Contents

1 Algorithms of Arithmetic

1.1 Lecture 1

1.1.1 Addition/Multiplication

First, let us consider the problem of adding two n-bit numbers, a and b. If both are a different amount of bits from each other, we can pad 0's to the left of the smaller one until it reaches the length of the larger one (note that padding 0's doesn't change the sum). The grade-school algorithm (add column-wise and do carries) has to compute at most $n + 1$ additions, which we can assume are all constant-time. Thus, we say addition has complexity linear in n, or $\Theta(n)$ (we drop the constant because 1 pales in significance to how great n can grow).

But can we do better for addition? The answer is no; since it takes $n + 1$ bits to write our answer, any algorithm returning the sum must require $n + 1$ operations. Thus, we say as a lower bound, addition is $\Omega(n)$ (the full definitions of these terms will come shortly).

Now we turn to the problem of multiplication. How fast is the grade school algorithm? First, we multiply digit-wise and then do a bunch of additions. In binary, multiplying by a 0 or 1 and then right-padding with 0s (bitshifting) corresponds to a constant time operation for each bit of b. Then, we have to add together n potentially $2n$ bit numbers. This adds n^2 time. Thus, the runtime is quadratic in n or $\Theta(n^2)$.

Now, can we do better for multiplication? It turns out we can. We do this by leveraging the idea of divide-and-conquer; breaking our problem into smaller subproblems that we can solve recursively and then using these pieces to build the final solution.

Here is our first attempt:

Algorithm 1.1 (Naive Divide and Conquer)
Suppose the numbers x and y that we wish to multiply are represented in decimal. Assume without loss of generality that both have the same number of digits n, and n is a power of two (if they aren't then we can just pad with 0s on the left until these requirements are met). Then, let x_H be the upper half of the digits of x and x_L be the lower half of the digits of x (and define y_H, y_L analogously). Note that

$$x = x_H \cdot 10^{n/2} + x_L$$
$$y = y_H \cdot 10^{n/2} + y_L$$

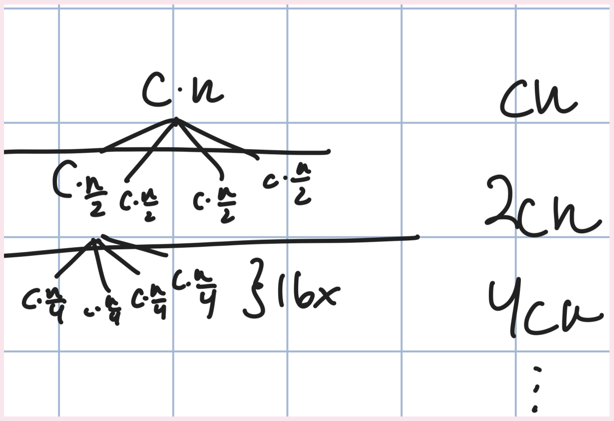
And all the subscripted letters are $n/2$ digits long. Multiplying these together then yields:

$$x \cdot y = x_H \cdot y_H \cdot 10^n + (x_H \cdot y_L + x_L \cdot y_H)10^{n/2} + x_L \cdot y_L$$

Note that to do this multiplication, we have to do 3 n-digit additions as well as 4 $n/2$-digit multiplications (Multiplying by powers of 10 is just digit shifts, which can be done in linear time). To do the additions, let us use the standard grade school algorithm. To do the multiplications, let us have the function call itself recursively on the $n/2$-digit numbers. As a base case, note that if x and y are both one-digit numbers, the multiplication can be looked up in constant time.
Runtime Analysis Now, to analyze the runtime, let the amount of time taken during the base case be c' and let c be another constant. Then, for the total running time $T(n)$, we know that:

$$T(n) = \begin{cases} 4T(n/2) + cn & n > 1 \\ c' & n = 1 \end{cases}$$

Since we make 4 recursive calls on an input of $n/2$ digits, and do a linear amount of work in every call. To analyze the runtime, we should draw a recursive tree.



$c \cdot n$
$c \cdot \frac{n}{2}$ $c \cdot \frac{n}{2}$ $c \cdot \frac{n}{2}$ $c \cdot \frac{n}{2}$
$c \cdot \frac{n}{4}$ $c \cdot \frac{n}{4}$ $c \cdot \frac{n}{4}$ $c \cdot \frac{n}{4}$ } 16x
cn
2cn
4cn
⋮

Summing the nodes in this tree will give us the total runtime. As we can see from the diagram, on layer i (considering the top layer as layer 0), there is $c \cdot n/2^i$ work done at each node, and there are 2^{i+1} nodes in that layer. Call $k = \log_2 n$. Then our total runtime is:

$$\begin{aligned} T(n) &= cn + 2cn + 4cn + \cdots + 2^k cn \\ &= cn\frac{2^{k+1} - 1}{2 - 1} \\ &\leq 2cn \cdot 2^k = 2cn^2 = \Theta(n^2) \end{aligned}$$

Thus, this algorithm is no better than our traditional grade-school algorithm.

However, there is a way to make this work. Gauss came up with a way to multiply two complex numbers (analogous to this setup) in 3 multiplications instead of 4. Similarly, Russian mathematician Karatsuba applied it to integer multiplication.

Algorithm 1.2 (Karatsuba's Algorithm for Multiplication)
Proceed similarly to last time, defining x_H, y_H, x_L, y_L. However, define the following:

$$A = x_H \cdot y_H, B = x_L \cdot y_L, D = (x_L + x_H) \cdot (y_L + y_H)$$

Then notice that the middle term from before is just $D - A - B$, i.e. we can write:

$$x \cdot y = A \cdot 10^n + (D - A - B) \cdot 10^{n/2} + B$$

This means that we only need to compute three multiplications recursively (and do a few more additions, but since those take linear time, it's fine to have extra of those).
Runtime Analysis The runtime analysis is similar to that of the naive algorithm. However, instead of the amount of work increasing by $4/2 = 2$ every level, instead the work will only increase by $3/2$ every time (3

subcalls of size $n/2$). Let us again define $k = log_2 n$. This gives us total runtime, $T(n)$, being:

$$\begin{aligned}
T(n) &= cn + \frac{3cn}{2} + \frac{9cn}{2} + \cdots + \frac{3^k cn}{2^k} \\
&= cn\frac{\left(\frac{3}{2}\right)^{k+1} - 1}{\frac{3}{2} - 1} \\
&\leq 2 \cdot 32cn\frac{3}{2}^k \\
&= 3c3^k \\
&= 3c\left(2^k\right)^{\log_2 3} \\
&= 3cn^{\log_2 3} \\
&= \mathcal{O}(n^{\log_2 3})
\end{aligned}$$

Note that $\log_2 3 \approx 1.585 < 2$, so this is better than our naive algorithm!

After Karatsuba's algorithm, people have continued to improve the worst case runtime of integer multiplication. In 2019, a $\mathcal{O}(n \log n)$ algorithm was found for multiplying two numbers together. However, this series of algorithms after Karatsuba's had such large constant factors that in practice, grade-school multiplication is still the one implemented most of the time.

As a note, Python currently uses Karatsuba multiplication, but only for numbers that are sufficiently large.

2 Divide and Conquer Algorithms

2.1 Lecture 2

Before we introduce some topics, let us set the stage for our analysis on the next algorithm. We define "Flops" as floating-point operations (additions, subtractions, multiplications, divisions, etc.). Now, we will consider the amount of flops that it takes an algorithm to run. We will use this to measure the runtime of certain algorithms.

2.1.1 Fibonacci Numbers

Consider the problem of computing the nth Fibonacci number. Recall the Fibonacci sequence is defined by the recurrence:

$$F_0 = 0, F_1 = 1$$
$$F_n = F_{n-1} + F_{n-2}$$

The simplest algorithm one can do is the follow the recurrence word-for-word.

TODO: Finish this section (Iteration, Fast Powering, Closed Form Solution)

2.1.2 Asymptotic Notation

Consider two functions $f, g : \mathbb{Z}^+ \to \mathbb{Z}^+$. Here is some information about common asymptotic notation used to analyze the size of these functions (these functions can maybe represent the runtime of an algorithm).

Name	Notation	Meaning	Analogy
"Big-Oh"	$f = \mathcal{O}(g)$	$\exists c > 0$ s.t. $f(n) \le cg(n)$	$\le$
"Little-Oh"	$f = o(g)$	$\lim_{n\to\infty} \frac{f(n)}{g(n)}$	$<$
"Big-Omega"	$f = \Omega(g)$	$g = \mathcal{O}(f)$	$\ge$
"Little-Omega"	$f = \omega(g)$	$g = o(f)$	$>$
"Theta"	$f = \Theta(g)$	$f = \mathcal{O}(g)$ and $f = \Omega(g)$	$=$

Here is an example to get a feel for how asymptotic notation works.

