\log n)$, that's usually going to be something along the lines of binary search: you want to check the middle and use that information to conclude you only care about one side of the array and recurse on that, while completing ignoring the other side. I wouldn't say this is always the case though.

Advice 10.2 — When the problem wants $O(n \log n)$, recall Merge Sort's recursion of $T(n) = 2T(n/2) + \Theta(n)$. So you can interpret this as having to recurse on both sides of the array and having $\Theta(n)$ work in combining the two solved portions. This isn't always the case, but may be a good starting point.

Advice 10.3 — Alternatively, when it is $O(n \log n)$, you can use Merge Sort once on the array without exceeding the time. The problem may be much easier when the array is sorted, so if you realize that's the case, do it.

Advice 10.4 — Use Master Theorem to verify your runtime for divide and conquer algorithms! Saves you time from expanding.

Warning 10.5. Remember that when you make a recursive call to one side of the array, you no longer have access to the other side of the array within the recursive work! An example would be if we needed to work on the subproblem provided by the left half of the array but for some reason in the subproblem, we needed the last value in the original array. We wouldn't be able to get that last value directly when working on the subproblem, so we'd need to use a parameter to pass the important information along recursive calls in that situation. After the subproblem is over, you get access to the whole array again, like when we did the merge after solving the two subproblems with merge sort.

§10.2 Problem Solving

Example 10.6 (Recitation)

You are given an integer array $A[1..n]$ with $n \geq 3$ and the following properties:

- Integers in adjacent positions are different
- $A[1] < A[2]$
- $A[n-1] > A[n]$

A position i is referred to as a local maximum if $A[i-1] < A[i]$ and $A[i] > A[i+1]$.
Example: You have an array $[0, 1, 5, 3, 6, 3, 2]$. There are multiple local maxes at 5 and 6.
Design an $O(\log n)$ algorithm to find a local maximum and return its index.

Let's understand the problem first. I propose to think of the array as a sequence of length $n-1$, where the sequence consists of up arrows or down arrows.

Have an up arrow at the ith position in the sequence when $A[i] < A[i+1]$ (modelling an increase) and a down arrow at the ith position in the sequence when $A[i] > A[i+1]$. So for the example array $[0, 1, 5, 3, 6, 3, 2]$, the arrow sequence would be $\uparrow\uparrow\downarrow\uparrow\downarrow\downarrow$. We don't have time to determine all the arrows because that would require $O(n)$ work, worse than the target runtime of $O(\log n)$; it's merely an easier way to think about the problem.

We're given $A[1] < A[2]$, meaning the first arrow in the sequence is $\uparrow$. We're also given $A[n-1] < A[n]$, meaning the last arrow in the sequence is $\downarrow$.

A local maximum occurs when we have $\uparrow$ then $\downarrow$, consecutively in that order.

We know the arrow sequence starts with $\uparrow$ and ends with $\downarrow$. So there MUST be some point where the sequence transitions from $\uparrow$ to $\downarrow$; it's inevitable considering the arrows at the endpoints of the sequence. But now, we have to figure out where. So the fact that a sequence starting with $\uparrow$ and ending with $\downarrow$ must have a transition point from $\uparrow$ to $\downarrow$, keep that fact in mind because it will be essential for our proof of correctness.

Also, remember we don't need to find all local maximums, just one. Let's determine the arrow in the middle. We can do this by checking two integers in the middle of the array at consecutive positions.

Let's say the middle arrow is $\uparrow$. So we know the arrow sequence is going to be $\uparrow$ (first arrow), something, $\uparrow$ (in the middle), something, $\downarrow$ (last arrow).

Remember how every sequence starting with $\uparrow$ and ending with $\downarrow$ must have a transition point? So we know the second half of the array has a local maximum considering what we know about the arrows. So we want to search there. As for the first half, well, there COULD be a transition point. But for all we know, it could just all be up arrows, so there is no guarantee we find a transition point there. So we don't want to bother searching that half of the array and focus on the half that we know has to have the transition point.

But what about when the middle arrow is $\downarrow$? By similar reasoning, we want to search the first half and don't bother with the second half.

As for the base case, that's when $n = 3$ and we have two arrows. Since the first arrow is $\uparrow$ and the second (which is the last) arrow is $\downarrow$, we have a transition point in front of us.

And there we have it, that's our algorithm.

Proof of correctness? Same old strong induction that we did for binary search. Base case is $n = 3$. Then, the inductive step relies on that fact where if the sequence starts with $\uparrow$ and ends with $\downarrow$, there's a transition point somewhere. Then, the two cases on the middle arrow, along with the recursion with the inductive hypothesis means it works out.

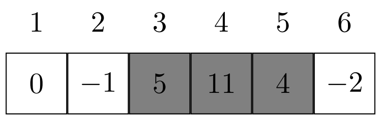
Runtime? We do constant amount of work to get the middle arrow and use that information to then solve 1 subproblem of size $T(n/2)$. Base case is obviously constant work, so we have $T(3) = k$ and $T(n) = c + T(n/2)$ for $n > 3$. Master Theorem implies $T(n)$ is $O(\log n)$. Alternatively, notice this is binary search's runtime.

Example 10.7 (Recitation)
You are given an integer array, with both positive and negative elements. Design an $O(n \log n)$ algorithm to return the sum of the continuous subarray with the maximum sum.

This is a hard problem, but let's think about it. In general, the largest continuous subarray is either going to be in one of three possibilities:

- It's entirely within the left half of the array
- It's entirely within the right half of the array
- It's partly in the left half and partly in the right half

Partly in the left half and partly in the right half would be something like this:



Anyway, we know that the largest continuous subarray is in one of those three categories. Let's find the largest for each respective category and compare the 3 at the end. The first two, we can get by recursively solving the problem on the two halves of the array, separately.

As for the subarray spanning on the middle? Not as easy to see, but we can cut a subarray spanning on the middle through the middle. So $A[3..5]$ in the example can be split in to $A[3..3]$ and $A[4..5]$. Not to mention the left half of any middle array must have the middle itself (3, in this case). The right half of any middle array must have the middle itself too (4, in this case).

So here's what we do to get the best subarray spanning on the middle. Consider the sum for $A[n/2, n/2]$, then $A[n/2-1, n/2]$, then $A[n/2-2, n/2]$, and so on until $A[1, n/2]$. Basically we check each subarray that starts at the middle and protrudes leftward. Keep track of the best sum we find as we go through them. So we take the best one, say $A[i, n/2]$.

We also do the same for the subarrays that start at the middle and protrude rightward: check $A[n/2+1, n/2+1]$, then $A[n/2+1, n/2+2]$, then $A[n/2+1, n/2+3]$, and so on until $A[n/2+1, n]$. Again, keep track of the best one of these and say the best one is $A[n/2, j]$.

We combine the best one that starts at the middle and protrudes leftward (which we called $A[i, n/2]$) with the best one that protrudes rightward (which we called $A[n/2, j]$) and combine the two to get $A[i, j]$, which necessarily passes through the middle of the array.

So we found the best subarrays for the three categories, we just compare the 3 to find the overall maximum.

As for the base case, that's when we have 1 element. Either we include it in the subarray, or we don't. If it's negative, don't include it. If it's positive, we include it.

Proof of correctness? Base case is pretty self-explanatory on why it works. Don't include an unnecessary negative that brings the sum down, but definitely include a sole positive.

As for inductive step, we again know the bets subarray is in one of the three categories. The recursive call and inductive hypothesis correctly gets us the best in the first two categories. As for proving we get the best in the third category, well, there's a part that protrudes leftward from the middle (call this part L) and there's a part that protrudes rightward from the middle (call this part R). Clearly, L has no effect on R, so they're independent. To optimize the overall middle array, both L and R should be optimal. And we optimize it by going through all the possibilities and cherry picking the best one.

So we correctly obtain the best from all three categories and all that's left is to compare them. This proves the inductive step.

Runtime? Well, when we get the best from both halves, that's two subproblems of size $\frac{n}{2}$. As for the best subarray spanning the middle, we check $n/2$ different subarrays protruding leftward and $n/2$ different subarrays protruding rightward. We can save time on sums by reusing previous work: the sum for $A[m-1, n/2-1]$ for example is the sum for $A[m, n/2-1]$ plus $A[m-1]$. So we're really just adding $n/2$

numbers together and doing some constant work in checking if we found a new best when going through the leftward protruding parts. Same with the rightward protruding parts.

So finding the best subarray spanning the middle is $\Theta(n)$ work. So we have $T(n) = 2T(\frac{n}{2}) + \Theta(n)$. This is merge sort's time, which is $O(n \log n)$.

§10.3 Summary

- We've seen before this section how algorithms like binary search and merge sort break the problem in to parts that progressively get easier to solve.
- Divide and conquer captures the general strategy behind those two algorithms. We divide the problem in to subproblems and then recursively solve those subproblems. Sometimes, we may combine the solved subproblems.
- We saw a problem where we only cared about one side of the array, so we didn't have a combine step.
- We also saw a problem where we needed to solve the subproblems provided by both sides of the array and combine them.

§11 Quick Sort

§11.1 Introduction

So Merge Sort's $n \log n$ runtime is cool and all. But there's an issue with it. It'll take up a lot of memory. Think about it: you have a problem of size n. You break that up in to two subproblems of size $n/2$ and need to allocate memory for the arrays corresponding to the would-be results of these subproblems. Then you break all of those in to two subproblems of size $n/4$ and need to allocate separate memory for all these subproblems. And so on.

The issue is that these subproblems don't get fully resolved until we break the subproblems into a small enough size that we reach a base case. So in breaking the problems into subproblems constantly, we use up a lot of memory, especially for a massive value of n.

Maybe we can try to get a sorting algorithm in $n \log n$ time that is in-place? Meaning we don't have to create these additional arrays when making recursive calls and we just do all the swapping and action in our original array?

§11.2 Main Idea

Here's a demonstration. We have this array. I'm going to choose an element at random from this array to be our "pivot", say 7 for this demonstration:

1	2	3	4	5	6	7
6	19	3	10	7	11	8

We want to switch the pivot with the last element in the array just to get it out of the way for now. Then, we consider the stretch of the remaining numbers. We label the left end with an L pointer and the right end with a right pointer.

L					R	
6	19	3	10	8	11	7

We're going to keep running this loop, until the L is directly to the right of R:

- Check the element where the L pointer is

  - If the element is less than the pivot, move the L pointer 1 slot to the right
  - If the element is greater than the pivot, swap the numbers at the L and R pointers and then move the R pointer 1 slot to the left.

When the above loop ends, the L and R pointers will have crossed. Insert the pivot in between the crossed pointers.

Let's work through the example. 6 is less than the pivot, just move the L pointer to the right:

	L				R	
6	19	3	10	8	11	7

19 is greater than the pivot, swap 19 and 11 and move the R pointer to the left:

	L			R		
6	11	3	10	8	19	7

11 is greater than the pivot, so swap and move R to the left:

	L		R			
6	8	3	10	11	19	7

Swap again:

	L	R				
6	10	3	8	11	19	7

and again:

	LR					
6	3	10	8	11	19	7

3 is less than the pivot, so we just move L to the right:

	R	L				
6	3	10	8	11	19	7

The two pointers have crossed, so we insert 7 back in between them:

	R		L			
6	3	7	10	8	11	19

The essential gist is we pick a pivot element. Then, we get everything less than the pivot to the left of the pivot in the array and everything greater than the pivot to the right of the pivot in the array.

The L and R pointers are a way to monitor our progress. Through a loop invariant, you can show anything strictly to the left of the L pointer is less than the pivot at every step. Similarly, anything strictly to the right of the R pointer is greater than or equal to the pivot at every step. Once the two pointers cross, you know you have everything less than the pivot on the left and everything greater than the pivot on the right, so you insert the pivot in that location.

I claim the pivot is now in the correct spot in the array and this would be the case for any choice of an array and pivot. Why? Because we already identified everything less than the pivot and greater than the pivot. If the array were in order, going left would mean smaller numbers and going right would mean greater numbers. So in the final sorted array, everything less than the pivot is left of the pivot and everything greater than the pivot is right of the pivot. So the pivot doesn't need to even move from this spot, and it boils down to sorting the two halves the pivot divides the array in to.

So we can use this idea in to an algorithm called Quick Sort. So we choose a pivot and partition the array about the pivot. This means we get everything less than the pivot to the left of it and everything greater than the pivot to the right of it, like we did in the example. Then, the pivot divides the array in to two halves, where we recursively solve each half. Eventually, every element will be a pivot and thus, get put in the right place. The base case would be if we have 1 element in the array and it would be already sorted, so we do nothing.

The neat thing about this algorithm is, it is in-place, meaning we didn't have to create any additional arrays through recursive calls: we do all the sorting within the original array. This means quick sort doesn't require much additional memory beyond the original array.

There are two types of quick sort:

- Deterministic: We pick the pivot based on some rule we decide on (like always the first element in the array, or always the middle)
- Randomized: We pick the pivot at random.

In proof of correctness and runtime though, there is no difference between deterministic and randomized. Because the first element being a pivot is equally likely to be as good or bad as the second element, or the third element, or the whatever element, considering random nature of an arbitrary array.

§11.3 Proof of Correctness

Same old strong induction. Base case of 1 element obviously works. When we use the pivot to partition the array, we reasoned earlier that everything to the left of it is less than the pivot and everything to the right of it is greater than the pivot. From that fact, we concluded the pivot is in the right position in the array and that it boils down to recursively sorting the two halves of the array. By IH, the two halves will get recursively sorted.

§11.4 Runtime

> **Review 11.1.** We're going to use random variables and Bernoulli trials here, along with LoE. Go back and review that from CIS 1600 if you need to.

Okay, so we can all agree, quick sort, in essence, is just a bunch of comparisons and swapping. One comparison with the additional possibility a swap follows it, is obviously constant time. So it boils down to how many we do.

Best case generally isn't very informative, as it doesn't really tell us how an algorithm may function in general. Instead, let's look at expected runtime.

To that end, let $y_1 < y_2 < \cdots < y_n$ be the n elements of the array in increasing order. Keep in mind, the originally array is more often than not, not going to be sorted already.

For integers i and j with $1 \le i < j \le n$, let $X_{i,j}$ denote a random variable on how many times y_i is compared to y_j throughout the entire process. Note that we don't have $i = j$ because it doesn't make sense to compare an element to itself in the context of quick sort. And $X_{j,i}$ is the same as $X_{i,j}$, so we do $i < j$. Anyway, the runtime is

$$T(n) = \sum_{1 \le i < j \le n} X_{i,j}$$

because this sum takes every pair of elements in the array, counts the number of times the two are compared, and contributes it to the total to get an overall count on the number of comparisons. Taking the expected value of both sides and using LoE (remember LoE allows us to separate expected value over sums!) implies

$$E[T(n)] = E\left[\sum_{1\le i<j\le n} X_{i,j}\right] = \sum_{1\le i<j\le n} E[X_{i.j}].$$

So now our goal is to find $E[X_{i,j}]$.

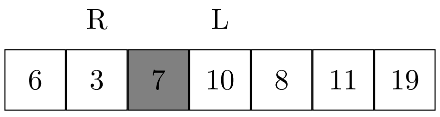
Remember how quick sort works? Whenever things are being compared, the pivot element is always involved. So a comparison between y_i and y_j would mean one of those two elements is currently the pivot.

I claim that if y_i and y_j are compared once, they'll never be compared again, meaning $X_{i,j}$ is at most 1. Why is this? Let's just say y_i is the pivot (the case of y_j being the pivot reasons similarly). We compare y_j to y_i (the pivot) inevitably and then move y_j to the appropriate half of the array. But then, we recurse on that half, completely ignoring y_i, as it is no longer part of that half. So once we compare the two once, we'll never do it again because of the recursion.

Okay, so $X_{i,j}$ is either 0 or 1, so it's essentially a Bernoulli random variable. Also, let $F_{i,j}$ be the event that $X_{i,j} = 1$ occurs. Now, it boils down to

$$E[T(n)] = \sum_{1\le i<j\le n} E[X_{i,j}] = \sum_{1\le i<j\le n} \Pr[F_{i,j}].$$

But also, because we recurse on both half of the arrays, the two sides of the array won't interact with each other at all during the recursive work. Let's take that finished example for demonstration:



So we partitioned everything about 7 and recurse on both halves. That means 3 won't interact with 8 because they're on opposite halves. Same with 6 and 11 and every pair of numbers on opposite halves. Can we use this idea to get a better understanding of when $F_{i,j}$ occurs?

So suppose we have k so that $i < k < j$. If y_k is a pivot element before both y_i and y_j become one, what will happen is we partition the array about y_k and the order means y_i and y_j end up on opposite halves. Then, the recursion ensures we never have the chance to compare y_i and y_j too each other (and we don't need to because of the purpose of a partition).

However, if we have $k < i < j$, y_k being the pivot doesn't mean we permanently lose the chance to compare y_i and y_j because then, both y_i and y_j end up on the same side of the partition. Same with $i < j < k$.

Okay, think about CIS 1600 probabilities. So for $F_{i,j}$ to occur, y_i or y_j must be selected as a pivot before any y_k with $i < k < j$ is selected as a pivot. So there are $j - i + 1$ possible pivot elements in question here: y_i, y_{i+1}, y_{i+2}, $\cdots$, y_j. Each one is uniformly likely to be the pivot first, since we select pivots arbitrarily. Only when y_i or y_j is the first of those possible pivots, will it allow $F_{i,j}$ to occur, only 2 possibilities of those choices. So $\Pr[F_{i,j}] = \frac{2}{j-i+1}$. Now, for some gritty math. Note that summing over all pairs (i, j) with $1 \le i < j \le n$ is basically summing over all pairs with $1 \le i \le n-1$ and $i+1 \le j \le n$ (think of it like a for loop if it's hard to see).

$$E[T(n)] = \sum_{1\le i<j\le n} \Pr[F_{i,j}] = \sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \frac{2}{j-i+1} = \sum_{i=1}^{n-1}\left(\frac{2}{2} + \frac{2}{3} + \frac{2}{4} + \cdots + \frac{2}{n-i+1}\right).$$

Those who haven't taken CIS 1600 with Rajiv may not know this, but $\sum_{a=1}^{b} \frac{1}{a}$ is basically $\log b$ (the Harmonic series). The stuff inside the parantheses is basically double a harmonic series up to $n - i + 1$, so

$$E[T(n)] = \sum_{i=1}^{n-1}\left(\frac{2}{2} + \frac{2}{3} + \frac{2}{4} + \cdots + \frac{2}{n-i+1}\right) = \sum_{i=1}^{n-1}(\log(n-i+1))$$

$$= \log(n) + \log(n-1) + \log(n-2) + \cdots + \log(2) = \log(n!) = \Theta(n \log n),$$

where we used a recitation problem saying $\log(n!) = \Theta(n \log n)$. That was a lot of work, but the takeaway is Quick Sort is expected $\Theta(n \log n)$. But that's only **expected**. What about worst case?

Well, it turns out the worst case is when the pivot is the largest or smallest element in the array. What will happen is we make all the $n-1$ comparisons between the pivot and all other elements and move stuff around. But all the elements will be in one side of the pivot. Then, we recurse on that side, which is an array of length $n-1$. So in essence, for the worst case, we have $T(n) = (n-1) + T(n-1)$. Base case is $T(1)$ is a constant. Expanding this gives

$$T(n) = (n-1) + (n-2) + \cdots + 2 + 1 + T(1) = \frac{(n-1)n}{2} + T(1).$$

This is $\Theta(n^2)$, which is insertion sort's worst case time. Okay, so the nice expected runtime comes with the issue of having a not so cool worst case time.

§11.5 Summary

- We saw how quick sort picks pivots at random. By moving elements around, we can get everything less than the pivot on the left and everything greater than the pivot on the right. This puts the pivot in the right spot in the array.
- We recurse on both sides to sort the halves to the left and right of the pivot.
- Quick sort is in-place, meaning we do all the action in the original array without much additional memory necessary.
- We found the expected runtime is $\Theta(n \log n)$, but the worst case is $\Theta(n^2)$.

§12 Selection

§12.1 Introduction

Suppose we want to find the smallest element in an array. Oh that's easy, just go through the array, keep track of the smallest we encounter so far and return it at the end. Takes $O(n)$ time.

2nd smallest? I guess, so through the array once and find the smallest and get rid of it. Then, the 2nd smallest is the new smallest. Takes two $O(n)$ passes, so still $O(n)$.

What about the median? This is basically the $\frac{n}{2}$th smallest. Well, first pass, we find the smallest among n elements. Second pass, we find the smallest among $n-1$ elements. Third pass, we find the smallest among $n-2$ elements. And so on until we have to find the smallest among $\frac{n}{2}$ elements. How long will that take? Well, we have $\frac{n}{2}$ passes and for each pass, we work with at least $\frac{n}{2}$ elements in the array, so that's already $\frac{n}{2} \cdot \frac{n}{2} = \frac{n^2}{4}$, which is $\Omega(n^2)$.

If we have to do that, we might as well merge sort, which takes $\Theta(n \log n)$ and get the median that way. But can we do better? Can we get the ith smallest element (for any i with $1 \le i \le n$) in $O(n)$ time? That's selection.

§12.2 The Algorithm

This is to find the ith smallest element in the array.

- Divide all n elements into groups of 5. Excess elements can go in their own group.
- Find the median element in each group of 5.
- Take the group consisting of the median element of each group. Find the median M of that group by recursive calling the algorithm.
- Partition the entire array about M like in quick sort.

- Let p be the resulting position number of M. If $i = p$, just return M. If $i < p$, recurse on the left half of the array, finding the ith smallest element. If $p < i$, recurse on the right half of the array, finding the $(i - p)$th smallest element.

Base case is when we have $n = 1$ and we just return whatever is the lone element in the array.

§12.3 Proof of Correctness

Why we go about a convoluted way in finding M to choose as a pivot isn't particularly important for proof of correctness. Moreso for runtime. Anyway, we know how partition works back from quick sort and the useful property of it: it gets everything in the array less than the pivot to the left of the pivot and everything greater than the pivot to the right of the pivot. The pivot is also in the correct spot if the array were to be sorted in order.

So if $i = p$, we know M, the pivot, is what we want because it's the pth smallest element by how a pivot works.

Otherwise, if $i < p$, we know the ith smallest element is less than the pth smallest element. By the pivot properties, that's to the left of the pivot, which is why recurse there.

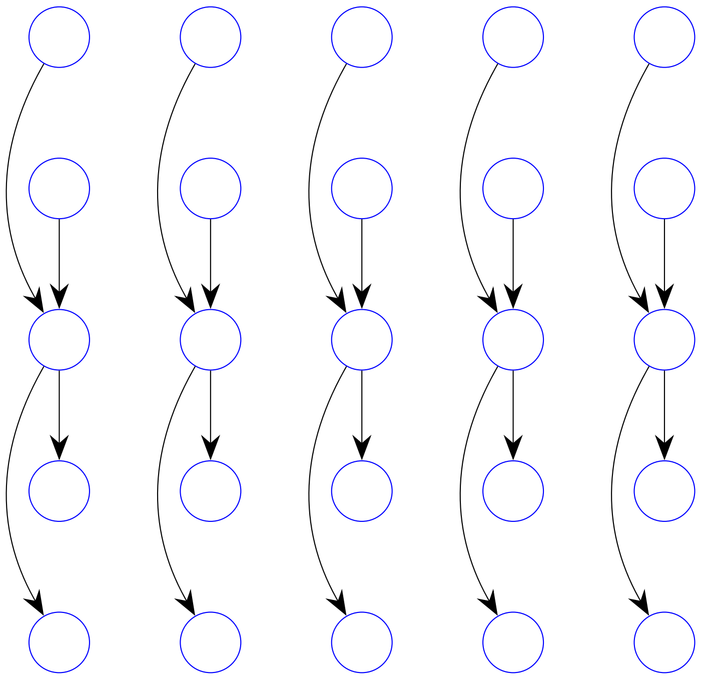
Otherwise, if $i > p$, we know the ith smallest element is greater than the pth smallest element. By the pivot properties, that's to the right of the pivot, which is why recurse on it. Except one thing. We completely lose access to the left side of the array during the recursion. So the ith smallest element in the whole array might not be the ith smallest element in the right half (with the left half deleted). But we know the pivot and everything to the left of it is less than anything in the right half, so deleting that turns the ith smallest element in the whole array to the $(i - p)$th smallest element in the right half.

So that justifies the recursive step, which is our inductive step. Base case is easy, so that's the strong induction needed for recursive algorithms.

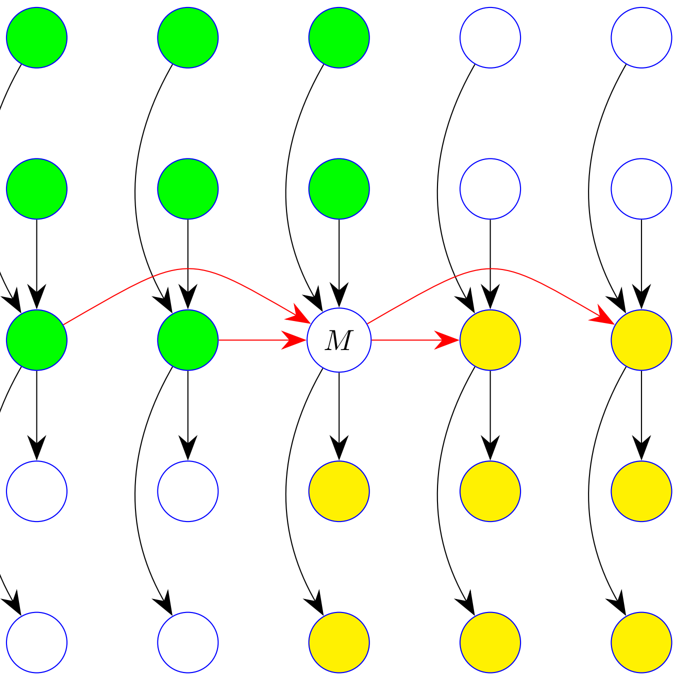
§12.4 Runtime

Let M be the median of the medians that we found as instructed in the algorithm.

Let's say we have 5 groups for demonstration without any leftover (leftover elements are negligible for runtime). In practice, we're going to have $\frac{n}{5}$ groups. I'll have groups represent columns. We can reorganize each column, so elements less than the median in its group are above the median in its column and elements greater than the median are below the median in its column. An arrow from one element a to another element b symbolizes $a < b$.



So the medians occupy the middle row. We figure out the median of the medians (which we called M). We can reorganize the columns so medians smaller than M are to the left of it and medians bigger than M are to the right of it. And we can draw arrows again.



Notice something about those elements I colored in yellow? Yes, we can get to all of them from M through a series of arrows, meaning these are all elements greater than M. How many of these are there? Well, they only show up for columns to the right of M and we have $\frac{n}{5}$ columns (corresponding to the number of groups). M being the median is at the halfway point, so $\frac{n}{10}$ columns contain these yellow elements. Each column that contains a yellow element has 3 of them (the 3 bottommost rows). So that's about $\frac{3n}{10}$ yellow elements, or elements we know are DEFINITELY larger than M.

Similarly, green elements are elements that are DEFINITELY smaller than M because you can follow a series of arrows to get to M. Similar logic means there are about $\frac{3n}{10}$ of these green elements.

So we have chosen M as a pivot for where we know it has at least $\frac{3n}{10}$ elements larger than it and at least $\frac{3n}{10}$ elements smaller than it (by the green element and yellow argument thing). So that means, worst case scenario, when we partition and do the pivot stuff, each side of the array can have at most $n - \frac{3n}{10} = \frac{7n}{10}$ elements (because the other side has to have at least $\frac{3n}{10}$ elements). So when we do the recursion, worst case, we solve a subproblem of size $\frac{7n}{10}$.

Enough blabbering, let's analyze what goes in to the runtime with time function $T(n)$:

- We find the median in each group of 5. Finding a median in a group of 5 is $O(1)$ because it doesn't depend on any variable. But we have $\frac{n}{5}$ groups, so this is $O(\frac{n}{5})$.
- We find the median of the medians, which is a subproblem of size $\frac{n}{5}$ because we have a median from each of the groups. This is $T(\frac{n}{5})$.
- We partition everything about the median of medians, which is $O(n)$ (check each element in the array)
- The array is in two halves and we know the size of either side doesn't exceed $\frac{7n}{10}$. We recurse on one, worst case, so this is $T(\frac{7n}{10})$.

So our runtime recurrence is $T(n) = O(\frac{n}{5}) + T(\frac{n}{5}) + O(n) + T(\frac{7n}{10})$. Solving this recursion formally is more trouble than it is worth and not particularly relevant. So I'll tell you $T(n)$ is $O(n)$.

Advice 12.1 — So we can get the median of an unsorted array in $O(n)$ time. This can be useful for partitioning when you don't care about the order within the partition.

Say like you wanted to identify all elements less than the median and all elements greater than the median and put them in separate piles. You can do just that by identifying the median in $O(n)$ time and the partition work gives you the two piles.

§12.5 Summary

- We took the partition intuition back from quick sort and made an algorithm that gets us the ith smallest element in an array in $O(n)$ time
- We chose the median of the medians (we called this M) as our pivot.
- It turns out M has the property that at least $\frac{3n}{10}$ elements are bigger than it and at least $\frac{3n}{10}$ are smaller than it. This limits the size of the recursive subproblem we need to solve.

§13 Lists as a Data Structure

§13.1 Introduction

> **Review 13.1.** You can review the Oracle JavaDocs for linked lists and array lists if you're rusty on them.

Back from CIS 1200, we used linked lists and array lists as essentially, resizable arrays. But now, let's not rely so much on Java's implementation of them and try to implement them from scratch, so we get a better grasp of runtime and space.

So a list as we know, is a finite sequence of ordered elements. In particular, the order aspect means each element has a position.

The list abstract data type needs to support the following operations:

- Append (add something to the back)
- Insert
- Delete
- Access

The array list and linked list both happen to be two implementations of a list.

§13.2 Operations

We know unlike an array, an array list can change in size even after it is declared. But how would we implement this? We would inevitably have to use an array, but move everything to a bigger array when the array fills up. That allows us to resize the array list.

So suppose we had this array list:

1	2	3	4
2	5	10	1

All's well and good until we want to add something else. So if we want to add 15, we have to copy everything to a bigger array and add 15 to the next empty slot:

1	2	3	4	5	6	7	8
2	5	10	1	15			

This resizing is going to be annoying, right? Well, we can do our resizings strategically.

If we resized from 4 to 5, we would have to resize again if we wanted to add another element. Having to resize every time we want to add something new to the array would be time consuming. If we resized from 4 to 1000, we won't have to resize again for a while. But that's a lot of space we're wasting on empty cells of the array that we might not ever use. So there has to be a balance between resizing large enough that it doesn't have often and saves time but not too much that it wastes memory.

Anyway, let's think about runtime of adding a single element in an array list. If we don't have to resize, it's just $O(1)$. But when we do, it's $O(n)$ (where n is the current number of elements we have) because we have to copy n elements over to a new array and then add it. But resizing only happens every so often. So saying "adding an element in an array list is $O(n)$ worst case" omits the fact that the worst case only happens every so often. So we need a way to analyze runtime in a way that is more informative for this situation.

§13.3 Intro to Amortized Analysis

Definition 13.2 (Amortized Runtime)**.** A way of analyzing runtime of a single operation by doing n operations and averaging them. This helps get around when there is a worst case but it happens every so often and we know when it happens.

It helps to give an example outside the context of computer science to understand this. Suppose I'm paying rent. I pay \$1 on every day except Sunday, but on Sunday, I pay \$22. Worst case, I pay \$22 one day, but that's only once every 7 days. Thinking about the average in the grand scheme of things over the week, it is

$$\frac{1+1+1+1+1+1+22}{7} = 4,$$

as my amortized pay because 6 times a week, I'm paying \$1 and on 1 day I'm paying \$22. So looking solely at the worst case doesn't give us the big picture because that alone omits the fact that I'm not really paying anywhere as much on the other days, so the average in the long run is much lower than what the worst case may suggest.

Warning 13.3. Do NOT think amortized and expected runtime are the same thing! The key difference is for amortized, we usually know EXACTLY when the worst case happens AND that it doesn't involve any randomness, like with my stupid rent example.

For expected runtime, it usually describes an algorithm that could be close to the best case today and then something close to the worst case tomorrow. Or vice versa. Or any sort of randomness. Who knows!

Anyway, let's look at an amortized analysis of the append operation to an array list. Suppose our rule for resizing is we start at an array of size 1 and double each time we need to resize. So it goes from 1 to 2, then 2 to 4, then 4 to 8, and so on.

Let's see how much time appending k elements to an initially empty array costs. Two things contribute to time: putting the element in the array when we have the space and resizing when we need to.