Example 2.1
Take $f(n) = 3n^3$ and $g(n) = n^4$. Then, notice,

$$\lim_{n\to\infty} \frac{f(n)}{g(n)} = \lim_{n\to\infty} \frac{3n^3}{n^4} = 0$$

So, $f = o(g)$. We can also conclude more. Realize that the above limit really means that there exists an N such that for all $n \ge N$, we have:

$$\frac{f(n)}{g(n)} \le 1 \implies f(n) \le 1 \cdot g(n)$$

(Note that 1 is not important for this argument; we could've chosen any $\varepsilon > 0$). Now, consider the values of $\frac{f(n)}{g(n)}$ for $n < N$; this has some maximum c. Thus, we can conclude that for ALL n,

$$f(n) \le \max(c, 1)g(n)$$

which implies $f = \mathcal{O}(g)$.

2.2 Lecture 3

2.2.1 Recurrences and Master Theorem

The idea of divide-and-conquer algorithms are to divide the input inot smaller parts, recurse on parts, and combine the parts to build an answer.

To analyze the runtime of divide-and-conquer algorithms, it is useful to derive the following result.

Theorem 2.1 (Master Theorem)
Suppose we have a recurrence

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

then, we have

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

Master theorem can be shown by drawing a recursion tree, and then summing up the work done in each level (proof omitted for brevity). We can also think of the cases as symbolizing the following:

Case	Interpretation
$a < b^d$	The root does most of the work
$a = b^d$	The root and the leaves do an equal amount of work
$a > b^d$	The leaves do most of the work

2.2.2 Matrix Multiplication

Another example of a divide and conquer algorithm is matrix multiplication.

Consider multiplying two n-by-n matrices A and B.

$$A = \begin{bmatrix} A_{11} & A_{12} & \dots & A_{1n} \\ A_{21} & A_{22} & \dots & A_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ A_{n1} & A_{n2} & \dots & A_{nn} \end{bmatrix}$$

Then the resultant C has entries given by:

$$C_{ij} = \sum_{k=1}^{n} A_{ik} B_{kj}$$

The natural implementation is then to to loop this summation over i and j. This means this will be three nested loop (a loop is needed for the summation). In flops, this runs in $\Theta(n^3)$ operations.

We can try to break our input instead into $n/2$-by-$n/2$ blocks, as shown:

$$\begin{bmatrix} A & B \\ C & D \end{bmatrix} \begin{bmatrix} E & F \\ G & H \end{bmatrix} = \begin{bmatrix} AE + BG & AF + BH \\ CE + DG & CF + DH \end{bmatrix}$$

To find the runtime of this algorithm, let us realize there are 8 multiplications (recursively) and then finally a $\Theta(n^2)$ addition at the end. This means our recurrence is:

$$T(n) = 8T\left(\frac{n}{2}\right) + \Theta(n^2)$$

Note that for our Master theorem setup, $8 > 2^2$, so we have

$$T(n) = \Theta\left(n^{\log_2 8}\right) = \Theta\left(n^3\right)$$

so this is no better than our naive approach.

Using a similar realization to Karatsuba, Strassen in 1969 found the following:

Algorithm 2.1 (Strassen's Algorithm)
Consider two matrices X and Y which are both n-by-n. Break them up into block matrix form of $n/2$-by-$n/2$ matrices as follows:

$$X = \begin{bmatrix} A & B \\ C & D \end{bmatrix}, Y = \begin{bmatrix} E & F \\ G & H \end{bmatrix}$$

Define the following:

$$\begin{aligned} P_1 &= A(F - H) \\ P_2 &= (A + B)H \\ &\vdots \\ P_7 &= (A - C)(E + F) \end{aligned}$$

Then,

$$Z = \begin{bmatrix} P_5 + P_4 - P_2 + P_6 & P_1 + P_2 \\ P_3 + P_4 & P_1 + P_5 - P_3 - P_7 \end{bmatrix}$$

Analyzing the runtime, we see that there are 7 $n/2$-by-$n/2$ multiplications, and some n^2 additions, meaning the total runtime is

$$T(n) = 7T(n/2) + \mathcal{O}\left(n^2\right)$$

which Master theorem brings to

$$T(n) = \mathcal{O}\left(n^{\log_2 7}\right) \approx \mathcal{O}\left(n^{2.81}\right)$$

However, Strassen has such a big constant factor that the normal n^3 algorithm is still the most widely used.

2.2.3 Sorting

Consider the problem of sorting a length n array A.

Algorithm 2.2 (MergeSort)
First, we define a procedure Merge that takes two sorted lists and merges them in linear time. To do this, we first keep a pointer on both lists that starts at the beginning of each list. We then compare the pointed-to elements of each list. The lesser element is then added to the output, and the pointer of the list with that element is incremented by one place. This keeps going until all the elements are used. We then use merge to divide-and-conquer the list as follows:

```
function MergeSort($A[1 \ldots n]$)
    if $n = 1$ then
```

```
            return $A$
        $B \leftarrow$ MergeSort($A[1 \ldots \frac{n}{2}]$)
        $C \leftarrow$ MergeSort($A[\frac{n}{2} + 1 \ldots n]$)
        return Merge($B, C$)
```

We get the following recurrence for MergeSort:

$$T(n) = 2T\left(\frac{n}{2}\right) + \Theta(n)$$

which through master theorem gives us a running time of

$$T(n) = \Theta(n \log n)$$

Another way of implementing this is a bottom up approach:

Algorithm 2.3 (Iterative Merge Sort)

```
function MergeSortIter($A[1 \ldots n]$)
    $Q \leftarrow$ Divide $A$ into $n$ lists of size one
    while $Q$.size() > 1 do
        $X, Y \leftarrow Q$.pop(), $Q$.pop()
        $Q$.push(Merge($X, Y$))
    return $Q$.pop()
```

Runtime Analysis Now we can think about the runtime of this algorithm. Think of the algorithm as running in phases. Phase 0 is when lists popped have size 1. Phase 1 is when lists popped have size 2. Phase i is when lists popped have size 2^i. Note that in each phase, each element is looked at exactly once. Thus, the total runtime must be proportional to $n \cdot$ number of phases. How many phases are there? There are $\log n$ phases, giving us the same $\Theta(n \log n)$ runtime!

The best way to see this is with an example:

Example 2.2
Suppose our initial list is:

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

We then split this into sublists of size one in our Q and start iterating:

$$\begin{aligned} Q &= [[8], [7], [6], [5], [4], [3], [2], [1]] \\ Q &= [[6], [5], [4], [3], [2], [1], [7, 8]] \\ &\vdots \\ Q &= [[7, 8], [5, 6], [3, 4], [1, 2]] \\ Q &= [[3, 4], [1, 2], [5, 6, 7, 8]] \\ Q &= [[1, 2, 3, 4], [5, 6, 7, 8]] \\ Q &= [[1, 2, 3, 4, 5, 6, 7, 8]] \end{aligned}$$

Our list has been sorted!

Can we sort faster than $n \log n$? It turns out we cannot do any better with an algorithm that uses comparisons to sort (the problem is $\Omega(n \log n)$).

Theorem 2.2 (Fastest Shorting in Comparison Model, Lower Bound)
We will show that $\Omega(n \log n)$ comparisons are needed even if promised A is some permutation of $\{1, \ldots, n\}$ (all distinct as well).

Proof
The first comparison such an algorithm might make might be: is $A_i < A_j$? Then we branch off into two cases for each, where we require another comparison. We can construct a binary tree that models the situation.
First, notice that each leaf is when the algorithm terminates. Note that since every run of the algorithm with a different input produces a different output permutation of the input, there must be at least $n!$ leaves. Consider the maximum depth of this tree T. There are at most 2^T leaves, meaning that $2^T \geq n!$. This means

$$\begin{aligned} T &\geq \log(n!) \\ T &= \Omega(n \log n) \end{aligned}$$

The last claim can be shown by realizing

$$\begin{aligned} n! &\geq \left(\frac{n}{2}\right)^{\frac{n}{2}} \\ \log(n!) &\geq \frac{n}{2} \log\left(\frac{n}{2}\right) \\ \log(n!) &\geq \frac{n}{2} \log n - \frac{n}{2} \\ \log(n!) &= \Omega(n \log n) \end{aligned}$$

However, there are way more operations than comparisons that can be used for sorting. An example of this is counting sort: if you have n integers and all the integers have values between 1 and b, then you can sort in $\Theta(n + b)$, by just keeping an array of all the elements that fit in each value "bucket" between 1 and b.