Well, putting an element to the array when we have the space is just $O(1)$, so simply adding the elements is $O(k)$.

And let's see how much time resizing adds. So we resize at 1, meaning we have to copy 1 element at that time. We resize at 2, where we copy 2 elements. And at 4, where we copy 4 elements. And so on. The last time we resize is at $2^{\log_2(k)}$. So adding all instances of having to copy elements over, we have

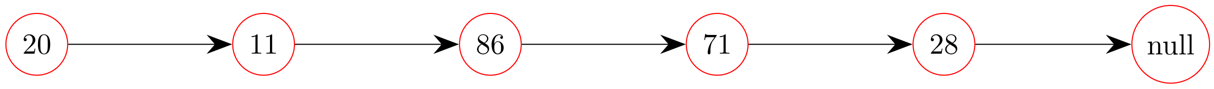
$$\sum_{i=0}^{\log_2(k)} 2^i = 2^{\log_2(k)+1} - 1 = 2k - 1.$$

This combined with the time it takes to put the k elements means the k append operations are $O(k)$. So the average is $O(1)$, so a single append operation is amortized $O(1)$.

§13.4 Runtime Analysis for Lists

Let's think about the other operations for an array list. Insert is worst case $O(n)$. Even with the possibility with resizing, what if we want to insert something at the front? We'd have to manually shift all the other n elements down. Remove? Same idea. Access? Luckily, that's $O(1)$ because it's an array.

As for linked list, we can think of this as a series of nodes. There is the pointer to the head, where we start. Each node has data of its own (like the entries in an array) and a next pointer directing us to the next node in the list. When we reached the end of the list, the last node's next pointer is simply set to null. Here's a simple linked list of size 5:



For now, assume we can only start a traversal of the linked list at the head. So if we need to access the end of it, we have to follow all the way through and can't skip to the end. Let's look at the operations.

Appending is $O(n)$, since we need to go all the way to the back. Insert is worst case $O(n)$ because we might need to go all the way to the back. Access is worst case $O(n)$ because again, we might need to go all the way back. And remove is worst case $O(n)$ for the same reason.

Operation	Append	Insert	Access	Remove
Array List	amortized $O(1)$	worst case $O(n)$	$O(1)$	worst case $O(n)$
Linked List	$O(n)$	worst case $O(n)$	worst case $O(n)$	worst case $O(n)$

It looks like an array list is better than linked list in most things in terms of time. But that doesn't necessarily render a linked list as obsolete because we need to analyze space.

§13.5 Space Analysis

Let's just say all elements in question are of the same size, whether they are put in an array list or linked list. Let's say a single such element is of size E. We should consider what we need to allocate space for in both an array list and linked list.

There may be n elements in an array list. But the actual array used to implement an array list is going to be much bigger than n because we resize but leave unused spaces we need to fill up. Regardless of the spaces being used or not, they're each all just as big as a single element. So if our actual array is of size D, the amount of space we use for the array list is $D \cdot E$.

For a linked list, we have the elements and pointers to the next one. Each element has a pointer to the next element (including the last one, which just points to null to signify the end of the list). So if a pointer is of size P, a linked list of n elements is $n(P+E)$ because for each element, we have the element itself and a pointer to the next.

I'll tell you this: for the most part, the linked list is going to be more space efficient than the array list. But there could be a time where the array list has less space than the linked list. So this would be when $n(P+E) > D \cdot E$ or $n > \frac{D \cdot E}{P+E}$. This is called the "break-even point." Maybe let's do a demonstration?

Suppose a pointer was 4 bytes and an element was 7 bytes, so $P = 4$ and $E = 7$. So the break-even point is when $n > \frac{7D}{11}$, as derived above. For n above the break-even point, the array list is better spacewise. For n below the break-even point, the linked list is better spacewise.

Here's the intuition behind this. Suppose our actual array was 256 so $D = 256$ and the break even point is roughly $n > 162$. Now, whether the array list has size 1 or size 100 or size 210, the actual array will always take up 256 spaces worth of elements (before we have enough elements to the point where we need to resize).

So if our list is of size 1, it's clear $D = 256$ for the array list is a massive waste of space and why the linked list is better. But when we add an extra element, the linked list would increase in space by adding a pointer and extra element, but the array list doesn't increase in space because an extra space gets allocated for the second element. That's the idea here: as we add more elements to the array list, we use up the previously wasted space, whereas we necessarily need more space for the linked list. So eventually, when the linked list gets big enough, we create more pointers and space for elements that it eventually makes up for the originally wasted space in the array list. With the numbers above, we hit this threshold (the break-even point) at $n = 163$ when the pointers for the linked list and elements outweigh all the 256 original slots in the array list (even with some slots being unused).

Also, to avoid wasting so much space like we did, we can implement a resize down when we have a ton of unused space. Suppose the actual array is of size D. If we find that we have less than $\frac{D}{4}$ elements, we should resize the array to size $\frac{D}{2}$ (half it essentially).

§13.6 Summary

- We saw how the linked list and array lists would be implemented and how they work. In particular, an array list has to secretly resize if the actual array being used reaches its maximum capacity.

- We learned about amortized runtime, which thinks about the average in the long run because the situation is that the worst case happens only so often. For example, we may need to resize the array to add a new element but only once in a while.
- We looked at space and how there are times where a linked list may be more efficient than an array list and vice versa, which is the break even point.
- An array list may waste a ton of space at first with unused elements but it gets made up for as new elements are added and as a linked list requires more space for pointers and elements.

§14 Stacks and Queues

§14.1 Introduction

So we've learned about array lists and linked lists. Can we go a step further and use them to implement other data structures? Yes, we can. We'll see that with stacks and queues.

Definition 14.1 (Stack)**.** A list that follows a "last in, first out" property. That means, when you add a new element in to the list, it always goes to the end. However, when you want to remove an element from the list, you can only remove the element at the end.

The analogy for stacks is, you have a stack of plates. You can add extra plates on top of the stack. But it would be dangerous to try to pull out a plate from the middle or the bottom. So the only safe plate to remove is the one from the top and that's how you remove plates. It's a useful data structure when you have stuff and stuff added more recently have priority.

Definition 14.2 (Queue)**.** A list that follows a "first in, first out" property. That means, when you add a new element in to the list, it always goes to the end. However, when you want to remove an element from the list, you can only remove the element at the start.

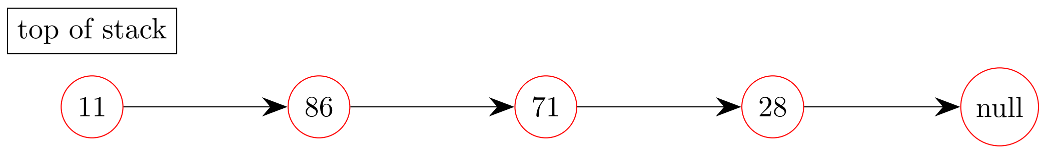
The analogy for queues is like a real world queue. Don't want to cut the line, as that would be rude. So you go to the back. Then, some people may arrive behind you while people up front get called to do whatever they were waiting in line for. It's a useful data structure when you have stuff and stuff found first have priority.
Now that we're acquainted to the definitions, let's examine the implementation and functions of stacks and queues.

§14.2 Stacks

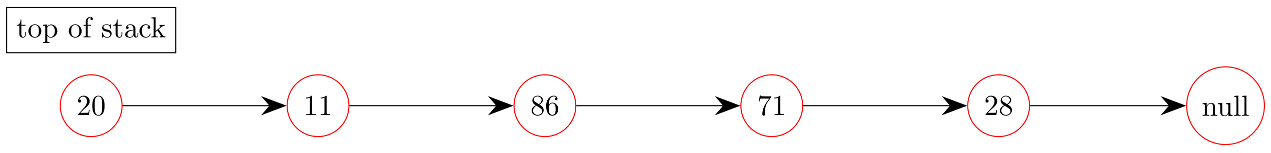
There are three operations that must be supported for it to be a stack:

- Push: add an element to the end of the list
- Pop: remove the element at the end of the list
- Peek: return the element at the end of the list

We can implement a stack with either a linked list or an array list. Let's think about both.
So for a linked list, we know the action is happening at the end of the list, or the top of the stack. While it may seem weird at first, let's have the "end of the stack" (or the top of it) be the start of the linked list. This way, we can have a pointer to where the action is happening, and the pointer can take us to the top of the stack in $O(1)$ time.

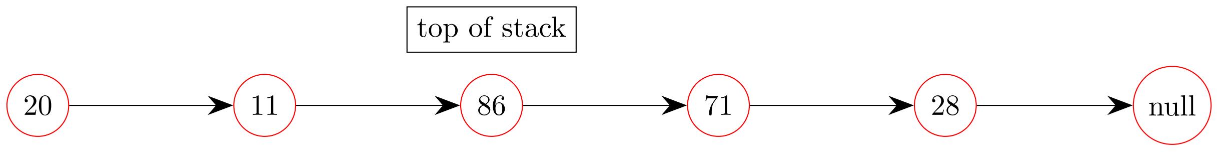


Say like we want to push 20. Easy way to implement this is by creating a new node whose next is the current top of the stack. Then, change the "top of stack" pointer so it goes to the new start:

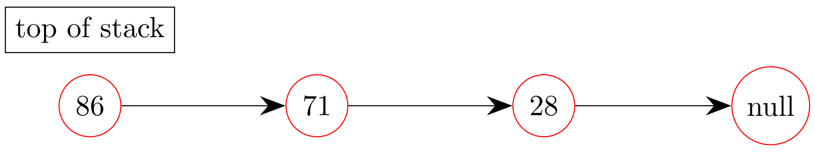


This is all $O(1)$ time: adding a new node and pointer and redirecting the top of stack pointer.

As for pop, we can we can have the top of stack pointer move to the right instead of the left with the next pointers guiding us to the next plate in the stack. So if we wanted to pop twice, we'd move the top of stack pointer:



But realistically, we no longer need the 20 and 11 nodes and having them stay there is just a waste of space. So before moving the top of stack pointer, we'd want a temporary variable storing the node we're about to destroy, move the top of stack pointer to the next node, and then destroy the unwanted node by setting it to null:



One push is $O(1)$: just redirect a pointer and destroy the node behind it after.

As for peek, that's easy. Just see what node the top of stack pointer (because the pointer should always be at the end of the list) takes you to and return the value there. That's $O(1)$ as well.

Using an array list is a bit trickier but still manageable. We can have some sort of counter keep track of how many elements we have as we add or remove them so we always know the position of the last element and get there in $O(1)$ time. Push is just append, while pop is just removing something in the last slot (which luckily, doesn't force you to shift any of the elements over). And peek is easy: just use the counter to get the position of the last element and go there.

As for runtime, push is amortized $O(1)$ (because it is append in an array list, which may run in to resizing issues). Pop is remove without shifting elements but also runs in to resizing issues (resize down), so this is also amortized $O(1)$. Peek is regular $O(1)$.

Also, for both implementations of a stack, we can have an isEmpty and size method. Both can easily be done through a counter monitoring the number of elements we have and thus, we just check a variable. For isEmpty, we would check if the counter is 0, while size, we just return the counter. Both are $O(1)$ time.

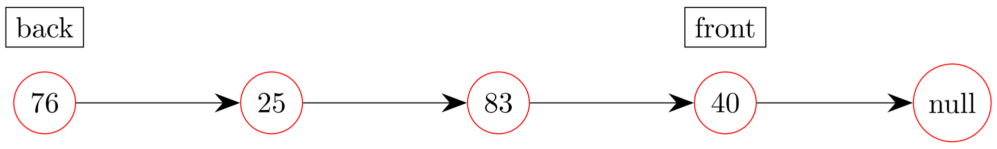
§14.3 Queues

There are three operations that must be supported for it to be a queue:

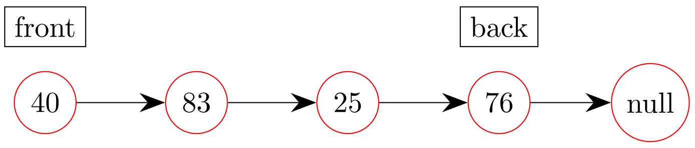
- Enqueue: add an element to the end of the list
- Dequeue: remove the element at the start of the list
- Peek: return the element at the start of the list

Again, we think about how we would implement this in both a linked list and array list.

Enqueue is basically the same as push in a stack. But the problem is the dequeue takes place in a different location then enqueue. So let's have two pointers: one for the front of the list and one for the back of the list. A pointer to the front of the list serves as a shortcut when we need to do something there because I don't want to have to traverse the entire list just to get from the back to the front.

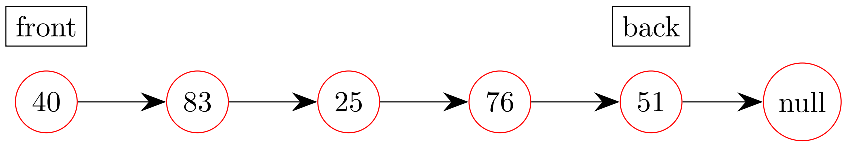


Okay, so enqueue works very similarly to push from a stack. We'd think dequeue is similar, move the front pointer to the left and then destroy the node behind... except we can't do that because the nodes don't have pointers to the left! Maybe let's reverse where the front and back of the queue is, instead?



Seems weird that the queue arrows are pointing from the front to back, but bear with me.

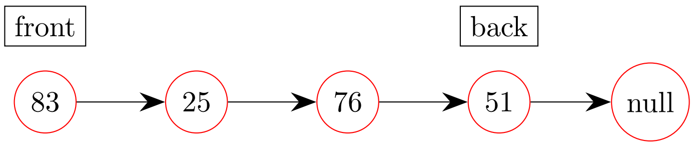
So how will enqueue work? Add a new node. For the current back, change its next to that new node and move the back pointer to the right. So let's enqueue 51:



This is $O(1)$.

As for dequeue, we implement it similarly to pop from a stack (even though popping takes place at the end of the stack and dequeue takes place at the start of a queue).

So dequeuing means remove 40 and the new front is 83:



Also $O(1)$. As for peek, that's easy. The front pointer takes us to the node with the value we want. Simple $O(1)$.

As it turns out, an array list will be quite tricky. There will be a problem that pops up that we need to address related to size. Okay let's have an array list of size 8 and enqueue 5, 7, 14, 23, then 2. We can keep track of what position we're at as we add in new elements.

1	2	3	4	5	6	7	8
5	7	14	23	2			

Eventually, we need to dequeue, so suppose we dequeue the first 3 elements. Well, if we dequeue 5, I don't want to have to shift everything over. So let's not shift stuff over as we dequeue.

1	2	3	4	5	6	7	8
			23	2			

Now, let's enqueue 37, 21, and then 15:

1	2	3	4	5	6	7	8
			23	2	37	21	15

Now let's try to enqueue 10. Well, we're at the end of the array, so the computer may think we're at full capacity and we need to resize... except that we're not actually at full capacity. We're just a bunch of space near the front because we were lazy in not shifting everything over. But shifting everything over takes time and we don't want to have to do it for every single enqueue.

I've got it! What if we say the next position in the array after the last one is the first one, so we can put the elements we need to enqueue in the empty space?

Definition 14.3 (Circular Array)**.** An array where we say the position after the last one is the first one.

Okay, so now if we want to enqueue 10, we put it in position 1. And if we want to enqueue 17 after that, we put it in position 2:

	B		F				
10	17		23	2	37	21	15

The F and B represent the front and back of the queue, respectively.

But how do we go about implementing this in code? After all when we want to enqueue 10, we don't put it in a non-existent 9th position. So we have to use modulus for m, where m is the size of the actual array. So if we're at b for back and we want to add something, the new back is $(b+1)\%m$ (the modulus is what allows the wrap around to happen). So if we exceed m, we just go back to the start of the array because of remainder.

Also, notice 37 is technically the 3rd element in the queue. But it's not at the 3rd position in the actual array. We know though that position in the queue is measured in relation to the front. So if we want the kth position in the queue, that's $k-1$ positions right of the front. But if we want the 7th position in the queue, 6 positions right of the front goes off the array... again, modulus saves the day! We do $(f+(k-1))\%m$, so if we go off the array, we go back to the start instead because of remainder.

Well, that's enough on the intuition of a circular array. I should actually tell you how to implement the queue operations. From the diagram above, it becomes obvious that we know the actual array is full when the B and F pointers are right next to each other (so that gives us an indicator of when we need to resize).

If we want to enqueue in the circular array, we just add the element to the spot right of the B pointer (where the spot right of the last spot is the first spot) and then move B one spot to the right. For dequeue, we remove whatever is currently at the F pointer and move the F pointer one spot to the right. For peek, we just access whatever is at the F pointer.

So enqueue and dequeue are both amortized $O(1)$ because we need to resize, but other than that, the stuff we do is constant time. Peek is also clearly $O(1)$.

Like with stacks, for both implementations of a queue, we can have an isEmpty and size method done in a similar way with a counter. Both are $O(1)$ time.

§14.4 Summary

So when using a linked list as a stack or queue:

- Push in a Stack: $O(1)$
- Pop in a Stack: $O(1)$
- Enqueue in a Queue: $O(1)$
- Dequeue in a Queue: $O(1)$
- Peek for both: $O(1)$
- isEmpty for both: $O(1)$
- Size for both: $O(1)$

but when using an array list:

- Push in a Stack: amortized $O(1)$
- Pop in a Stack: amortized $O(1)$
- Enqueue in a Queue: amortized $O(1)$
- Dequeue in a Queue: amortized $O(1)$
- Peek for both: $O(1)$
- isEmpty for both: $O(1)$
- Size for both: $O(1)$

As for the conceptual knowledge:

- Linked list was relatively easy for both a stack and a queue. However, we did have to orient the list in such a way that we could conveniently add and remove elements at the correct spots when necessary.
- Most of the action in a stack or queue takes place at one particular location (front or back), so establishing pointers helped us quickly get there.
- An array list as a stack ran into the resizing problems we learned about previously, but is otherwise nothing new.
- As a queue, however, an array list needed a solution. Shifting elements over every time we dequeue wastes time, but leaving unused slots at the start wastes space. So we solve both in one swoop by using a circular array to cover the front that would otherwise be wasted and not have to shift everything over.

§15 Heaps

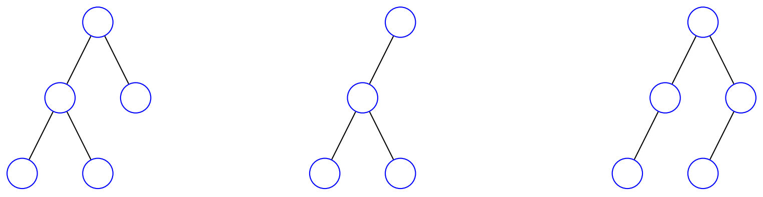
§15.1 Introduction

So let's say we have some video game tournament and we want to have a real-time leaderboard. But we have 1000 players and only want to display the top 10. It would be a real hassle to have to sort scores of 1000 players, regardless of what sorting algorithm we use. Not to mention if a player's score updates, we would have to update the ordering quickly because it's a real-time leaderboard. But remember, we only care about the ordering of the top 10. The bottom 990? We don't care about the ordering from one another, just that none of them have a high enough score to make it to the top 10. Introducing heaps! Which are useful for getting the max (or min) at any given point but don't care too much about the relative order of the other stuff.
First off, some binary tree vocabulary:

Definition 15.1 (Full binary tree)**.** A binary tree where all internal nodes (non-leaf nodes) have exactly 2 children.

Definition 15.2 (Complete binary tree)**.** A binary tree where all levels are full except the lowest level. Furthermore, all nodes on the lowest level are as far to the left as possible. Note that a complete binary tree with exactly k nodes has exactly 1 possible shape.

Here's are three binary trees:



The first one fits the definition of a complete binary tree. The second one doesn't fit the definition because one of the levels (the second to last one here) isn't full. The third one also doesn't fit the definition because the nodes on the last level are not as far left as possible.

Also, we're going to make a distinction between a min heap and a max heap.

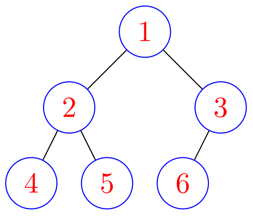
§15.2 Properties of a Heap

First of all, here are two properties a min heap has to maintain:

- Must be a complete binary tree
- Any internal node has a smaller number than its two children. It doesn't matter if the smaller of the two children are on the left or right.

A max heap is the same, except every internal node has a bigger (not smaller) number than its two children.

The binary tree stuff is nice to visualize the heap. But when we implement in Java, we're going to be using an array. The complete binary tree properties make implementation via an array easy. Let's take a complete binary tree of size 6 and number the positions in a left to right, top to bottom fashion:

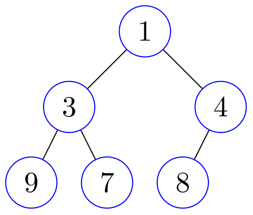


The complete binary tree properties make this numbering easy. There's no gaps in any of the levels because all levels before the last one are as full and the last level has all nodes as far left as possible. In fact given a node at position i:

- Its parent is at position $\lfloor \frac{i}{2} \rfloor$ ($\lfloor x \rfloor$ is the floor function, which means if x isn't an integer, round it down to the next integer less than x)
- Its left child is at $2i + 1$ (provided i isn't a leaf node)
- Its left child is at $2i + 2$ (provided i isn't a leaf node)
- Its left sibling is $i - 1$ for odd i (it doesn't have one if i is even)
- Its right sibling is $i + 1$ for even i (it doesn't have one if i is odd)

This works for any complete binary tree of any size because of the whole "no gaps" intuition. Try a few examples for yourself if you're not convinced. All this position stuff makes the array implementation even more practical because we have a surefire way of knowing where to find the parent, child, sibling, etc of whatever node we want.

Anyway, let's take that complete binary tree and fill it with numbers in each node (instead of labeling positions). In fact, I chose numbers so that it would actually be a min heap:



Well, with numbers given to each node, as well as the corresponding position system we have, we can easily make an array representation:

1	2	3	4	5	6
1	3	4	9	7	8

And again, our position system allows us to get parents, children, and whatever in $O(1)$ time.

Also, let's consider how many levels a complete binary tree of n nodes has. 1 node? Just 1 level. 2-3 nodes? 2 levels. 4-7 nodes? 3 levels. 8-15 nodes? 4 levels. Not hard to see by drawing pictures. You can catch the pattern that if there are n nodes, we have $\lfloor \log_2(n) \rfloor + 1$ levels. Point is, the number of levels will be $\log(n)$, give or take. This will be needed for analyzing runtimes later.

§15.3 Overview of Operations

I'm going to be using max heaps to demonstrate all the operations and intuition. Min heaps have a very similar set of operations that follows the same logic. So here are some operations that we need to implement:

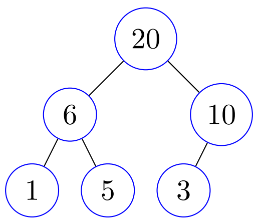
- Insert (add a given number into the heap)
- Remove the maximum (we don't care about removing anything other than the maximum)
- Max Heapify (given a complete binary tree that may not satisfy the heap property, move nodes around until it does)
- Build Max Heap (given an array, create a complete binary tree out of it and move nodes around until it satisfies the heap property)
- Peek (return the maximum)

With insert and remove, where we're necessarily changing the collection of elements in the heap, we have to make sure we preserve the heap property (any internal node being greater than its two children).

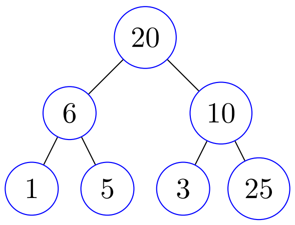
§15.3.1 Insert

- Insert the new element in the last slot of the complete binary tree. If the last level is full, that means creating a new level and inserting the new element in first slot available there.
- Compare the new element to its parent. If the new element is larger than its parent, swap the two elements. Keep doing these swaps between the new element and its parent, until the parent is greater than the new element, or it reaches the root.

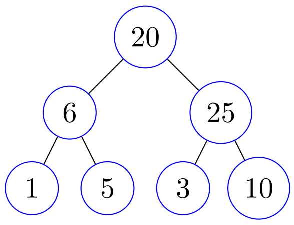
Allow me to demonstrate with this max heap:



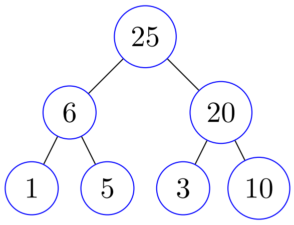
Now let's insert 25:



Well, 10 isn't happy because it's a parent less than one of its two children. That's why we have the swapping steps. So $10 < 25$, meaning we swap the two.



And then we check if 25's new parent is satisfied. $20 < 25$, so we need to make another swap:



The swapping business is easy to implement in the array because again, we have formula to find a node's parent.

Okay, we can tell this is a max heap. But can we be sure this algorithm always gives us a max heap at the end?

Yes. We can consider induction where given a max heap of size k, this insertion leads to a max heap of size $k + 1$. One key observation is, a parent is greater than its two children, so its greater than the children of its children, and the children of its children of its children. And so on. This means any node is greater than anything in either of its two subtrees.

So consider when we did the swap for 20 and 25. 20 having the 3 and 10 subtrees as its ancestors in the original heap meant it was greater than both of them. So there was no problem in 20 becoming the new parent to both of them instead of 25. Also, we saw 25 become the new parent to the 6 subtree. 20 was already big enough and 25 is even bigger, so it doesn't cause problems becoming the new parent of that subtree.

Basically, as we make swaps for 25 upward, the new numbers that are displaced along the way do not cause problems. And 25 itself does not cause a problem when it reaches its final position. That's the intuition, the formal proof is a pain to write up.

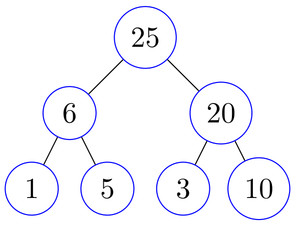
As for runtime, the worst case is we make swaps all the way. One swap is constant time, but we can only make as many swaps as there are levels because we stop once we reach the root (the top). So this is $O(\log n)$ because there are that many levels.

Of course, we could stop prematurely. if we inserted 4 instead of 25, then we don't do any swapping at all because it's already a max heap without problems.

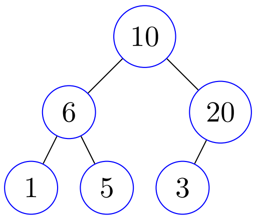
§15.3.2 Remove

- Swap the numbers in the root node and last node
- Delete the new last node
- Track the number currently in the root. If it's greater than its two children, don't do anything. Otherwise, swap it with the larger of its two children. Keep making swaps until that number being tracked is greater than its two children or it reaches the bottom.

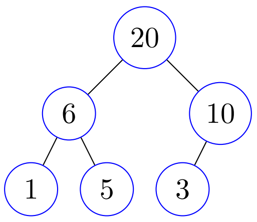
Okay, so we have that tree from the insert example:



Let's call remove, which in essence, should get rid of 25 (the maximum) and adjust the tree so it is a heap. So we swap 25 with 10 (the last node) and then delete 25:



Obviously, the 10 causes problems, which is why we have our swapping procedure. Okay, between 6 and 20, 20 is bigger, so we make the swap:



Okay, 10 no longer causes problems, so we're good.

Proof of correctness that this operation always yields a max heap at the end is similar in spirit to insert, where we make sure any numbers displaced along the swaps do not cause problems and the number being repeatedly swapped doesn't cause problems in its final position. Take note though of why we always chose the bigger of the two children to swap with. Had we swapped 10 and 6 originally instead of 10 and 20, we would have a problem where $6 < 20$, meaning the smaller of the two children becomes the parent for the bigger child, which is bad.

So we have this intuition where we have a complete binary tree and all nodes are happy and satisfy the heap property, all except possibly the root. But with a series of swaps with the root, we can always make it into a heap. This intuition will be necessary to understand max heapify.

Runtime is also $O(\log n)$, similar to insert. Worst case, we have to swap all the way down and the single swap and delete we make at the beginning is constant work.

§15.3.3 Max Heapify

When I say a node is "happy" that means, it's greater than its two children. Anyway, take a rooted complete binary tree, where the root may or may not be happy but we know everything else in the tree is. We can turn it into a tree where all the nodes are happy through this procedure (and thus a heap):

- Track the number in the root. Do the series of swaps like in the last step of remove. If it's greater than its two children, don't do anything. Otherwise, swap it with the larger of its two children. Keep making swaps until that number being tracked is greater than its two children or it reaches the bottom.

It basically uses the intuition in remove for why the swaps do not cause any problems. You can reuse the example for when 10 is the root and 25 is deleted and trace the work from there. Clearly, this is $O(\log n)$ in the worst case where we have to swap all the way down.

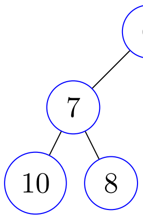
§15.3.4 Build Max Heap

Take any complete binary tree that may or may not be a max heap because of the greater than its two children property being violated. We can turn it into a max heap through this algorithm. Going in reverse order by node position number (from largest position number to smallest in the tree):

- Check the rooted tree that has the node at position i as the root.

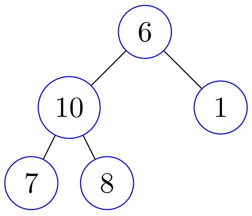
- Use max heapify on the rooted tree

So I'll walk you through an example, while giving commentary on why this works so that it doubles as a proof of correctness.

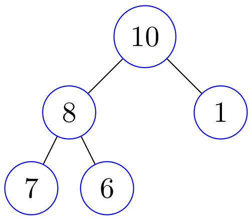


Okay, so we check the rooted tree at position 5, which is just 8. Already a heap. Same with the trees at positions 4 and 3. Now, check the rooted tree at position 2, which is in a situation similar to remove. We have the root at position 2, which may or may not be happy. But the nodes in both of its subtrees are because we already managed those beforehand.

Like we went over in max heapify, whenever we have a rooted tree where the root may or may not be happy, but all the nodes in the subtrees are, the swapping procedure always gives us a heap, making the whole rooted tree happy. So we do the swaps appropriately and now, the rooted tree at position 2 is happy.



So the rooted trees at positions 2-5 are all happy and we worked through them. Now, the rooted tree at position 1. This is once again a situation where the root may or may not be happy but the two subtrees are. So we pull our swapping procedure to get:



Did you catch the inductive logic here and why we went in reverse order by position? We know max heapify works any time we have a situation where the root may or may not be happy but everything in the subtrees are. So we can always fix the rooted tree so that the whole rooted tree is happy. We apply that here where we work backwards specifically because it ensured lower rooted trees are happy before we get to upper ones. The base case are the leaves on the lowest level, which are happy by default.

Now, you would be forgiven for thinking this is $O(n \log n)$ time, where we have n nodes and worst case scenario, max heapify is $O(\log n0$. You're not wrong, but we can get a better, more informative upper bound.

Not all nodes have to swap the height of the entire tree down in the worst case. If a node is in the 2nd to last level, worst case, it's only going to be swapped once. If a node is in the 5th to last level, worst case, it's only going to be swapped 4 times. Only the nodes closer to the top will have to go the height of the entire tree down worst case.

Label the levels from top to bottom as level 0, then level 1, then level 2, and so on, until level $\log(n)$. It can be seen through drawing some pictures that level i has 2^i nodes. Also, in level i, exactly $\log(n) - i$ swaps are required to reach the bottom. Worst case, all 2^i nodes in level i swap all the way down, accounting for $2^i(\log(n) - i)$ swaps. Summing across all levels, our worst case for the number of swaps is

$$T(n) = \sum_{i=0}^{\log(n)} 2^i(\log(n) - i) = 2^0(\log(n)) + 2^1(\log(n) - 1) + 2^2(\log(n) - 2) + \cdots + 2^{\log(n)-1}(1).$$

Some unmotivated math here. Multiply this equation by 2:

$$2T(n) = 2^1(\log(n)) + 2^2(\log(n) - 1) + 2^3(\log(n) - 2) + 2^{\log(n)}(1).$$

Subtracting this with the equation for $T(n)$ above cancels stuff out neatly. For example, the $2^1(\log(n)) - 2^1(\log(n) - 1)$, which becomes just 2^1. so

$$2T(n) - T(n) = -2^0(\log(n)) + (2^1 + 2^2 + \cdots + 2^{\log(n)-1}) + 2^{\log(n)}(1)$$

We can make this

$$T(n) = -\log(n) + 2(2^0 + 2^1 + 2^2 + \cdots + 2^{\log(n)-1}) = -\log(n) + 2(2^{\log(n)} - 1) = -\log(n) + 2(n - 1).$$

This is $O(n)$, a more informative bound.