The Word RAM model: suppose your machine can store words of size w and you can do any common C operations. The fastest known algorithm following this model (not just comparisons) is: $\mathcal{O}\left(n\sqrt{\log \log n}\right)$. This is also a randomized algorithm.

There are two types of randomized algorithms (which will be revisited). A Monte Carlo randomized algorithm is one whose output may be incorrect with small probability. A Las Vegas algorithm is one whose runtime is fast in expectation, but may be slow with small probability.

2.2.4 Selection/Medians

We now consider the problem of selection. Suppose we want to select the kth smallest integer in a list A. Without loss of generality, assume all elements of A are distinct (since we could replace $A[i]$ with the tuple $(A[i], i)$). For selection, there is Quick Select, which we will explore later. Notably, quick select requires knowing the median in linear time. We will instead focus on that problem, (the same as the selection problem for $k = n/2$).

Algorithm 2.4 (Median of Medians)
Take an array A. Then break up the array into subarrays of size 5. Next, we will recursively compute the median of each subarray. Note that this takes constant time to complete since 5 is a constant. Now we have a $N/5$ size array. We then find the median recursively of this smaller problem. Call this median m_1.
Now, we change the array such that all the elements bigger than m_1 end up on the right of m_1, elements smaller than m_1 end up on the left, and m_1 is in the middle of these two parts (this only requires a linear scan). If m_1 is in position less than $n/2$, then the true median sits on its right, so we can recurse on the right half. If m_1 is in position greater than $n/2$, then the true median sits on its left, so we can recurse on the left half. Finally, if m_1 is at exactly position, $n/2$, then we have found the median.
Runtime Analysis The claim is that at least 30% of the elements are filtered out by comparisons to m_1. To

show this, consider m_1 compared to the other medians. Note that it is bigger than 3 of the elements in every median it is bigger than, so, it is bigger than $\frac{3}{5} \cdot \frac{N}{10} = \frac{3}{10}$ of the elements. Thus, if m_1 is in the first half of the array, then it will filter out at least $\frac{3}{10}$ of the numbers. Similarly, you can make a symmetric argument that if m_1 is in the second half, then it must be less than $\frac{3}{10}$ of the numbers and thus will filter out 30% of them. Either way, we can then produce the following recurrrence:

$$T(n) \leq T\left(\frac{7n}{10}\right) + T\left(\frac{n}{5}\right) + \Theta(n)$$

This recurrence gives $T(n) = \mathcal{O}(n)$. We can give an inductive argument:

Proof
We will show that $T(n) \leq Bn$ for sufficiently large B, which will imply our big-$\mathcal{O}$ runtime.
Base Case: if n is 1, then we just return the input, so if B is greater than the time needed to return then the base case holds.
Inductive Hypothesis: Suppose that the claim holds for $k < n$.
Inductive Step: By the recurrence and the inductive hypothesis, we have that

$$T(n) \leq B\frac{7n}{10} + B\frac{n}{5} + Cn$$

where C is some other constant. Now, we have

$$\begin{aligned} T(n) &\leq \left(\left(\frac{7}{10} + \frac{1}{5}\right)B + C\right)n \\ &\leq \left(\frac{9}{10}B + C\right)n \\ &\leq Bn \end{aligned}$$

as long as $C \leq \frac{B}{10}$. Since C is fixed, we can set $B \geq 10C$ to make this true. ■

2.3 Lecture 4

2.3.1 Polynomial Multiplication

Suppose we have two polynomials as inputs:

$$A(x) = a_0 + a_1 x + a_2 x^2 + \cdots + a_{d-1} x^{d-1}$$

$$B(x) = b_0 + b_1 x + b_2 x^2 + \cdots + b_{d-1} x^{d-1}$$

Then we want the output polynomial C in the following form:

$$C(x) = c_0 + c_1 x + \cdots + c_{2d-2} x^{2d-2}$$

Define $N = 2d - 1$ for simplicity, and notice that these can all be considered $N - 1$ degree polynomials if we pad A and B with 0 coefficients on higher order terms.

There is a relationship between polynomial and integer multiplication. Given integers α, β, if we want $\gamma = \alpha \times \beta$, we first write them digit-wise as

$$\alpha = \alpha_{N-1}\alpha_{N-2}\ldots\alpha_0$$

$$\beta = \beta_{N-1}\beta_{N-2}\ldots\beta_0$$

$$A(x) = \alpha_0 + \alpha_1 x + \cdots + \alpha_{N-1} x^{N-1}$$

$$B(x) = \beta_0 + \beta_1 x + \cdots + \beta_{N-1} x^{N-1}$$

Note that $\alpha = A(10)$ and $\beta = B(10)$, and $\gamma = (A \cdot B)(10)$ plugging in integers for the polynomials is fairly fast (just some additions and multiplication). This shows that integer multiplication and polynomial multiplication are fairly connected.

Algorithm 2.5 ("Straightforward" Algorithm for Polynomial Multiplication)

$$C(x) = c_0 + c_1 x + \cdots + c_{2d-2} x^{2d-2}$$

What are these coefficients in terms of a_i and b_i?

$$\begin{aligned} c_0 &= a_0 b_0 \\ c_1 &= a_0 b_1 + a_1 b_0 \\ &\vdots \\ c_k &= \sum_{j=0}^{k} a_j b_{k-j} \end{aligned}$$

Then the algorithm looks something like this:

- Loop over $k = 0$ to $N - 1$
  - Compute c_k with a loop from $j = 0$ to k

Note that this algorithm runs $\Theta(N^2)$.

However, we can do better, since integer multiplication is close to polynomial multiplication.

Algorithm 2.6 (Karatsuba for Polynomials)
Call:

$$\begin{aligned}
A_l(x) &= a_0 + a_1 x + a_2 x^2 + \cdots + a_{N/2-1}x^{N/2-1} \\
A_h(x) &= a_{N/2}x^{N/2} + \cdots + a_{N-1}x^{N-1} \\
B_l(x) &= b_0 + b_1 x + b_2 x^2 + \cdots + b_{N/2-1}x^{N/2-1} \\
A_h(x) &= b_{N/2}x^{N/2} + \cdots + b_{N-1}x^{N-1}
\end{aligned}$$

Note that $A(x) = A_l(x) + x^{N/2}A_h(x)$ and $B(x) = B_l(x) + x^{N/2}B_h(x)$. Using the Karatsuba trick, you see that you need 3 multiplications, giving the recurrence:

$$T(N) \leq 3T\left(\frac{3}{2}\right) + \Theta(N)$$

which solves to: $T(N) = \Theta(N^{\log_2 3})$

Here is a fact from elementary algebra:

Note 2.1 (Polynomial Interpolation)
A degree $< N$ polynomial is fully determined by its evaluation on N distinct points.

Proof
Represent polynomial $C = c_0 + c_1 x + \cdots + c_{N-1}x^{N-1}$ as the vector:

$$c = \begin{bmatrix} c_0 \\ c_1 \\ \vdots \\ c_{N-1} \end{bmatrix}$$

Suppose your points are represented as $(x_0, y_0), (x_1, y_1), \ldots, (x_{N-1}, y_{N-1})$. Then we want $y_i = C(x_i)$ for all i. This is equivalent to the following matrix vector product

$$\begin{bmatrix} 1 & x_0 & x_0^2 & \ldots & x_0^{N-1} \\ 1 & x_1 & x_1^2 & \ldots & x_1^{N-1} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_{N-1} & x_{N-1}^2 & \ldots & x_{N-1}^{N-1} \end{bmatrix} \begin{bmatrix} c_0 \\ c_1 \\ \vdots \\ c_{N-1} \end{bmatrix} = \begin{bmatrix} y_0 \\ y_1 \\ \vdots \\ y_{N-1} \end{bmatrix}$$

I.e. we can call this $Vc = y$ and solving this equation is only possible if V is full rank.
However, a fact for the "Vandermonde" matrix V is that

$$\det(V) = \prod_{i<j}(x_i - x_j) \neq 0$$

so we can solve $c = V^{-1}y$, so since we chose distinct x_i, there is a unique polynomial that interpolates, represented by the vector c.

This gives rise to the following idea: rather than multiplying directly, we instead evaluate $C(x_0), C(x_1), \ldots, C(x_{N-1})$ for distinct x_i.

To do this evaluation, just evaluate $A(x_i)$ and $B(x_i)$, then finally combine to get $C(x_i)$. Finally, interpolate to set back coefficients from C in terms of these points.

However, interpolation is way too slow. You have to use inversion which takes $\mathcal{O}(n^3)$ flops. Instead, what if we choose V carefully such that it's faster to invert?

Let us establish some types:

1. The Discrete Fourier Transform (DFT) is a **matrix**.
2. The Fast Fourier Transform (FFT) is a **algorithm**.

Definition 2.1 (Discrete Fourier Transform (DFT))
Define $\omega = e^{2\pi\sqrt{-1}/N}$ (primitive root of unity). Now define the DFT matrix F such that $F_{ij} = (\omega^i)^j = \omega^{ij}$.
Imagine evaluating a polynomial at points $1, \omega, \omega^2, \dots, \omega^{N-1}$
This gives the Vandermonde matrix:

$$V = \begin{bmatrix} 1 & 1 & 1 & \dots & 1 \\ 1 & \omega & \omega^2 & \dots & \omega^{N-1} \\ 1 & \omega^2 & \omega^4 & \dots & \omega^{2(N-1)} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & \omega^{N-1} & \omega^{2(N-1)} & \dots & \omega^{(N-1)(N-1)} \end{bmatrix}$$

i.e. the DFT matrix.

Here is the most important property of the DFT matrix:

Note 2.2 (Inverse of the DFT matrix)

$$F^{-1} = \frac{1}{N}\overline{F}$$

Note that we can view the following algorithm in two lenses: either a fast way to multiply by F^{-1}, or a fast way to calculate $P(\omega), P(\omega^2), \dots$. We take the latter interpretation.

Algorithm 2.7 (Fast Fourier Transform (FFT))
The goal of this algorithm is to multiply by the DFT quickly. We will take a polynomial interpretation. Consider our polynomial, assuming without loss of generality that N is a power of 2:

$$\begin{aligned} P(z) &= p_0 + p_1 z + p_2 z^2 + \dots + p_{N-1} z^{N-1} \\ &= \left(p_0 + p_2 z^2 + p_4 \left(z^2\right)^2 + \dots + p_{N-2}\left(z^2\right)^{N/2-1}\right) + z\left(p_1 + p_3 z^2 + p_5 \left(z^2\right)^2 + \dots\right) \\ &= P_{\text{even}}(z^2) + z P_{\text{odd}}(z^2) \end{aligned}$$

For all N roots of unity, squaring any of them will just give you another Nth root of unity. In fact, it'll give you a $N/2$ root of unity. This means that we only have to evaluate P_{odd} and P_{even} on $N/2$ roots of unity.
Runtime Analysis As we stated before, we only have to evaluate P_{odd} and P_{even} on $N/2$ roots, and they also have degree less than $N/2$, so we make two subcalls of size at most $N/2$. Furthermore, multiplying by z and adding two polynomials takes linear time. This means our recurrence becomes:

$$T(N) \le 2T\left(\frac{N}{2}\right) + \mathcal{O}(N)$$

which solves to:

$$T(N) = \mathcal{O}(N \log N)$$

Finally, we give an algorithm for our initial problem of multiplying polynomials.

Algorithm 2.8 (Polynomial Multiplication Via FFT)
First, we use the Fast Fourier Transpose to compute $\hat{a} = Fa$ and $\hat{b} = Fb$.
Then, for $i = 0$ to $N-1$, we compute, $\hat{c_i} = \hat{a}_i \times \hat{b_i}$.
Finally, we have to bring c back into the original basis, i.e. compute $c = F^{-1}\hat{c}$. To do this, notice

$$\begin{aligned} c &= \frac{1}{N}\overline{F}\hat{c} \\ &= \frac{1}{N}\overline{F\overline{\hat{c}}} \end{aligned}$$

which requires just one more use of FFT to multiply $F\overline{\hat{c}}$.
The runtime is thus dominated by the 3 FFTs, giving us: $\mathcal{O}(N \log N)$ runtime, assuming we can multiply/add/-conjugate complex numbers in constant time.

It may seem paradoxical that since it takes N^2 entries to write down F, how come we have come up with a faster way to multiply by F? The heart of this is that we **never explicitly write down** F. Instead, we just use FFT to multiply F by a vector (quickly).

2.3.2 Cross Correlation

Next we consider the problem of cross correlation. Suppose you have two vectors: x and y:

$$x = \begin{bmatrix} x_0 \\ x_1 \\ \vdots \\ x_{m-1} \end{bmatrix}, y = \begin{bmatrix} y_0 \\ y_1 \\ \vdots \\ y_{n-1} \end{bmatrix}$$

where $n \geq m$. The cross correlation is all shifted dot products of x with y, i.e.

$$\begin{aligned} & x_0y_0 + x_1y_1 + \cdots + x_{m-1}y_{m-1} \\ & x_0y_1 + x_2y_2 + \cdots + x_{m-1}y_m \\ & \vdots \end{aligned}$$

However, we can reduce cross correlation to a problem we have already solved, polynomial multiplication!

Algorithm 2.9 (Cross Correlation Via Polynomial Multiplication)
Define the following:

$$\begin{aligned} X(z) &= x_{m-1} + x_{m-2}z + \cdots + x_0z^{m-1} \\ Y(z) &= y_0 + y_1z + y_2z^2 + \cdots + y_{n-1}z^{n-1} \\ Q(z) &= (X \cdot Y)(z) = q_0 + q_1z + \ldots \end{aligned}$$

Then let us investigate the coefficients of Q:

$$\begin{aligned}
q_0 &= x_{m-1}y_0 \\
q_1 &= x_{m-1}y_1 + x_{m-2}y_0 \\
&\vdots \\
q_{m-1} &= x_{m-1}y_{m-1} + \cdots + x_1y_1 + x_0y_0 \\
q_{(m-1)+1} &= x_{m-1}y_m + \cdots + x_1y_2 + x_0y_1 \\
&\vdots
\end{aligned}$$

Thus, we can multiply the polynomials X and Y, then take the coefficients $m-1$ and bigger to get all of our cross correlation terms.

3 Graph Algorithms

3.1 Lecture 5

3.1.1 Graph Representation

Definition 3.1 (Graph)
A graph is a pair $G = (V, E)$ where V is the set of vertices and E is the set of edges. We generally call $n = |V|$ and $m = |E|$.
If G is a directed graph, then $E \subseteq V \times V$. G is simple if (a, a) (a self loop) is not allowed.
If G is an undirected graph, then E is a set of unordered pairs from V. If there are no self-loops, G is simple.

Example 3.1 (Examples of graphs)
Graphs are often used as convenient ways to represent data.

1. Road network where vertices are intersections, and edges are road segments connecting intersections. (Would be directed, also maybe "weighted" according to distance)
2. Social networks where vertices are people, and edges are friendships. (Facebook would undirected, Twitter/IG would be directed)

How do we represent graphs on a computer? We will assume: $V = \{1, \ldots, n\}$. Then to store edges, we will either:

a Adjacency Matrix: A is an n-by-n matrix where

$$A_{ij} = \begin{cases} 1 & (i,j) \in E \\ 0 & (i,j) \notin E \end{cases}$$

for a weighted graph this becomes:

$$A_{ij} = \begin{cases} w_{ij} & (i,j) \in E \\ \infty & (i,j) \notin E \end{cases}$$

b Adjaceny List: represent E as an array B of linked lists. Then, $B[i]$ is a linked list containing all j such that $(i, j) \in E$.

We can compare the cost of these representations as follows:

	Adjancency Matrix	Adjancency List
Space	n^2 bits	$\Theta(m+n)$ words
$(u,v) \in E$?	$\mathcal{O}(1)$	$\Theta(1+d_u)$
Print all the neighbors of u	$\Theta(n)$	$\Theta(d_u)$

where d_u is the degree of u, i.e. $|\{w \mid (u, w) \in E\}|$.

Note that we could also choose alternative representations. Remember that graphs are abstractions used to store data, so there is no one-size-fits-all solution.

3.1.2 Depth First Search (DFS)

We discuss graph exploration, i.e. visiting all vertices in a graph.

Algorithm 3.1 (Depth First Search)

```
function DFS($V, E$)
    global clock = 1
    global visited = boolean[n]
    global preorder, postorder = int[n], int[n]
    for $v \in V$ do
        if visited[v] is false then explore($v$)
function EXPLORE($v$)
    visited[v] = true
    preorder[v] = clock
    clock = clock + 1
    for $(v, w) \in E$ do
        if visited $w$ is false then explore($w$)
    postorder[v] = clock
    clock = clock + 1
```

The time window between postorder[v] and preorder[v] is exactly the amount of time we spend in recursive calls from v.
We have a claim about the subroutine EXPLORE. Namely, EXPLORE(u) explores exactly: $\{v \mid \exists$ a path from u to $v\}$, i.e. the connected component of u.
An argument for this claim is as follows:

Proof
We need to show two directions.
First, if we explored v, there must be a path from u to v, since every call in the recursion is from one neighbor to another. We can construct the path by just following the path in the recursion tree.
In the other direction, for the sake of contradiction, suppose there exists a reachable v that doesn't get explored. Let the path from u to v be:

$$(u \to x_1 \to x_2 \to \cdots \to x_r = v)$$

Let x_j be the first vertex on the path which isn't explored. Then, look at x_{j-1}, which was explored, which means we looped over all of x_{j-1}'s neighbors. This means we had the opportunity to visit x_j, but we didn't. This means we must've visited x_j and failed the if check. This is a contradiction, we visited x_j and didn't. Thus, we must have that all reachable v's are explored.