§15.3.5 Peek

Just look at the first element in the array. We know its the largest because it's greater than anything in the two subtrees by the heap property. So this is $O(1)$.

§15.4 Heap Sort

So we have min and max heaps. Suppose we have n elements in a min heap. For a min heap, we can get extract the minimum by removing it and the heap makes adjustments so that it still remains a heap. By then, we have a new minimum, which if we remove again, we should get the new minimum. This new minimum should be the second smallest element from the original n elements. If we do this enough times, we can get the position numbers for all elements in increasing order.

Okay, maybe we can make a sorting algorithm out of this? We know we can build the heap in $O(n)$ time. Then, we keep removing n times, which are each $O(\log n)$ worst case, so that's $O(n \log n)$ total.

So the whole sorting algorithm is $O(n \log n)$ and that's worst case. Better than quick sort being $O(n \log n)$ only in expectation and in worst case, it's $O(n^2)$.

§15.5 Summary

- We learned about the operations of a heap. We can turn a collection of numbers into a min or max heap.
- The heap is a complete binary tree, which makes it easy to represent as an array: given a node's position, we then know the positions of its parent, children, and sibling.
- The maximum is conveniently stored at the top of a max heap (and minimum for min heap).
- Then, we can add numbers all we want to the heap to maintain the key properties of a heap.
- We can also remove the maximum from a max heap at any time (or minimum from a min heap) and still be able to fix the heap.
- We can also create a sorting algorithm out of a heap.
- The heap is again, useful for keeping track of the top 10 or so elements, when you don't care about the order of anything not in the top 10. Because you can have anything not big enough to be in the top 10 excluded from the heap and sort the top 10 in $O(1)$ time.
- We will see algorithms later that necessitate the relative quickness of a heap when we care about the minimum but not the order of anything else.

§16 Recap on All Our Sorting Algorithms

We know 4 sorting algorithms now. Let's think about each of them.

I'll say this: it would be foolish to think that merge sort obviates quick sort just because merge sort is reliably $O(n \log n)$ compared to quick sort only attaining that time in expectation.

We need to introduce some vocabulary. The first one was alluded to before. The second one isn't.

Definition 16.1 (In-place Algorithm)**.** All the action happens within the input itself

Definition 16.2 (Stable Sorting Algorithm)**.** A sorting algorithm that maintains relative order on elements with the same attribute being sorted. Say we had a directory of names, where we had "John Brown" and "John Smith," and we could sort by either first name or sort by last name. Suppose we sort by last name first so we have "John Brown" before "John Smith". When we sort by first name (with the two Johns) now, will "John Brown" always come before "John Smith"? If so, then it's a stable algorithm. Otherwise, if it doesn't always happen, it's not stable.

In particular, stability is super important for searching when we want to have more than one different attribute we use as the sorting basis. The example above with search by first name order or search by last name order demonstrates that. A real world application would be a UPenn directory, where we would want to sort students in different ways: by name in alphabetical order, by graduation year, by major, and so on.

Anyway, let's talk about in-place. Insertion sort, quick sort, and heap sort are all just moving stuff around in the array. So they're all in-place. Is merge sort in-place? No because we have to allocate all that memory for all those recursive calls until we reach the base case. That's going to use up a lot of memory and most of the action happens in the merging of all the arrays obtained recursively, not the original array.

And let's talk about stability. Insertion sort? Yes. We don't move an element any further than we need to. So John Brown gets inserted somewhere and then John Smith stops before John Brown because we notice the two Johns being the same in order by first name. Merge sort? Yes. When we merge two arrays, if we have a tie, we could prioritize the thing from the left array over the thing from the right array. So that preserves relative order of John Brown and John Smith.

Quick sort? Not stable. The pivots are random and when we do the partition, quick sort essentially just shoves elements to either side of the pivot without regards to their original relative order.

Heap sort? Not stable either. Especially when elements in consecutive positions could either be siblings sometimes but not all the time. So relative order won't be accounted for.

And runtimes in terms of best, average, and worst. We didn't do average for insertion. It's going to be $O(n^2)$, just like worst case because we expected are going to insert halfway through the possible positions for each element. But halve the sum of the first n integers and you still get $O(n^2)$.

Merge sort doesn't ever stop prematurely. It always breaks it down to base cases and merges. It's not binary search where we stop prematurely if we accomplish the objective early. So its best and average are the same as the worst case.

Quick sort, best runtime is when the pivots are always in the center, so we have the recursion $T(n) = 2T(n/2) + \Theta(n)$, which is merge sort's time.

Heap sort? Well, we always have to build the heap, which is $O(n)$. Best case, when we extract the minimum, we don't do any swapping at all, so it is $O(1)$ per getting the minimum. So $O(n)$ best case. On average, a swap chain will probably be halfway down the tree, so $\frac{\log(n)}{2}$, but that's still $O(\log n)$. So average is $O(n \log n)$.

Sorting Algorithm	Best Runtime	Average Runtime	Worst Runtime	Stability	In-Place
Insertion Sort	$O(n)$	$O(n^2)$	$O(n^2)$	Yes	Yes
Merge Sort	$O(n \log n)$	$O(n \log n)$	$O(n \log n)$	Yes	No
Quick Sort	$O(n \log n)$	$O(n \log n)$	$O(n^2)$	No	Yes
Heap Sort	$O(n)$	$O(n \log n)$	$O(n \log n)$	No	Yes

An informed programmer is going to look at the situation where they need a sorting algorithm, weigh the importance of the characteristics, and make their choice on the sorting algorithm based on that. For example, we might not have enough memory to merge sort, but we also need an $O(n \log n)$ time to do it fast enough. So we might look at heap sort. Maybe we don't care about runtime too much, but we need stability and not use up too much memory. Then, we'd do insertion sort.

Advice 16.3 — This will most likely appear on the final where they may ask you on the attributes of different sorting algorithms.

§17 Huffman Trees

§17.1 Introduction

So we may need to send a large text file over the internet. Problem is, it may be so big that it could be faster to just FedEx a flash drive with the file instead. Maybe we can compress the file into something smaller to make it faster to send and then decompress it once it reaches its destination?

You may have heard of ASCII or American Standard Code for Information Interchange. This is a way of assigning a sequence of 7 bits to each of the various characters used by a computer. For example, 'H' is represented as 1001000, while '7' is represented as 0110111. There are 95 characters in the ASCII system. With 7 bits, there are $2^7 = 128$ possible different binary strings. So we can assign each of those 95 characters a unique 7 digit sequence of bits.

However, there's a good chance we're not going to need EVERY single character in ASCII. So for this large file, why not create our conversion system to change the characters to binary using only the relevant characters? Also, there's no reason why each character's corresponding binary sequence all have to be the same length.

Suppose our file consisted of a ton of 'a's and a couple 'b's and 'c's but not nearly as many 'a's. One conversion system is to let 'a' be 0, 'b' be 10, and 'c' be 11. While b and c have longer strings compared to a, it won't be needed as often, since as said, a appears much more. So in this system, we have efficiency in needing less bits. But we want a generalize this.

§17.2 The Algorithm

To set things up, we need the alphabet we want to convert into an encoding system with their corresponding frequencies. The frequencies can appear as a probability, or as numbers. For example, suppose the file we want to convert has 100 characters, 90 of which are 'a's, 6 'b's, and 4 'c's. The numbers for each character are the frequencies in of itself. Or we can say 'a' for example has frequency of 0.9, because that's how many 'a's we have relative to the total ($\frac{90}{100} = 0.9$).

Suppose we have n total characters in our alphabet. Here's how we construct the tree:

1. Create n nodes, one for each character that shows up. Put its corresponding frequency on each node.

2. Find the two nodes available with the two smallest frequencies.

3. Have those two nodes as children to a parent node. Have the frequency of this parent node be the sum of the frequencies of its two children.

4. Place this new parent node back in the collection with the remaining nodes.

5. Repeat steps 2-4, decreasing the number of remaining nodes available by 1 each time, until we have 1 node left. This 1 node is the root of the whole tree.

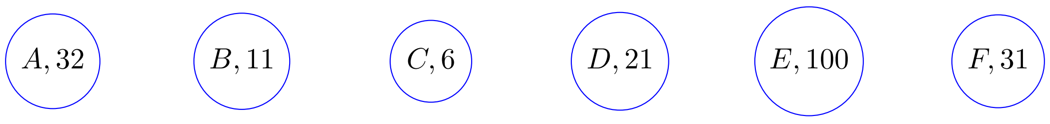
If you're doing this on paper and you have, let's say, 5-6 characters in your alphabet. It's pretty easy to eyeball which are the two smallest frequencies each for each time you do step 2. However, for larger alphabets and in code, you want to use a binary min heap to help speed up step 2.

Example 17.1

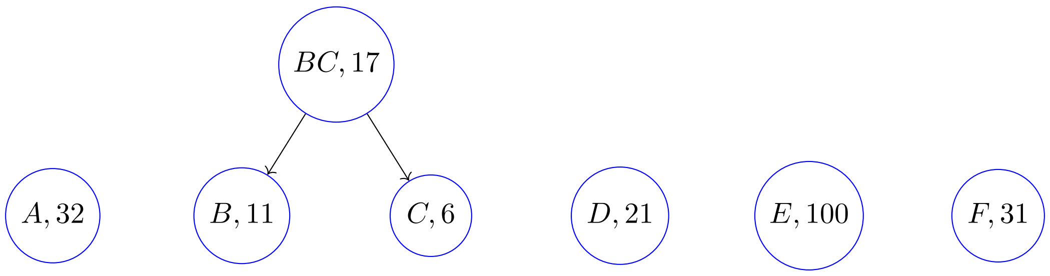
Build a Huffman Tree of an alphabet with the following frequencies:

Letter	A	B	C	D	E	F
Frequency	32	11	6	21	100	31

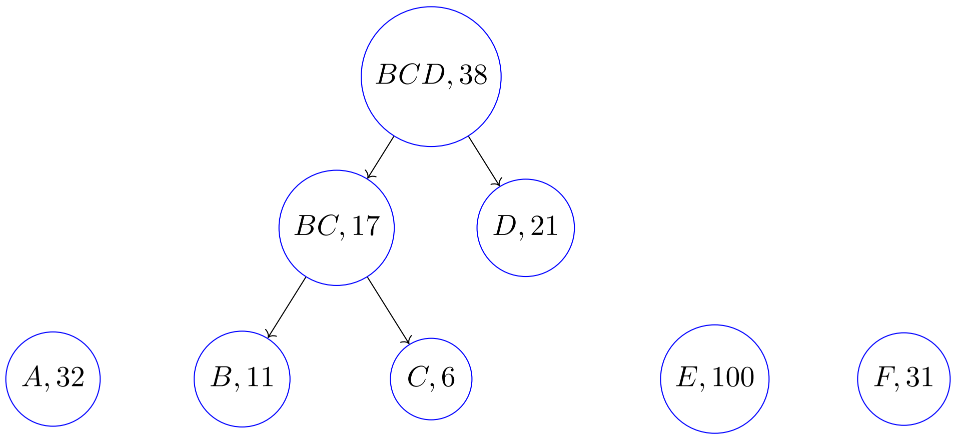
First, we create the 6 nodes as said in step 1.



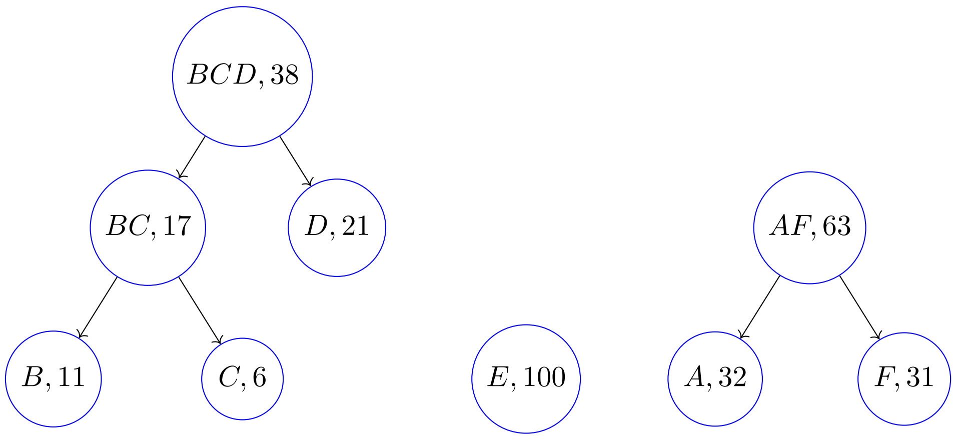
Now, we look at which 2 have the lowest frequency, which are B and C. So we create a parent node (I'm labelling it BC for convenience) with a frequency being the sum of the frequencies of B and C:



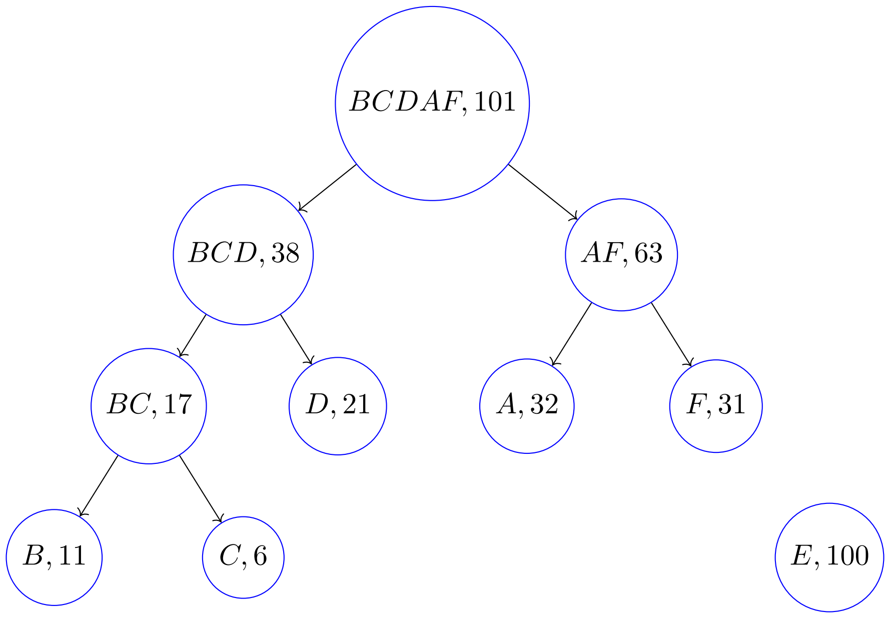
At this point, the nodes for B and C are no longer in the collection and are treated as they are "merged" into the node BC. But we can't delete the B and C nodes outright because they'll be important for the full tree. Anyway, just pretend BC is a single node that secretly has 2 children. So we have 5 nodes left: A, BC, D, E, F. Now, we take the two lowest frequencies, being BC and D and do steps 3 and 4 again:



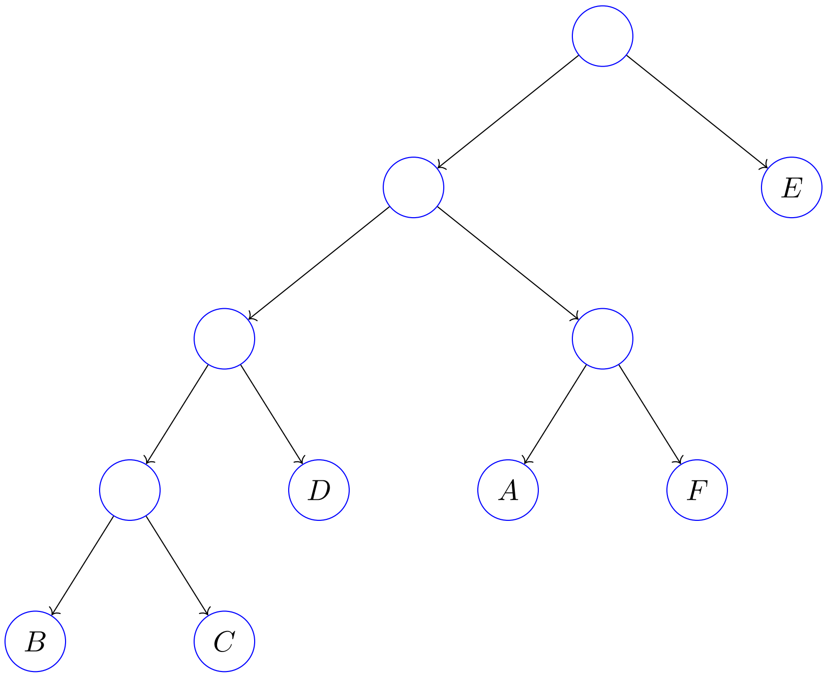
I think you get the hang of it, but I'll show the remaining merges we need to do. First, merge A and F:



Now, merge BCD and AF:



Now, merge $BCDAF$ and E for our final tree (with labels removed on the internal nodes and removing frequencies):



Now, to generate the set of binary codes for each letter. We do this by considering the path from the root of the tree to said letter and the sequence of left and right movements necessary to get there. Once you write out the sequence, change each "left" movement to a 0 and every "right" movement to a 1. That gives you the code.