Now we look at the runtime of the routine. First, note that the outer for loop runs n times. Then, we have to enumerate the neighbors of u for all vertices u in the graph. We only have to do this once, since we visit each vertex only once.
This means that the total running time is:

$$T(n) = \Theta(n) + \sum_{u \in V} \text{time to enumerate neighbors}$$

which depends on our graph representation. With our adjacency matrix, the second term is quadratic. In the adjacency list, it is just the sum of (degrees + 1) which will be exactly $2m + n$. (Since by adding degrees we double count the number of edges).

	Adjancency Matrix	Adjancency List
DFS time	$\Theta(n^2)$	$\Theta(m+n)$

TODO: Add a pictoral example of DFS from lecture.

There are many applications of the DFS:

- Reachability - Identifying the separate connected components
- Articulation points - The set of vertices whose removal disconnects the graph

- Finding biconnected/triconnected components - if there are two/three disjoint paths between any two vertices
- Strongly connected components - In a directed graph, two vertices are strongly connected if there is a path from one vertex to another and from that other vertex back to the original
- Planarity testing - Testing if a graph is planar, i.e. you can draw it without crossings
- Isomorphism of planar graphs - Telling whether two planar graphs are isomorphic, i.e. we can turn one into the other with a bijection

The first set of problems we have already solved. Reachability is everything we visit in one iteration of the outer loop. The amount of connected components is the amount of explore calls in the outer loop.

Definition 3.2 (Preorder, Postorder)
The notation $\text{pre}(u)$ and $\text{post}(u)$ denote the preorder and postorder number of a given vertex u in a run of the DFS algorithm on some graph containing u.

Now let us explore another claim about the DFS.

Note 3.1
For some vertex u, the set of intervals $[\text{pre}(u), \text{post}(u)]$ are either pairwise nested or disjoint. The argument is that pairwise, either two are in the same connected component or different components. In the same component, one must have started before the other, then the recursion finished the inner one, then it must've ended. In different components, the intervals are disjoint.
Let us denote previsiting a vertex u as $[_u$ and postivisiting that vertex as $]_u$.

It helps us to classify the graph edges during a DFS.

Definition 3.3 (Types of Graph Edges)
These are the types of edges in a DFS traversal of G.

1. Tree edge: Traversed edge during DFS (in the DFS tree).
2. Forward edge: Goes from an ancestor to a descendant in the DFS tree, and is not a tree edge.
3. Back edge: Goes from a descendant to an ancestor in the DFS tree, and is not a tree edge.
4. Cross edge: An edge that is not any of the above.

The useful facts about these edges are as follows:

Theorem 3.1
Suppose $(u, v) \in E$. $\text{post}(u) < \text{post}(v)$ if and only if (u, v) is a back edge.

Proof
The backwards part of the claim is simpler. Basically u is a decendant of v, so the order is something like $[_v \ldots [_u$, so $]_u \ldots]_v$ must happen, i.e. the postorder numbers have the given order.

Theorem 3.2
G has a cycle if and only if it has a back edge.
We again take the backwards case first. By the definition of a back edge, there must be a series of tree edges from some vertex u to v and then a back edge from v to u. This implies there is a cycle from u to u.

Proof
Now the forward part of the claim, consider the cycle:

$$u_0 \to u_1 to \cdots \to u_k \to u_0$$

Take u_i with the lowest postorder number. Then the edge:

$$(u_i, u_{(i+1) \mod k})$$

goes from a higher postorder number to a lower postorder number, which means that by the previous result, this edge is a back edge, showing our claim.

3.2 Lecture 6

3.2.1 Topological Sort

We consider the problem of topological sort. We take as input a directed acyclic graph (DAG). We seek to find an ordering of V such that $(u, v) \in E \implies u$ must come before v in the ordering. Note that such an ordering of the graph is not necessarily unique. Intuitively, it represents the order that dependencies must be filled in order to solve a problem.

Algorithm 3.2 ("Brute-force" Search)
Try all permutations of the vertices. Return the first one that is a topological sort.
The runtime is $\mathcal{O}n!mn$, because for each of $n!$ permutations, we have to check m edges that the edge is respected, and finding each endpoint of the edge needs to be found in the sorted order.

To find a faster algorithm, let us define some terms.

Definition 3.4 (Source, Sink)
In a directed acyclic graph, a source is a vertex with no incoming edges. A sink is a vertex with no outgoing edges. Note that every DAG has a source and a sink.

Algorithm 3.3 (Source Peel-Off)
We can iteratively "peel-off" source vertices one at a time. It is possible to do this algorithm in linear time: $\mathcal{O}(m + n)$.
To do so, have n linked list nodes, one for each vertex. Then we keep an array B where the ith entry of the array stores a pointer to node i. Then, we also keep an array B of linked lists where the ith entry of that array is a doubly-linked list that has i incoming edges. To peel off a source, you take anything in the 0th entry of the array and take it out, call it u. Then, for each outgoing edge (u, v), move v to the lower bucket in the array (since it now has one less incoming edge). Rinse and repeat.
This is a bit too complicated. There is an easier linear-time algorithm.

Consider the following pre and postorder traversals (subscripts dropped for clarity):

$$[[][]][][[]]$$

then, it's easier to see that the vertex associated with last closing bracket is a source; it has nowhere else that lead to it. This leads to the following result:

Theorem 3.3 (Finding a Source with DFS)
The vertex v with the largest postorder number must be a source.

Proof
Suppose for the sake of contradiction that v is not a source. That means there must exist a $u \in V$ such that $(u, v) \in E$.
We know that the only possibilities are that $[_u]_u[_v]_v$ or $[_v[_u]_u]_v$. The latter means that (u, v) is a back edge, which would mean there is a cycle. However there are no cycles since this is a DAG, so this cannot be the case. The former means that u and v are disconnected, but there is clearly an edge between them or that v was already visited, which is also not the case.
By exhaustion of cases, we have a contradiction, so v must be a source. ∎

Algorithm 3.4 (Topological Sort)
We begin by doing a DFS traversal on G. Then, we sort by postorder number. This exactly a topological sort

of the graph.
This works because peeling off the source causes the DFS to be the exact same, so the order of postordering numbers does not change.
Note that postorder number is bounded between 2 and $2n$, so it is easy to sort in linear time. Thus the runtime is dominated by DFS, $\mathcal{O}(n+m)$.

3.2.2 Strongly Connected Components

Next we try to find strongly connected components in a directed graph.

Definition 3.5 (Strongly Connected)
For some directed graph $G = (V, E)$, $u, v \in V$ are strongly connected if u has a parth to v and v has a path to u.

Definition 3.6 (Strongly Connected Component (SCC))
A strongly connected component in a graph G is a maximal subset of strongly connected vertices.

An easy algorithm to find SCCs would be to do n DFS's from each vertex and check strong connectivity. However, this is fairly slow, about $\mathcal{O}(mn+n^2)$.

Theorem 3.4 (SCC Graph is a DAG)
The graph made from treating the SCCs as nodes is acyclic (a DAG).

Proof
Suppose there was a cycle. Then, all the vertices in those components forming a cycle are strongly connected, which would contradict the fact that the SCCs were maximal. Thus, there cannot be a cycle.

We want to find a sink of this reduced DAG. In particular, running a DFS from the sink SCC, we can peel it off and recurse. This means we want to find the SCCs in reverse topological sorted order. Imagine we had a subroutine that could find a vertex in a sink in constant time. Then, the runtime would be: $\mathcal{O}(n+m)$ because we have to DFS over every single strongly-connected component, visiting every vertex and edge once.

To do this, first let us reverse the graph (make all the edges go the other direction). This will turn any source into a sink and vice versa. Now we have to find a source SCC in the reversed graph G_{rev}. The claim is that the highest postorder number still works.

Theorem 3.5
If u has the highest postorder number, then u is in the source SCC.

Proof
Suppose that u is not in the source SCC. That means there is another SCC that point into that SCC of u. This means that $(v, w) \in E$, where w has a path to u and u has a path to w. Since v thus has a path to u but u has the highest postorder number, the intervals cannot be disjoint. Furthermore, the intervals cannot be inside each other, as this would imply u would have a path v; but that would mean they're in the same SCC, which they're not. Thus, the edge (v, w) cannot exist, meaning that u is in the source SCC.