For example, to get to E, we start at the root and make on movement right. So E's code is 1. To get to A, the sequence is left, right, left. So A's code is 010. Here is a table of codes:

Letter	A	B	C	D	E	F
Code	010	0000	0001	001	1	011

You use the above logic for any Huffman Tree to generate codes, not just this one example.

So when encoding, what we do is we just use the table to see how we convert a character to bits.

When decoding, we traverse the tree starting at the root, using the 0s and 1s as a guide until we hit a node with a character. Then, we go back to the root.

For example, take 00011011. So the three 0s say go left three times. Still no character yet. Then, the 1 says go right. We hit C. So first character in the message is C and we go back to the root. We have a 1, which says go right. We hit E, meaning it's the next character in the message. Return to the root. Now, we have 011, which says go left once and then right twice. This takes us to F. So the original message is CEF.

It's easy to see the length of a character's encoding is simply the number of edges in the unique path from the character to the tree's root, or the level that the leaf node is located in. (This intuition is very important for proofs)

§17.3 Proof of Correctness

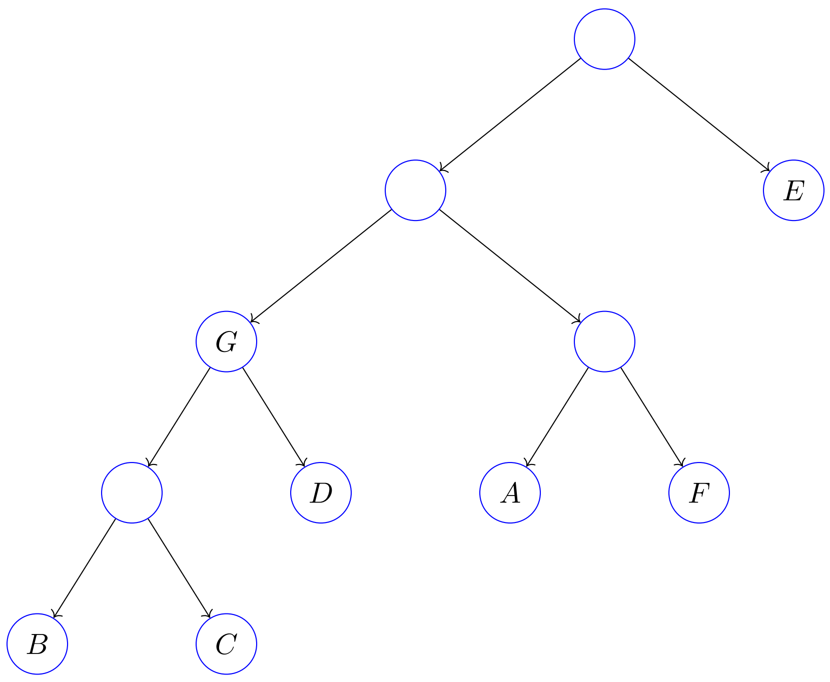
So there are two important things we need to prove:

- That this algorithm gives us an encoding that can be used to both encode and decode (as in, get the original message back from the 0s and 1s)
- That this specifically does it in the most optimal manner

Let's worry about the first one for now. Clearly, from the algorithm, every node will be added to the full tree at some point, so each letter will have a code. So it's clear we can convert a sequence of these letters into a sequence of bits.

But the thing to think about is, can we always get the original message back? Hypothetically speaking, what if we had $A - 011$, $B - 01$, and $C - 1$ and we needed to convert the bits '011' back to letters? Well, this could be either 'A' or 'BC'. Who knows which one it is! So we never want a situation like this, where there could be two or more possible original messages.

For demonstration purposes, I'm taking the Huffman tree we got at the last example and adding a G at an internal node just because it will teach us something.



Let's suppose we had a message that started with 'D', so that when it becomes bits, the bit sequence starts with 001. But when we convert back to characters, what will happen is, we start at the root and go left twice, as the first two 0s imply. We hit a character node G, so the first character in the message back is 'G', except we know that's not true because our original message started with 'D'! So what went wrong here?

Well, we always stop when we hit a character node and as you can see, D is "locked behind" G. So we can never actually reach D because G is at an internal node, blocking the path to D. Aha! So we never want character nodes to be at internal nodes because they block paths to other characters, so we may end prematurely and get the wrong character.

Also, we can clearly see that leaves function as dead ends, so if we always have character nodes at leaves, we never create this situation where a character node blocks the path to another. And by how Huffman works, we always have character nodes at leaves because we merge character nodes with some other node as two children of a parent, and that is not a character node. So we're safe here. In fact, for this reason, we call Huffman a prefix-free tree.

Definition 17.2 (Prefix-free tree)**.** A tree with codes where no two codes are prefixes of one another. For example, '011' and '01100' aren't allowed together in the same tree because the former is a prefix of the latter. If one code is a prefix of another, it will be visible in the tree as some character node being an internal node, blocking the path to another character node.

So this prefix-free aspect is what allows to decode bits without ambiguity because again, we don't reach some other character node prematurely before we can reach the node that was intended in the original message.

Now, we consider the second part. That this is the best way we can accomplish the encoding. To measure how well we can accomplish it, we introduce:

Definition 17.3 (ABL (Average bits per letter))**.** The expected length of the binary code of some random letter chosen from the alphabet sample (with frequencies taken into account). The smaller this is, the more optimal our encoding is.

The formula for ABL (which I will denote as $E(L)$ for some alphabet set L with frequencies) is reminiscent of the expected value formula. Let $f(x)$ be the frequency of some letter x in the alphabet, and $P(x)$ denote the length of x's corresponding binary string. Then,

$$E(L) = \sum_{x \in L} (f(x) \cdot P(x))$$

Back to that example at the beginning where we have 100 characters, 90 of which are 'a's, 6 'b's, and 4 'c's. I'll just tell you the corresponding binary strings from the Huffman tree is $a - 0$, $b - 10$, and $c - 11$. Then, the ABL is

$$E(L) = \sum_{x \in L} (f(x) \cdot P(x)) = f(a) \cdot P(a) + f(b) \cdot P(b) + f(c) \cdot P(c)$$

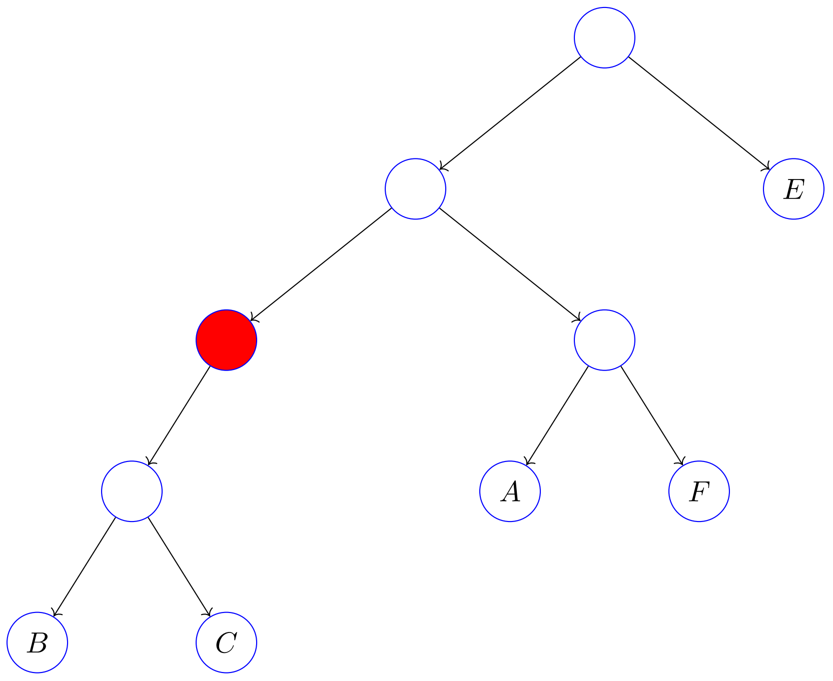
$$= 0.90 \cdot 1 + 0.06 \cdot 2 + 0.04 \cdot 2 = 1.10.$$

As you can see, it's a weighted average just like expected value is, where more frequent letters have bigger weights.

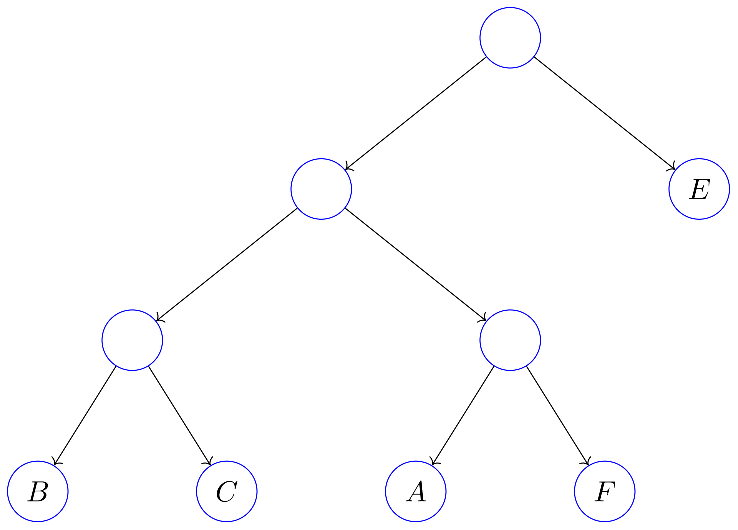
Advice 17.4 — You may get a midterm question where you are asked to compute the ABL for a Huffman tree, so just remember it's like the expected value formula. Don't want to lose points on something relatively intuitive and easy to remember.

Okay, so the formal proof of Huffman's optimization is more trouble than it is worth, so I'll just give you the intuition.

First off, all internal nodes should have exactly 2 children to help with optimization. Why? Let's again, steal the tree from the example, but delete the D node for demonstration purposes. So here, we have a Huffman tree where as you can see, an internal node has only 1 child (which I colored in red).



Well, since the red node only has 1 child, what I can do is move its left subtree up and not change the fact that this tree is prefix-free.



Moving that subtree up reduced the distance from B and C to the root, which means less lengths for those codes and thus, lower ABL. So it's no good if we have an internal node with 1 child because it protracts the tree for no reason. In this regard, every internal node in a Huffman tree has two children, meaning it is a full binary tree.

Also, we can technically switch the characters around within the leaf nodes without changing the fact that the tree is prefix free. Like it makes no difference if we swapped the codes for E and B when it comes to being prefix free. But it may affect ABL. Keep this in mind.

Advice 17.5 — This technique of switching around stuff to get something that is valid but may be more optimal is called an "exchange argument." There will be a topic later on where we use this.

Lemma 17.6 (Exchange Argument)
If $f(x) > f(y)$ in an optimal tree, then $P(x) \leq P(y)$ necessarily follows.

Proof. Here, we use the exchange argument. Suppose for the sake of contradiction that $f(x) > f(y)$ in some optimal Huffman tree, but $P(x) > P(y)$. So somewhere in the ABL sum, we have $f(x) \cdot P(x) + f(y) \cdot P(y)$.

Suppose we switched the nodes for x and y in the Huffman tree. The frequencies don't change, but the path lengths of x and y do. $P(x)$ becomes $P(y)$ and vice versa. So somewhere in the new ABL sum, we have $f(x) \cdot P(y) + f(y) \cdot P(x)$. What is the net change from the original ABL to the new ABL? Well, that is

$$(f(x) \cdot P(y) + f(y) \cdot P(x)) - (f(x) \cdot P(x) + f(y) \cdot P(y)) = (f(x) - f(y))(P(y) - P(x)).$$

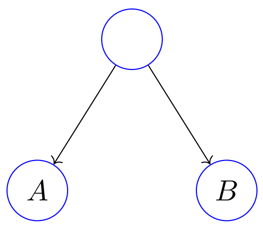
With $f(x) > f(y)$ and $P(x) > P(y)$, this quantity is negative. So the net change in making this switch is a reduction to the ABL! Remember, switching character nodes doesn't change the fact that we have a prefix free tree. But we showed we can make a simple switch that creates a better ABL if we ever have $f(x) > f(y)$ and $P(x) > P(y)$. So we never want that to happen because we can always do better when that occurs. The unoptimality of the tree before the switch was made serves as the contradiction. □

Now for the main part of the proof.

Lemma 17.7

Huffman produces the optimal tree for any alphabet on size $n \geq 2$.

Proof. Consider induction on n. The base case of $n = 2$ involves the Huffman making a tree looking like this:



I mean, the algorithm aside, we literally can't do any better than this for $n = 2$, right? 1 digit codes for both of the two letters, regardless of their frequencies. No prefixes. So the base case works for $n = 2$.

Now for the inductive step. So we assume Huffman always produces the optimal tree for an alphabet of size $n = k - 1$ and want to show that implies the IH holds for $n = k$.

Remember we can move the characters in the leaf nodes around without changing the fact that it's prefix free. We can use this later to argue the nodes with the two smallest frequencies should be at the bottom.

What Huffman will do is merge the two lowest frequencies among the k nodes to make a new node and place it back in the collection. Now, we have $k - 1$ nodes.

By the IH, Huffman will sort everything out for the $k - 1$ nodes in the optimal manner and create a tree T'. Let L' be the alphabet set involving the $k - 1$ nodes (the merged node can just be some character of its own). So we know $E(L')$ is minimal by IH.

If N is the first merged node created in the Huffman process for T, we know N is a leaf node somewhere in T'. So to get from T' to T, we just add N's two children. Obviously, the frequency of N is the sum of its two children.

Let's figure out how to get from $E(L')$ to $E(L)$. We have $f(N) \cdot P(N)$ somewhere in the ABL sum for L'. Nothing else will change except N is no longer and internal node and has two character nodes. These two new character nodes in T obviously have path length $P(N) + 1$ (one longer than its parent, N) and the two character nodes have a frequency summing to $f(N)$ because that's how the Huffman merging works. So basically, the $f(N) \cdot P(N)$ becomes $f(N) \cdot (P(N) + 1)$ in the ABL sum when we transition from L' to L, resulting in a net change of $f(N)$, so $E(L') + f(N) = E(L)$.

We could have the Huffman process merge the two largest frequencies each step or the two middle frequencies for all we care and still get prefix free codes. But it always merges the two smallest frequencies which means $f(N)$ is as small as it can be. We also don't want only 1 node in the deepest level of the tree because that would imply its parent has only 1 child (which we saw earlier is not optimal), which is why we make N have 2 children and not 1.

With $E(L') + f(N) = E(L)$ and $f(N)$ as small as it can be (as well as $E(L')$ by IH), $E(L)$ is as small as it can be. This completes the induction. □

§17.4 Runtime

Note that we should use a min heap to store all the nodes in the collection, as they will save us time.

Building the min heap is $O(n)$. Then, we extract the minimum twice ($O(\lg n)$), do some constant work to make a new merged node with the two chosen nodes as children, and then put the new merged node back into the heap ($O(\lg n)$). We do the extracting, merging, and insert back a total of $n-1$ times because we have 1 less node each time, until we have only 1 node in the collection and that root serves as the tree. So this is

$$O(n) + (n-1)(O(\lg n)) + O(\lg n) = O(n \lg n).$$

§17.5 Problem Solving

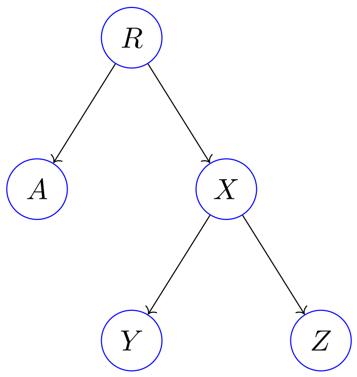
Huffman problems will often involve proof by contradiction and probability bounding. A key trick is that in every point in the process, the sum of the frequencies of all available nodes will always be 1 (shouldn't be too hard to see because the new node after merged is the sum of two previous ones, so the overall sum never changes). It's also important to remember Huffman always chooses to merge the two smallest nodes, which can help lead to a contradiction.