Finally our algorithm to find the SCCs is as follows:

Algorithm 3.5
1. Reverse the graph and run topological sort on it. This will give you the ordering S of sinks in the original

graph.

2. Run DFS on each sink s in order. The vertices reached are in SCC of s, so we can remove them from the graph (mark them) and keep going.
3. The SCCs removed are all the SCCs.

This algorithm requires a topological sort and then small DFS's which amount to a single big DFS. This is $\mathcal{O}(m+n)$.

3.3 Lecture 7

3.3.1 Single Source Shortest Paths

We now consider shortest paths. Suppose we are given a directed graph G and a start vertex s. We wish to find the shortest path from s to all other vertices. More precisely, we want two arrays:

- $\text{prev}[1, \dots, n]$, where $\text{prev}[v]$ is the previous vertex to v on the shortest path from s to v.
- $\text{dist}[1, \dots, n]$, where $\text{dist}[v]$ is the length of the shortest path from s to v.

Note that the prev array has enough information to give us the actual shortest path from s to v.

There are many algorithms for single-source shortest paths. Here are a few:

- Breadth-First Search - Assumes edges all have weight 1 ("unweighted")
- Dijkstra's Algorithm - Assumes edge weights are all non-negative.
- Bellman-Ford Algorithm - Arbitrary edge weights.
- Dynamic Programming on DAGs - Arbitrary edge weights, but G must be a DAG.

Note that depth-first search does not work because going deep first may yield a longer path than some other traversal. Consider the graph:

$$V = \{S, A, B\}, E = \{(S, A), (A, B), (S, B)\}$$

Then suppose the DFS traversal was S, A, B. Then the path to B would seem like it's distance 2, when in reality it's 1, since the (S,B) wouldn't be traversed by DFS.

Algorithm 3.6 (Breadth-First Search)
Here is the main algorithm:

```
function BFS($G, s$)
    dist$[1 \dots n] \leftarrow \infty$
    prev$[1 \dots n] \leftarrow$ null
    vis$[1 \dots n] \leftarrow$ False
    Q $\leftarrow$ queue($s$)
    dist$[s] \leftarrow 0$
    vis$[s] \leftarrow$ True
    $Q$.push($s$)
    while $Q$.size$> 0$ do
        $u \leftarrow Q$.pop()
        for $(u, v) \in E$ do
            if !vis$[v]$ then
                vis$[v] \leftarrow$ True
                dist$[v] \leftarrow$ dist$[u] + 1$
                prev$[v] \leftarrow u$
                $Q$.push($v$)
    return dist, prev
```

Runtime Analysis

Proof
The first 3 operations are linear in n, and the last 4 are constant time. Then note that every vertex is added to

the Q once, and all of its edges are looped over. So the total runtime is:

$$T(n) \leq \Theta(n) + \sum_{v \in V} C \cdot (1 + \text{outdegree}(v))$$

Note that the sum of the outdegrees counts every edge once. Thus, $T(n) = \mathcal{O}(m + n)$.

The interesting thing about BFS is that it is implemented the exact same as iterative DFS, but the stack is replaced with a queue.

To show correctness, we require a few intermediate results:

Theorem 3.6 (BFS Lemma 1)
$\forall v \in V$, $\text{dist}[v] \geq \delta(s, v)$ (the true shortest distance).

Proof
We proceed by induction on k, the number of push operations to Q so far. $k = 1$ is trivial, since the dist of s is 0 and everyone else's distance is infinity, satisfying the inequality. Consider the $k + 1$st push (with the induction holding for $\leq k$), during the edge (u, v). We push v when we visit u. By the inductive hypothesis, $\text{dist}[u] \geq \delta(s, u)$, so

$$\text{dist}[v] = 1 + \text{dist}(u) \geq \delta(s, u) + 1 = \delta(s, u) + \delta(u, v) \geq \delta(s, v)$$

completing the induction.

Theorem 3.7 (BFS Lemma 2)
Look at any point in time i. Say $Q = [v_1, \ldots, v_r]$. Then

1. $\forall i, \text{dist}[v_i] \leq \text{dist}[v_{i+1}]$
2. $\text{dist}[v_r] \leq \text{dist}[v_1] + 1$

Proof
The proof is similar to the theorem above. Induct on the number of queue operations.

Now we can show the correctness of BFS.

Theorem 3.8 (The Correctness of Breadth-First Search)
We will show that BFS finds shortest paths from s.

Proof
For the sake of contradiction, suppose the dist arry is incorrect. Then, there is some $v \in V$ such that $\text{dist}[v] \neq \delta(s, v)$. By BFS Lemma 1, we must have $\text{dist}[v] > \delta(s, v)$. This may be the case for many such v. Let us pick the v such that $\delta(s, v)$ is minimum (note that $v \neq s$). Then, let us take the shortest path from s to v.

$$s \longrightarrow v_1 \ldots v_{r-1} \ldots v$$

This means for all intermediate vertices until v_{r-1}, the dist array was set correctly. Look at the point in time when v_{r-1} was popped off Q. But this means that v was not put into the Q (since the distance was resolved incorrectly) at this point. This means that v was visited already by some other vertex u and by BFS Lemma 2, this means that $\text{dist}[u] \leq \text{dist}[v_{r-1}]$. But this would mean that v got set to some value:

$$\text{dist}[v] = \text{dist}[u] + 1 \leq \text{dist}[v_{r-1}] + 1 = \delta(s, v)$$

However, we initially claimed $\text{dist}[v] > \delta(s,v)$, so this is a contradiction! So we cannot have any place where the dist array is incorrect.

3.3.2 Weighted Graphs

Note that if all weights $w(e) \in \mathbb{N}$, then we can reduce finding the SSSP to the unweighted case by just subdividing edges into $w(e)$ fake vertices in the middle. If $w(e) \leq L$, then the BFS runtime is $\mathcal{O}(n + mL)$. We can do better (and also use $w(e) \in \mathbb{R}$).

To do this, we use heaps (or priority queues). A min-heap is a data structure that maintains a set of (key, value) pairs S subject to the following three operations:

1. delMin(), returns (k, v) from S with the smallest k and removes it from S.
2. decKey(O, k'), where O is a pointer to the v object, replaces the old key with a smaller key k'
3. insert(k, v), inserts (k, v) into S

We can now use these heaps to solve SSSPs for arbitrary non-negative weighted graphs.

Algorithm 3.7 (Dijkstra's Algorithm)

```
function DIJKSTRA($G, s$)
    dist$[1 \dots n] \leftarrow \infty$
    prev$[1 \dots n] \leftarrow$ null
    $H \leftarrow$ heap()
    for $v \in V$ do
        $H$.insert$(\infty, v)$
    dist$[s] \leftarrow 0$
    $H$.decKey$(s, 0)$
    while $H$.size$> 0$ do
        $u \leftarrow H$.delMin()
        for $(u, v) \in E$ do
            if dist$[u] + w((u, v)) <$ dist$[v]$ then
                $H$.decKey$(v, \text{dist}[u] + w(u, v))$
                dist$[v] \leftarrow$ dist$[u] + w((u, v))$
                prev$[v] \leftarrow u$
    return dist, prev
```

Runtime Analysis We do n insertions and thus must do n deleteMins, and we are doing potentially deg(v) insertions for each, so overall, considering t_I as the runtime of insert, t_{dK} for decKey and t_{dM} for delMin, we have the runtime is something close to: $T(n) = \mathcal{O}(n + m + nt_I + nt_{dM} + mt_{dK})$ which is:

$$T(n) = \mathcal{O}((m + n) \log n)$$

for a binary heap implementation.

Proof of Correctness First realize the following: Any non ∞ dist$[u]$ value corresponds to some $s \to u$ path. This can be shown formally by induction on the main loop of the algorithm.

The main claim is that the final dist and prev arrays are correct, so for all u, dist$[u] = \delta(s, u)$. Note that if we do this, then the prev array is correct because note that we change the prev arrays exactly when the dist arrays are set, so the path traced out is the correct one.

To show the claim, let

$$A = \{\text{all vertices that have been popped off the heap so far}\}$$

at the end of the algorithm, the heap is empty so all the vertices have been popped off. Thus, we will show the following invariant: that for any $u \in A$, dist$[u] = \delta(s, u)$. We proceed by induction.

Base case: If $|A| = 1$, then only s has been removed off the heap. Since we set its distance initially, we know dist$[s] = 0 = \delta(s, s)$.

Inductive step: Say $|A| = k + 1$, so we just popped a vertex v off the heap. So, we just need to make sure dist$[v]$ is correct; the rest are correct by inductive hypothesis ($|A| = k$ without v). Then, v must've been the minimum key in the heap, so its dist must've been set last by some $u \in A$ (since it was popped off previously). Thus, there is an edge (u, v). Furthermore, there is a path from s to u called p by the inductive hypothesis. We claim that appending (u, v) to p yields the shortest path. Suppose it wasn't and we could do better, with some other path p'. Then at some point, this path must leave A (since v was still outside A at this point). Consider the last vertex before it leaves A as x and call the first vertex after it leaves as y. Let the subpath from s to x be q. Then, the length of p' is as follows:

$$\begin{aligned} L(p') &\geq L(q) + w(x, y) \\ &= \delta(s, x) + w(x, y) \\ &= \text{dist}[x] + w(x, y) \end{aligned}$$

But since y is a neighbor of x, then we had to have updated it in the past, at least through the update at vertex x. Thus, the dist value is at most the last line, since that is what an update in dijkstra's looks like.

$$L(p') \geq \text{dist}[y]$$

However, since v was the last thing popped off the heap and y wasn't, its dist value is lower.

$$\begin{aligned} L(p') &\geq \text{dist}[v] \\ &= L(p) \end{aligned}$$

Which means that p' can't be any shorter than p, completing the induction and the proof.

3.4 Lecture 8

3.4.1 Minimum Spanning Trees

We look at finding the minimum spanning tree in some connected graph G. First, we define these notions.

Definition 3.7 (Tree)
A tree is an undirected graph that is connected and acyclic.

Definition 3.8 (Spanning Tree)
The spanning tree of some undirected graph $G = (V, E)$ is a subgraph of G called $T = (V, E')$ with the same vertices and edges $E' \subseteq E$.

Then, the notion of a minimum spanning tree is finding a spanning tree whose edge weights added up have minimal cost.

Here is a nice result about trees.

Theorem 3.9
Consider some graph T. Any of the following two implies the third:

1. $|E(T)| = n - 1$.
2. T is connected.
3. T is acyclic.

As a corollary, any two of these define a tree.

Here is a slow algorithm to tackle the problem.

Algorithm 3.8 (Brute Force MST)
Take all subgraphs with $n - 1$ edges. Next, check if each is connected (using DFS), if it is connected, then calculate the weight. Finally take the minimum of the weights.
The runtime is roughly:

$$\mathcal{O}\left(\binom{m}{n-1}(n-1+n)\right) \leq \mathcal{O}\left(\binom{n^2}{n-1}n\right) \leq \mathcal{O}(n^n)$$

Next, let's discuss a faster algorithm; it's a meta-algorithm that we can use to make other algorithms by filling in key implementation details.

Algorithm 3.9 (MST Meta-algorithm)

```
function MetaAlg($G$)
    $X \leftarrow \emptyset$
    while $|X| < n - 1$ do
        Pick $S \subsetneq V$, $S \neq \emptyset$ such that no edge in $X$ cross $(S, V \setminus S)$
        Let $e = (a, b)$ be one of the min-weight edges in $G$ crossing the partition
        $X \leftarrow X \cup \{e\}$
    return $(V, X)$
```

Proof of Correctness We will show at all points in time, there exists an MST T containing X. If we show this, this means that at the end of the while loop, since T conatins X and is the same size, X becomes T. We proceed

by induction on $|X|$.
Base case: $|X| = 0$ works because a connected graph G always has an MST, which trivially contains the empty edge-set.
Inductive step: Suppose that for X so far, it was contained by T. Now, we are adding one more edge $e = (a, b)$ where $a \in S$. There are two cases:
Case 1: T had the edge (a, b). Then X is still contained by T.
Case 2: T did not have the edge (a, b). Note that since T is a spanning tree, there must be a path from a to b, i.e. it must pass the partition V and $V \setminus S$ somewhere. If we combine this path with (a, b), we get a cycle. Then, there must be a family of edges which all cross the partition; removing any one of them forms a tree. Suppose now we remove any edge (x, y). We define

$$T' = T \cup \{(a, b)\} \setminus \{(x, y)\}$$

However, the weight of $T' \leq$ weight of T since the weight of (a, b) is at most the weight of (x, y) because by construction it is the lightest edge across the partition. This means that T' is also an MST, which also contains X, so the claim holds.

Now, we are left with a choice: how do we construct our paritioning set S?

Algorithm 3.10 (Prim's MST Algorithm)
Prim's partitions the set based off a starting vertex s.

```
function Prim($G, s$)
    $X \leftarrow \emptyset$
    $S \leftarrow \{s\}$
    for $n - 1$ times do
        $(a, b) \leftarrow$ min-weight crossing($S, V \setminus S$), where $b \notin S$
        $S \leftarrow S \cup \{b\}$
        $X \leftarrow X \cup \{(a, b)\}$
    return $(V, X)$
```

To implement this efficiently, we get the min-weight crossing by using a heap. We greedily take the cheapest edge that's not yet in our tree; this is precisely that min-weight crossing. Every time we add something new to S, all we should do it scan the edges and update it's distance from our tree accordingly. The implementation is ommitted here.
Runtime Analysis The runtime becomes the exact same as Dijkstra's algorithm, since we update distances and pop things off the heap the same way (except updating distances is the distance to the tree, instead of doing an addition), so with a binary heap, the runtime is the same $\mathcal{O}((m + n)\log n) = \mathcal{O}(m \log n)$ since $m \geq n - 1$ since the graph is connected.

To present another approach, we first discuss a new data structure.

Note 3.2 (Union-Find Data Structure)
Suppose we want to maintain a partition of $\{1, \ldots, n\}$ subjects to 2 operations.

1. find(a) returns the name of the partition that a is in.
2. union(a, b) merge the partitions containing a and b.

Now we discuss an even more greedy approach.

Algorithm 3.11 (Kruskal's Algorithm)
Kruskal's algorithm uses a global approach.

```
function KRUSKAL($G$)
    Sort $E$ in increasing order of weight.
    $X \leftarrow \emptyset$
    Initialize a UnionFind data structure.
    for $(a, b) \in E$ (in increasing order of weight) do
        if find$(a) \neq$ Find$(b)$ then
            $X \leftarrow X \cup \{e\}$
            union$(a, b)$
    return $(V, X)$
```

4 Greedy Algorithms

4.1 Lecture 9

A greedy algorithm is not super mathematically well-defined property. Generally, we can separate the problems that greedy can solve into two types of problems:

1. Search problems: which try to find an object in a large set.
2. Optimization problems: which try to find the object (or objects) in a large set that have some maximal or minimal property.

So, we then define:

Definition 4.1 (Greedy Algorithm)
A greedy algorithm is one that builds the solution to a problem iteratively using a sequence of local (or locally optimal) choices.

Note that brute-force search is not greedy; in a greedy algorithm, you generally stick to your local decisions, never looking back.

We now discuss three problems that one can solve with a greedy approach.

4.1.1 Scheduling

We take as input as a collection of jobs that need to be done. Each job has a time interval $[x_1, y_1], \dots, [x_n, y_n]$ where $x_i < y_i$. Now, we want to find the maximal amount of jobs that can be done without any time conflicts (e.g. with one thread).

To be greedy, what local choice should be make?

One idea is to greedily keep doing the shortest possible remaining job; it unfortunately does not work. Consider the jobs $[1, 10], [9, 11], [11, 20]$, where this algorithm will choose only the middle interval as one job, but clearly the optimal solution is taking the first interval and the last one.

Instead, let us make a different choice.

Algorithm 4.1 (Scheduling)
Greedily pick the next job to have the shortest y_i (end time) without conflicting with already-done jobs.
Runtime Analysis We can implement this by sorting by the end-times. Then take the first element $[x, y]$ and consider the next element $[x', y']$. Since $y \leq y'$ then checking for no conflict is just checking that $x' \geq y$. Thus, we have to just do a for loop over the array to implement the above logic. The bottleneck is the sort, giving us $\mathcal{O}(n \log n)$.
Now, to prove correctness for greedy algorithms, we generally use an exchange argument, where we postulate the existence of a solution strictly better to the output produced by the algorithm, and show a contradiction.
Proof of Correctness Suppose our algorithm gives J, giving jobs $j_1, j_2, \dots, j_k$ (in sorted order by endpoint) and this not optimal. Take some optimal solution S such that $|S \cap J|$ is maximum. We will show there exists another optimal solution S' such that $|S' \cap J| > |S \cap J|$, giving us a contradiction of maximality.
Let us sort by endpoint on S, making $s_1, s_2, \dots, s_k, s_{k+1}, \dots$. The j's are not the same as the s's because otherwise the greedy algorithm would've taken more s's (since the s's are not conflicting and sorted by end time). Thus, there must exist some first t such that $j_t \neq s_t$. Now, let us introduce a new solution S' with s_t is replaced by j_t. j_t's end-time is earlier or at the same time as s_t, so there cannot be any conflicts after j_t (otherwise there would've been a conflict with s_t) and there cannot be any conflict before j_t (because the rest of the s's agree with j, and there is no conflict among the j's). Furthermore, $|S'| = |S|$. Thus, S' is also an optimal solution; but $|S' \cap J| = |S \cap J| + 1 > |S \cap J|$, as required for contradiction.