Example 17.8 (Recitation Problem)

You have an alphabet with $n > 2$ letters and frequencies. You perform Huffman encoding on this alphabet, and notice that the character with the largest frequency is encoded by just a 0. In this alphabet, symbol i occurs with probability p_i; $p_1 \geq p_2 \geq p_3 \geq \ldots \geq p_n$.

Given this alphabet and encoding, does there exist an assignment of probabilities to p_1 through p_n such that $p_1 < \frac{1}{3}$? Justify your answer.

I claim there does not exist an assignment of probabilities. Assume for the sake of contradiction that there did. Let's draw out the Huffman tree to get a better understanding of what's going on here.



R is defined to be the root of the tree. Since we have a character with an encoding of 0 (which is length 1), we have node A to represent that, which will be a leaf. X will be the sibling node of A, which has to have two children (or else we will only have 2 letters in the alphabet, contradicting $n > 2$). So X has children Y and Z. These could have children of their own, but they are irrelevant to the solution.

Let $f(n)$ be the frequency of a node n, whether that node is a leaf or internal node.

By the tree's construction, only one node is of distance 1 to the root. Intuitively, the character with the highest frequency is closest to the root. So $f(A) = p_1 < \frac{1}{3}$.

Anyway, let's work backwards. The last merge is obviously A and X to get R. Remember that the sum of the frequencies of the available nodes at any given point is 1. So $f(A) + f(X) = 1$. With $f(A) < \frac{1}{3}$, that means $f(X) > \frac{2}{3}$.

Since A is a leaf node, it cannot have been the result of a merge during the second to last step. So the second to last step must have been merging Y and Z to get X.

By how Huffman constructs a parent node's frequency, we have $f(X) = f(Y) + f(Z)$. WLOG, suppose $f(Y) \geq f(Z)$. We must have $f(Y) > \frac{1}{3}$ (because if $f(Y) \leq \frac{1}{3}$, then that with $f(Y) \geq f(Z)$ would mean $f(X) = f(Y) + f(Z)$ is not greater than $\frac{2}{3}$, contradicting prior info).

Irrespective, $f(A) < f(Y)$ and $f(Y) \geq f(Z)$. So in the second to last step, where we have nodes A, Y, and Z, the ones with the two lowest frequencies are A and Z. But here's the contradiction: Huffman is supposed to merge the nodes with the two lowest frequencies each time, so it should have merged A and Z in the second to last step. However, information earlier says it merged Y and Z in the second to last step. So this completes the solution.

§17.6 Summary

We saw how Huffman can be used to create a coding system for any given alphabet set with different frequencies. It allows us to both convert the letters into bits and obtain the original message back without conflicts. Here are the main things from this section:

- We start out with one node for each letter. The algorithm involves repeatedly taking the two nodes with the smallest frequencies and merging them in a tree. Repeat until we have a full tree built.
- Codes for a character are generated by looking at the path from the root to the character. Decoding involves using the 0s and 1s to move along the tree until we get to a character.
- Character nodes being only at leaf nodes prevents a situation where they could be two possible original messages from the same sequence of bits.
- Intuitively, optimization is shown via ABL. We objectively want to save the longer codes for less frequent letters and more frequent ones should have shorter codes.
- The formal proof by induction involves recursively thinking about the Huffman process where we merge one node and then it's an alphabet size of one less character.
- Huffman proof problems involve using probabilities, the Huffman process, and proof by contradiction.

§18 Graphs

§18.1 The Basics

Review 18.1. Obviously, CIS 1600 review would be helpful here for graphs, but I will be more thorough on review in this section. This is because CIS 1600 content differs in the fall versus spring, so it's best everyone is on the same page.

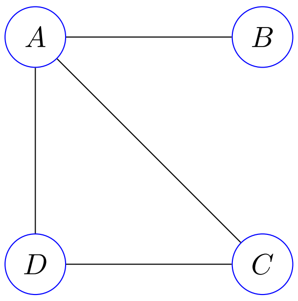
Definition 18.2 (Graph)**.** A set of nodes (usually denoted as V) where some pairs of nodes may be connected by edges (the set of edges is usually denoted as E). In this course, we will never have the same edge twice.

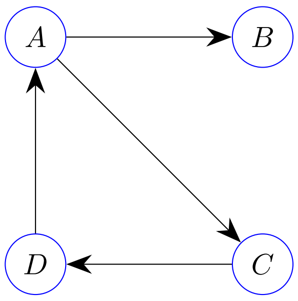
Now, we need to clear up some distinctions on graphs.

Definition 18.3 (Undirected graph)**.** A graph where the edges don't have directions, meaning they are all 2-way.

Definition 18.4 (Directed graph)**.** A graph where the edges have directions, meaning they are all 1-way. We can have "anti-parallel edges," which are two edges between the same pair of vertices but running in opposite directions. However, we aren't ever allowed to have two edges between the same pair of vertices in the same direction.

In the two graphs below, the left graph is undirected, while the right graph is directed.





Definition 18.5 (Unweighted Graph)**.** Graphs where there are no weights assigned to the edges

Definition 18.6 (Weighted Graph)**.** Graphs where there is a real number (representing its weight) assigned to each edge

You can also think of an unweighted graph as a weighted graph with all the edges having weight 1.

§18.2 Representations of a Graph

§18.3 Space

§18.4 More Definitions

Definitions applying for UNDIRECTED graphs:

Definition 18.7 (Connected vertices)**.** Two vertices a and b are connected in an **undirected** graph if there exists a path from a to b.

Definition 18.8 (Connected component)**.** A set of vertices in an **undirected** graph such that any two vertices in the set are connected, and the component is maximal (meaning you can't add another vertex to the component so that all vertices in the component are pairwise connected).

Definitions applying for DIRECTED graphs:

Definition 18.9 (Reachability)**.** We say v is reachable from u in a **directed** graph if there exists a directed path from u to v. We note reachability from u to v as $u \twoheadrightarrow v$.

Definition 18.10 (Strong connectivity)**.** An extension of reachability is strong connectivity. We say u and v are strongly connected in a **directed** graph when u and v are both reachable from each other.

Definition 18.11 (Strongly connected component)**.** Similar to a connected component in an undirected graph. In a directed graph, any two vertices in a strongly connected component are strongly connected, and the component is maximal (meaning you can't add another vertex to the component so that all vertices in the component are pairwise strongly connected).

Definition 18.12 (Directed cycle)**.** Similar to a cycle in an undirected graph: a directed walk with no repeating vertices except the first and last ones. Self-loops count as directed cycles. Two edges between the same two vertices in opposite directions (anti-parallel edges) also count as directed cycles.

Definition 18.13 (Directed Acyclic Graph (DAG))**.** A directed graph without any cycles

Definition 18.14 (Outdegree)**.** As noted by out(u), the outdegree of a vertex u is the number of directed edges coming out of u

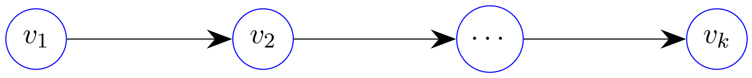
Definition 18.15 (Indegree)**.** As noted by in(u), the indegree of a vertex u is the number of directed edges coming in to u

Definition 18.16 (Sink)**.** A vertex with outdegree 0. Meaning all edges connected to it point in to it.

Definition 18.17 (Source)**.** A vertex with indegree 0. Meaning all edges connected to it point out of it.

Lemma 18.18
All DAGs have at least one source and one sink.

Proof. Let's use the Maximal Path technique back from CIS 1600. Let $v_1 \to v_2 \to \cdots \to v_k$ be a maximal path in the DAG.



I claim that v_k is a sink. Suppose for the sake of contradiction it wasn't. Then, there would need to be some directed edge going out of v_k and to some other vertex. Two cases, either this vertex is outside the maximal path or inside the maximal path.

In the first case, $v_k \to w$, where w isn't already in the path.

$$\begin{tikzcd} v_1 \arrow[r] & v_2 \arrow[r] & \cdots \arrow[r] & v_k \arrow[r] & w \end{tikzcd}$$

Since w isn't already in the path, we can extend the maximal path to have $v_1 \to v_2 \to \cdots \to v_k \to w$. But this contradicts the definition of a maximal path (a path that cannot be extended at all). So this case leads to a contradiction.

Let's try the second case. So v_k has an edge pointing out of it that goes to some vertex already in the path.

$$\begin{tikzcd} v_1 \arrow[r] & v_2 \arrow[r] & \cdots \arrow[r] & v_k \arrow[l, bend right] \end{tikzcd}$$

This creates a cycle though, contradicting the definition of a DAG. So v_k cannot have edges going out of it, so it is a sink, meaning the graph has a sink.

A similar proof pattern holds for source, where if there were an edge going in to v_1, similar contradictions occur in the two cases. □

§18.5 Summary

§19 Breadth First Search

§19.1 Introduction

So we have a graph. Why don't we explore it? Check every nook and cranny and see what we can find.

We'll get our first taste of a graph algorithm. It turns out that these graph algorithms can have other applications beyond the obvious.

Here, we'll do Breadth First Search, or BFS for short. The objective is to pick some starting node S and find all nodes that can be reached from the starting node.

§19.2 The Algorithm

First, establish a starting node S.

Suppose the graph has n nodes. Create two arrays of size n, one being a boolean array called "discovered" (with each entry initially set to false), and a node array called "parent" (with each entry set to null).

Have a queue and add S to it. In "discovered" for S, set it to be true.

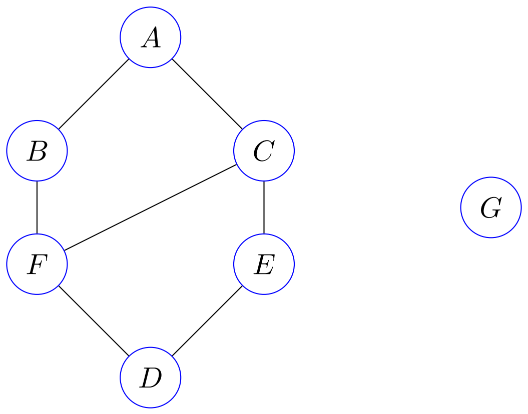
Run the following while the queue is not empty:

- Dequeue the queue and suppose v is the vertex we get from doing that
- Check all neighbors of v in the adjacency list. Suppose u is some neighbor of v. If we check the discovered array and see u is discovered already, ignore it. Otherwise, do the following:
  - Set the discovered status of u to be true
  - Add u to the queue
  - Set the parent of u to be v in the parent array

In plain English, basically we search the starting node's neighbors and add them all to the queue. Then, one by one, we look at each of those neighbors in the queue and add their neighbors (only ones we didn't discover yet). We keep adding neighbors upon neighbors upon neighbors of nodes to the queue until we discover everything we can. The parent array is optional; it is more of a way to keep track of the node from which we first discovered some node, which has applications I'll get to later. But the discovered array is not optional. We'll see when we do the algorithm in action.

§19.3 In Action

Let's do BFS on the following graph with A as the starting node: (notice that G is a different connected component than A)



Let's do the initial set up:

Node	A	B	C	D	E	F	G
Discovered	True	False	False	False	False	False	False
Parent	null	null	null	null	null	null	null

And the queue so far is just A. Now, the loop begins, where the action unfolds. We take A out of the queue. So now, we check all neighbors of A, which are B and C. Neither are discovered yet, so we set them to be discovered, add them to the queue, and their parent node to be A. Here's the new table:

Node	A	B	C	D	E	F	G
Discovered	True	True	True	False	False	False	False
Parent	null	A	A	null	null	null	null

The queue is B, C. Again, dequeue, which takes B out of the queue. We check all neighbors of B, which are A and F. We ignore A as we discovered it already. But we add F to the queue, since we didn't discover it yet and set its parent to be B. Here's the new table:

Node	A	B	C	D	E	F	G
Discovered	True	True	True	False	False	True	False
Parent	null	A	A	null	null	B	null

The queue is C, F.

Warning 19.1. Do you now see why the discovered array is essential? Suppose we didn't have it. We would check A's neighbors and add B to the queue. But upon eventually getting to B in the queue checking B's neighbors, we would add A back. Then, we eventually get to A in the queue, check its neighbors, and add B back. So we get stuck in an infinite loop. Also, there's literally no point in processing the same vertex more than once anyway.

So we dequeue C and check its neighbors. Only E is undiscovered among its neighbors. New table:

Node	A	B	C	D	E	F	G
Discovered	True	True	True	False	True	True	False
Parent	null	A	A	null	C	B	null

The queue is F, E. Now, we dequeue F and check its neighbors. Only new neighbor is D. New table:

Node	A	B	C	D	E	F	G
Discovered	True	True	True	True	True	True	False
Parent	null	A	A	F	C	B	null

The queue is E, D. Checking both nodes, we discovered all their neighbors already. So we remove both from the queue. Queue is empty, so we stop, and the above table is the final result. Notice we never discovered G, and it was in a different connected component than A. Maybe there is causation between those two things? We'll see in the proof of correctness.

Also, the parent of A is null because that's where the source of the BFS is and wasn't discovered by some predecessor node.

§19.4 Proof of Correctness

§19.5 Runtime

§19.6 Properties of BFS

§19.7 Applications of BFS

Warning 19.2. Do NOT use BFS when considering connected components in a DIRECTED graph. The reason it works for undirected graphs is because if you can get from u to v, that automatically means you can get from v to u. But with directed graphs, just because you can get from u to v, that doesn't necessarily mean you can get from v to u. Don't worry, we'll have an algorithm later that will get you connected components in a directed graph.

§19.8 Summary

§20 Depth First Search

§20.1 Introduction

§20.2 The Algorithm

§20.3 Proof of Correctness

§20.4 Runtime

§20.5 DFS Forest and Edge Classification

§20.6 Parentheses Theorem

§20.7 White Path Theorem

§20.8 Applications of DFS

§20.9 Summary

§21 Kahn's Algorithm

§21.1 Introduction and Topological Sorts

§21.2 The Algorithm

§21.3 Proof of Correctness

§21.4 Runtime

§21.5 Summary

Advice 21.1 — Note that topologically sorting is $O(n + m)$ and most graph algorithms you're asked to do on homework or test will have a target runtime of $O(n + m)$ (or worse). So you don't lose anything by topologically sorting a DAG. In fact, you usually want to do it because it makes the DAG feel more organized and easier to work with.

§22 Tarjan's Algorithm

§22.1 Introduction

§22.2 The Algorithm

§22.3 Proof of Correctness

§22.4 Runtime

§22.5 Summary

§23 Kosaraju's Algorithm

§23.1 Introduction

§23.2 The Algorithm

§23.3 Proof of Correctness

§23.4 Runtime

Advice 23.1 — Remember G^{SCC} is a DAG too! So you can topologically sort it. In fact, there are problems where you will see Kosaraju's and then Kahn's in tandem, especially involving strong connectivity or reachability in directed graphs.

§23.5 Problem Solving

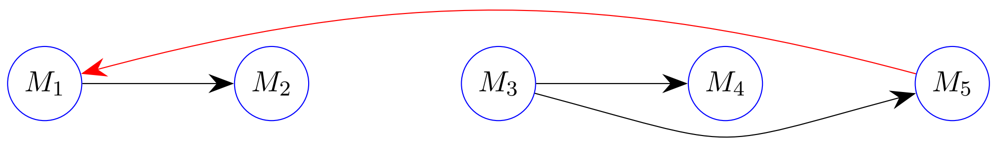
I shall demonstrate the beauty of graph algorithms in tandem, since we've learned a good number so far.

Example 23.2 (Recitation)
A directed graph is called "almost strongly connected" if adding a single edge makes the entire graph strongly connected. Design an $O(n + m)$ algorithm to determine whether a graph is almost strongly connected.

Okay, the problem is talking about strong connectivity, so maybe we should think about this in terms of strongly connected components. Let's run Kosaraju's to get G^{SCC}. Oh wait, G^{SCC} is a DAG, so let's topo sort it! Say T is the topo sort.

We know by definition of an SCC that any two vertices in the same SCC are strongly connected. So the issue now is being able to get from SCC to SCC and back.

Remember how in a topo sort, the last node L is a sink and the first node F is a source. So at the current moment, there is no way to leave L and no way to enter F. If we want any chance of the graph being strongly connected, we need a way to get from L to F with only one edge, so suppose we draw an edge from L to F. However, that doesn't necessarily make the graph strongly connected. Just look at this G^{SCC}, where adding the edge I mentioned doesn't necessarily make the graph strongly connected:



So how do we check that this is strongly connected? Run Kosaraju's on the graph with the added edge. If we get 1 SCC, the new graph is strongly connected, making the original graph almost strongly connected. If not, the original graph is not almost strongly connected.

Proof of Correctness? I alluded it as I talked through the thought process, but the idea is(there necessarily has to exist both a sink mega vertex and source mega vertex in the G^{SCC} because G^{SCC} is a DAG and all DAGs have at least one. And the topo sort properties allow us to locate an example of a sink and source (even though there could be more than one).

I also said how you can never leave the sink and never enter the source. Let u be some vertex in the sink mega vertex and v be some vertex in the source mega vertex. So at the moment, u cannot get to v, but we need that to occur to ever have a chance at the graph being strongly connected (where any two vertices are mutually reachable from one another). So we justify the necessity of drawing the edge to even have a chance. And to show whether or not drawing the edge actually works, the new graph is strongly connected if and only if it's 1 SCC, which is why we use Kosaraju's again and check the number of SCCs.

Runtime? Well, Kosaraju's is $O(n + m)$. Topo sorting is also $O(n + m)$. Kosaraju's again is $O(n + m)$. So the algorithm is 3 back-to-back $O(n + m)$ operations, which is still $O(n + m)$.

Advice 23.3 — See the beauty of turning a directed graph into G^{SCC}? Because a directed graph may not be a DAG, but G^{SCC} always is. And G^{SCC} not only makes thinking about strong connectivity easier, but the topo sort (which you can always do for a DAG) gives nice properties to get us on the right track.

§23.6 Summary

§24 Dijkstra's

§24.1 Introduction

§24.2 The Algorithm

§24.3 Proof of Correctness

§24.4 Runtime

§24.5 Summary

§25 Kruskal's Algorithm

§25.1 Introduction

§25.2 Minimum Spanning Trees

§25.3 The Algorithm

§25.4 Proof of Correctness

§25.5 Runtime

§25.6 Summary

§26 Union-Find

§27 Prim's Algorithm

§27.1 Introduction

§27.2 The Algorithm

§27.3 Proof of Correctness

§27.4 Runtime

§27.5 Summary

§28 Hashing

§29 Tries

§30 Balanced Binary Tree

§31 Test Section and Cheat Sheets

Before I get in to the details, keep in mind all these tests are closed notes. Again, remember that content may be different depending on the iteration of the course.

This is how it's going to work for each of the three tests: I'll briefly recap the main topics. Then, I'll have bullet point lists over all the content that was covered. Yes, the lists will be long, but whether you like it or not, this course is content-heavy. Most of the bullet points should be stuff you're familiar with anyway, but it doesn't help to have a good refresher every couple of times in the days before the test. Go back to the appropriate sections if you don't feel confident on something. I'll also give test-specific strategies because there may be types of problems you're not used to, or non-standard ways of applying the material you learned.

§31.1 Good Sources to Review, In General

- Your notes
- Lecture notes
- Past HW problems (because intuition from such problems could help you with coming up with solutions)
- Recitation slides and problems
- Practice tests, if they post them

§31.2 Midterm 1

This is a 90 minute test, takes place just over a month in to the course.

§31.2.1 Main Topics

- Asymptotic Analysis
- Recurrence Relations and Code Snippets
- Divide and Conquer
- Quicksort, Select
- Stacks, Queues, and Heaps

§31.2.2 List of Content

- Euclid's algorithm: $\gcd(a, b) = \gcd(b, c)$, where $c \equiv a \pmod{b}$ and $c < \frac{a}{2}$. Runs in $O(\lg n)$.
- $f(n) \in O(g(n))$ means there exists a positive real c and positive integer n_0 such that $f(n) \leq cg(n)$ for all integers $n \geq n_0$
- $f(n) \in \Omega(g(n))$ means there exists a positive real c and positive integer n_0 such that $f(n) \geq cg(n)$ for all integers $n \geq n_0$
- $f(n) \in \Theta(g(n))$ means $f(n)$ is both $O(g(n))$ and $\Omega(g(n))$.
- Use induction when they ask you explicitly for n_0 and c. Go about the inductive step first to get an n_0 that fits your needs. Then, choose a c so that your base case works.
- Polynomials of degree d are always $\Theta(n^d)$
- $\lg n$ is faster than n
- Use strong induction for POC in recursive algorithms.
- Insertion Sort: We place in elements in order as we go. Worst case is $\Theta(n^2)$ (backwards order), while best case is $\Theta(n)$ (already in order).
- For POC in loops, show three things: initialization, maintenance, and termination.
- Expansion Method: For a recurrence relation, keep plugging it in to itself, and it will eventually reach a base case.
- Subset-Superset Method: Use it to find the runtime for nested for loops when the code inside the for loops runs in constant time (like printing) and each loop's variable increments by 1 each iteration.
- Table and Summation Method: Use it when the for loop does NOT increment by 1 each iteration and does something wacky like double or square each iteration.

- Merge Sort: Takes two sorted arrays (that should be sorted recursively) and combines them into one final sorted array. Runs in $\Theta(n \lg n)$ without much nuance between a worst or best case scenario.
- Divide and Conquer: Break the problem into parts (usually 2). Recursively work on both parts. Then, combine the solved parts.
- Quick Sort: Chooses a pivot element and then elements are moved around. At the end, all elements less than the pivot are to the left of it, and all elements greater are to the right of it.
- If pivots are selected randomly, the expected runtime is $\Theta(n \lg n)$, but worse case is $\Theta(n^2)$.
- Select/Partition: We can find the ith smallest element in $O(n)$ time, as well as determine which elements are greater and which are smaller than the ith smallest element.
- Select relies on finding the median of the medians and using that as the pivot. After partitioning around the pivot, both sides are guaranteed to have less than $\frac{7n}{10}$ elements and then we recurse on the appropriate half.
- To increase the size s of an array, we can either copy everything to a new array of either size $s + c$ (for some fixed constant c) or size $2 \cdot s$. Both time to copy elements and space that is wasted by empty slots in the array need to be considered.
- Amortized time looks at the long run average because while something like copying takes up time, it's only done so many times compared to adding in new elements.
- Stack
  - Last In, First Out
  - Push inserts element to the back (amortized $O(1)$)
  - Pop removes last element and returns it (amortized $O(1)$)
  - Peek ($O(1)$)
- Queue
  - First In, First Out
  - Enqueue inserts element to the back (amortized $O(1)$)
  - Dequeue removes first element and returns it (amortized $O(1)$)
  - Peek ($O(1)$)
- A circular array helps for implementing queues because otherwise, there could be unused space in the front that we don't know about.
- Complete Binary Tree: All levels before the last level are totally full. In the last level, all nodes are as far left as possible.
- Max Heap is a CBT (complete binary tree) where each parent is greater than both its children. Min Heap is the same but each parent is less than both its children.
- MaxHeapify is for when you aren't sure about the root node, but the two subtrees connected to the root are definitely max heaps. You sift the root node down appropriately and get a max heap. Runs in $O(\lg n)$ time.
- BuildMaxHeap turns an unsorted array into a Max Heap. Read off the elements in the array into a heap without worrying about the heap invariant yet. Then, sift internal nodes down appropriately, starting from the rightmost one on the lowest level and then working your way left. Go to the next level up for more internal nodes when you're done with one level. Runs in $O(n)$ time.
- To insert a number n into a heap, place n in the next available spot in the lowest level. Then, sift n up appropriately. Takes $O(\lg n)$ time.

- To delete the largest element in a max heap (or smallest for min heap), switch the root r with the rightmost node in the lowest level. Then, delete r, and sift the switched node down appropriately. Takes $O(\lg n)$ time.
- To turn a max heap into an array that is sorted from lowest to highest, switch the root with the last element in the lowest level. Then, detach the last element from the tree, and sift the new root down appropriately. Rinse and repeat until all nodes are detached.

§31.2.3 Test Specific Strategies

- They'll provide Master Theorem. Use it as a timesaver for finding the runtime of a recursive algorithm. BUT THEY MAY SAY NOT TO USE IT, IN WHICH CASE, DO NOT CITE IT. In that case, use expansion, but you can use Master Theorem to check your work.
- When ask to expand, try to do 2-3 expansions before you generalize it (not including the line with the original recurrence relation).
- They'll provide log rules, but it helps to be familiar with them, so you know when to use where. It often helps to know $\lg(a) + \lg(b) = \lg(ab)$ to combine logs, $\lg(a^b) = b\lg(a)$ to move exponents in and out of logs, and $a^{\log_a(b)} = b$ to remove logs in exponents.
- If they want an algorithm done in $\lg n$ time, that's usually a sign to use Divide and Conquer, but recurse on only one side (like binary search) and not both.
- If you have to write a recurrence relation or recursive algorithm, DO NOT FORGET TO WRITE THE BASE CASE.
- Remember that Merge Sort is done in $\Theta(n \lg n)$. Sometimes the problem may be so much easier if the array were sorted, so if Merge Sort fits in the given time, go for it.
- Similar to above, remember that Select runs in $O(n)$. This may be useful for finding the median, min, or max if it fits in the given time as part of an algorithm.
- Remember common recurrences and their runtimes because it helps for designing new algorithms. You know Merge Sort is $\Theta(n \lg n)$ and has the recurrence $T(n) = 2T(\frac{n}{2}) + \Theta(n)$. So if asked to design a $n \lg n$ algorithm and you decide to divide and conquer on both halves of an array, make sure the combine step doesn't exceed $O(n)$ (else, the whole algorithm exceeds Merge Sort's time).
- $T(n) = 2T(\frac{n}{2}) + O(1)$ with $T(1) = O(1)$ implies $O(n)$ time
- $T(n) = T(\frac{n}{2}) + O(n)$ with $T(1) = O(1)$ also implies $O(n)$ time

§31.3 Midterm 2

This is a 90 minute test, takes place just over two months in to the course.

§31.3.1 Main Topics

- Heap runtimes
- Huffman
- Graph representations and space
- BFS
- DFS
- Topological sorts
- Kosaraju
- Dijkstra

§31.3.2 List of Content

- Building a min heap is $O(n)$. Removing the min or adding an element is $O(\lg n)$.
- Huffman:
  - Huffman is a "prefix tree", where the character nodes are at leaves, preventing a situation where two messages can create the same sequence of bits.
  - To create a Huffman tree, you repeatedly merge the two smallest nodes and traverses the edges from the root to get codes.
  - ABL is essentially an expected value for the length of the codes.
  - A min heap is generally used to help get the two smallest frequencies in an efficient manner.
  - Huffman is $O(n \lg n)$ with a heap
  - Try proof by contradiction for Huffman proof problems.
- For space problems, let a be the number of bytes for a vertex index, b be the number of bytes for a pointer, and c be the number of bytes for an edge weight. Then, an adjacency matrix takes up $c \cdot |V|^2$ bytes, while an adjacency list takes $b \cdot |V| + (a+b+c) \cdot |E|$. Note that for undirected graphs, you have to double E because an edge in an adjacency list has to appear twice for both directions.
- BFS:
  - Input is a graph (undirected or directed) and a source node. Output is the BFS tree of the source's connected component.
  - BFS traverses the graph one layer at a time, branching outwards. Nodes that are closer to the source get caught first.
  - It uses the FIFO properties of a queue to ensure nodes closer to the source are prioritized.
  - Nodes in layer k are a distance k away from the source.
  - Applications of BFS:
    - Reachability - finding all nodes for which there is a path from u to v
    - Shortest path (using the layers, but only in unweighted graphs)
    - Bipartitiness (using the layers)
  - BFS is $O(n+m)$, where $O(n)$ comes from processing every node and then each neighbor of each node is processed, which is $O(\deg(v))$ work for a node but $O(m)$ work overall by Handshaking lemma.
- DFS:
  - Input is any graph (undirected or directed). Output is a DFS forest.
  - DFS is another graph traversal but involves going as far as you can until you hit a dead end and then backtracking and exploring alternate routes that were missed along the way.
  - Start time in DFS is when you discover a node for the first time. Finish time occurs when there's no more undiscovered neighbors and then you backtrack.
  - Edges in the original graph fall in to one of 4 categories, using the DFS forest:
    - Tree edges: this edge is also in the DFS forest
    - Back edge: edge is $u \to v$, where u is a descendant of v
    - Forward edge: a non-tree edge in the form $u \to v$, where u is an ancestor of v
    - Cross edge: edge is $u \to v$, where u and v have no ancestor-descendant relationship. Usually between different connected components of the DFS forest, or different branches in the same connected component.
  - In an undirected graph, there are only tree and back edges.

- Parentheses Theorem: Suppose $d[u] < d[v]$. Then, $d[u] < d[v] < f[v] < f[u]$ if v is a descendant of u. Or $d[u] < f[u] < d[v] < f[v]$ if u and v don't have an ancestor-descendant relationship.
- White Path Theorem: In DFS forest, v is a descendant of u if and only if at $d[u]$, there is a path of white vertices from u to v
- Above two theorems are super important for proofs on algorithms that will involve DFS (Kosaraju and Tarjan for example) and are good to cite in general when necessary.
- Popular use of DFS: detecting cycles (which happens if and only if DFS detects a back edge)
- DFS is $O(n + m)$ by the same intution as BFS.

• Topological Sorts:
  - Topological sort is a permutation of the vertices such that all edges point from left to right.
  - Only DAGs have topological sorts; cycles create a conflict with trying to order them.
  - Kahn's algorithm: Find all sources. Remove sources from the graph and add them to the sort. This opens up new sources, and then rinse and repeat. Runs in $O(n + m)$.
  - Proof involves that every DAG has a source and sink (by Maximal Path) and removing sources still gives a DAG.
  - Tarjan's algorithm: Run DFS on the graph. The topological sort is given by the finish times of the vertices, in decreasing order. Runs in $O(n + m)$.
  - Proof involves Parentheses and White Path, where if $u \to v$, then $f[u] > f[v]$. Cases on which of $d[u]$ or $d[v]$ is smaller.

• Kosaraju:
  - Input is a directed graph G and output is G^{SCC} (the graph of strongly connected components of G)
  - A strongly connected component is a subset of vertices in a directed graph where for any two vertices in the subset are reachable from one another, and this subset is maximal.
  - Kosaraju is done by:
    * Doing DFS and noting finish times
    * Computing the transpose of G, call this G^T
    * Keep doing DFS on G^T but in order of finish times on G from highest to lowest to get each SCC.
  - Proof involves if we have $A \to B$ in G^{SCC}, then $f[A] > f[B]$. Proof is similar to Tarjan's in which we use Parentheses and White Path in tandem along with cases on which of $d[A]$ or $d[B]$ is smaller.
  - Runs in $O(n + m)$

• Dijkstra's
  - Input is a directed/undirected graph that is weighted and a source node. Output is the shortest path from source to all other vertices.
  - The idea involves creating a set S of nodes where we can be confident nodes in S have the shortest path found. S starts out by only having the source. But we slowly expand out and update possible paths as we go. The vertex v we find with the shortest distance thus far can safely go into S because essentially, all other routes into v already suck.
  - Dijkstra's is $O((V + E) \lg V)$ specifically with a min heap: creating the min heap is $O(V)$, extracting min for each vertex is $O(V \lg V)$, and possibly updating distances when we traverse each edge is $O(E \lg V)$.

§31.3.3 Test Specific Strategies

- Remember applications of each algorithm
- Think about how each part of the algorithm contributes to the runtime. For example, examining neighbors over all vertices is $O(m)$ by Handshaking Lemma.
- Be comfortable with the DFS process as there could be a question involving it. Also, be able to identify classify edges in the DFS based on the forest.
- Toposort is a good strategy for DAGs
- It may be helpful to use Kosaraju and then toposort G^{SCC}, since G^{SCC} is always a DAG. Especially useful in reachability in a directed graph.
- Transpose is also something good to think about when dealing with reachability in a directed graph. Because testing whether u can be reached from v in G is equivalent to whether you can get from u to v in G^T (which can be done with BFS)
- Don't merely memorize graph algorithm runtimes: understand why they are that way. Funny story: I remember saying to my neighbor before the midterm that they could ask something about different implementations of Dijkstra's because it could be done with an array, just not really used in the class. Lo and behold, they did ask such a question to troll those who merely memorized runtimes without understanding where the runtime comes from. We joked about it after the test.

§31.4 Final