Now, working through the example above, we will select $[1, 10]$ first, then the second interval won't be added since it's conflicting, then the third interval will be added since it's not conflicting.

4.1.2 Huffman Encoding

We now discuss the problem of efficient encoding. Suppose we have some alphabet Σ, $|\Sigma| = n$ (e.g. $\{A, \dots, Z\}$) and some text w whose characters come from Σ. Now there are character frequencies:

$$freq(\sigma) = \text{Number of occurences of } \sigma \text{ in text}$$

Now, how can we encode the text as efficiently as possible using these characters (minimizing codeword length)? One concern for encoding is that certain codewords may have the same word that created it. We want our encoding to be unambiguous; one way to ensure this is using prefix-freeness.

Definition 4.2 (Prefix-Freeness)
An encoding is prefix-free if no character's encoding is a prefix of any other character's encoding.

Note that any code that is prefix-free cannot be ambiguous, because the unique prefix will tell you which character to look at. Thinking in terms of bits, the following encoding:

$$A = 0, B = 01, C = 001, \dots$$

can be represented by a binary trie where each branch is a 0 or 1; the leaves are all characters.

Now, we want to find the optimal prefix-free encoding. Naively, we could find all binary trees on n leaves ($2n - 1$ nodes) and assignments of characters to leaves. The number of binary trees is exponential, about 16^n and there $n!$ assignments. We also have to do a linear check of length to check cost; this means our total runtime is $\mathcal{O}(n!)$. Note that even we assigned all characters to leaves greedily, this would still be an exponential-time algorithm!

Furthermore, being fully greedy and letting the highest frequency character hang at the top of the tree is also not optimal. In the case of equal frequency, we want a perfectly balanced tree (the best compression of 26 characters is to use 5 bits, if they are equal frequencies).

Here is a better way:

Algorithm 4.2 (Huffman Encoding)
We try to build the tree bottom-up. Note that at the lowest depth, any node v has a sibling (otherwise we could delete the parent of v and replace v with that to have less bits). At these two leaves, let us place the least-frequent characters here. We claim this is optimal; suppose there was another optimal way to do things where a different pair was at the bottom of the tree, then you can switch the one of the least-frequent to the bottom, saving you characters in your encoding.
To do this algorithm greedily, we simply repeat this choice over and over iteratively. To see this in action, we present an example.
First, notice that we have to do $n-1$ iterations. To find the smallest characters in the set, we can keep a min-heap, requiring 1 $\Theta(\log n)$ insertion and 2 $\Theta(\log n)$ removals. Then, building the tree is done in constant time in each iteration. Our total runtime is $\Theta(n \log n)$.

Example 4.1
Consider the following frequencies on the alphabet of capital vowels:

$$A : 60, E : 70, I : 45, O : 50, U : 20, Y : 30$$

Placing the two smallest nodes U and Y at the bottom of the tree then creates a certain "meta-character" $\{U, Y\}$ with frequency $20 + 30 = 50$. Our frequencies then become:

$$A : 60, E : 70, I : 45, O : 50, \{U, Y\} : 50$$

Now we take the next two smallest nodes (I and $\{U, Y\}$) and place it at the bottom of tree, creating:

$$A : 60, E : 70, O : 50, \{I, U, Y\} : 95$$

Continuing, we have:

$$\begin{aligned}&A : 60, E : 70, O : 50, \{I, U, Y\} : 95\\&E : 70, \{I, U, Y\} : 95, \{A, O\} : 110\\&\{E, I, U, Y\} : 165, \{A, O\} : 110\\&\{A, E, I, O, U, Y\} : 275\end{aligned}$$

Then, we've build the tree; we can traverse with DFS to then get the encoding per character.

4.1.3 Set Cover

Now we consider another problem. We are given a Universe $\{1, \ldots, n\} = [n]$ and a collection $C = \{S_1, \ldots, S_m\}$ of subsets of $[n]$. We want to find a minimum-size subcollection to cover $[n]$. Generally, we don't expect there to be a polynomial-time algorithm to solve this. The natural greedy approach (where we take the biggest subset every time) does not give the optimal solution (easy to see with a counterexample).

Let the optimal number of sets be OPT. Feige showed that if there exists a polynomial-time algorithm for set cover, which always uses less than $OPT \times \ln n$ sets, then 3-SAT can be solved in time $\leq n^{\log\log n}$ (which we don't believe to be true).

This makes greedy even more tantalizingly close:

Theorem 4.1
The natural greedy approach uses $\leq OPT \times \lceil \ln n \rceil$ sets.

The greedy algorithm for set cover is as follows:

Algorithm 4.3
```
function GreedySC($C$)
    $A \leftarrow \{1, \ldots, n\}$ // Not covered yet
    $B \leftarrow \emptyset$ //Sets taken
    while $|A| > 0$ do
        Let $j \in [m] \setminus B$, be s.t. $|A \cap S_j|$ is max
        $A \leftarrow A \setminus S_j$
        $B \leftarrow B \cup \{j\}$
    return $B$
```
Now we prove our earlier claim. Say that OPT uses k sets. We want to bound $|B|$.

Proof
Let A_t be A after t times through the main loop. Note $|A_0| = n$. There must be some set S_t^* in OPT covering $\geq \frac{1}{k}|A_t|$ elements in A_t, because on average, every set covers that many elements on A_t, so there must be at least one that is at least the average. This means that greedy took some set covering $\geq \frac{1}{k}|A_t|$ elements in A_t. Therefore:

$$|A_{t+1} \leq \left(1 - \frac{1}{k}\right)|A_t|$$

By induction on t, we just have:

$$|A_L| \leq \left(1 - \frac{1}{k}\right)^L |A_0| = n\left(1 - \frac{1}{k}\right)^L$$

Now, we just want to understand when this quantity is less than 1. Since $1 + x < e^x$, then:

$$|A_L| < n(e^{-L/k}) < 1$$

Which means $|B| = L^* \leq \lceil k \ln n \rceil$.

4.2 Lecture 10

4.2.1 Union Find

We now investigate how to build a union find data structure that we described earlier (disjoint sets where find$(\cdot)$ tells you the name of the set that some number is in, and union$(\cdot, \cdot)$ unions together the associated sets). See the Kruskal's section for more information.

First, think of a naive approach. We could potentially store an array $A[1 \dots n]$, where $A[x]$ tells you the name of x's set. find(x) is easy, just return $A[x]$. This runs in constant time. To union(x, y), we find $a = A[x]$, $b = A[y]$ and then change all of the indices having value a to b (by looping over them). This is linear time.

Secondly, let's try an array of linked lists. Represent x by a linked list node. $A[x]$ is a pointer to a linked list node that corresponds to x (which is itself part of some circular doubly-linked list). Thus, we end up with a collection of linked lists; make each of these one of the sets.

Then, to find(x), we follow the pointer $A[x]$ all the way up its linked list to the head. This is worst-case linear time. To union(x, y), then put the head of one linked list to point to the tail of another linked list. This also takes linear time to traverse, and then changing the pointers takes constant time.

Let us think of an optimization. How about if every node stored a pointer to its list's head node? Well, during a union, we may need to update all the head pointers in some list; this would make union linear time and find constant time. Another optimization is to make sure the smaller list always goes under the bigger list. To do this, we can have the head pointers store their size.

Now the claim is that this optimized version, any sequence of operations consisting of at most m finds and at most n unions takes total time $\Updownarrow + \backslash \log \backslash$. This is slower than the sorting step in Kruskal's and is actually enough to get optimal runtime.

Proof
First, doing a find takes constant time. But a single union takes:

$$\mathcal{O}(1) + \mathcal{O}(\text{head pointer changes})$$

Thus, the total runtime is:

$$\mathcal{O}(m + n + \text{total head pointer changes}) = \mathcal{O}\left(\sum_{x=1}^{n} (\text{number of times I changed } x\text{'s' head pointer})\right)$$

Note that whenever I change a head pointer, the size of the list that x is a part of at least doubles. Thus, the maximum amount of times that list can double is $\log_2 n$, which will thus be at least amount of times I changed each node's head pointer. Thus, we end up with:

$$\mathcal{O}(m + n \log n)$$

as we wanted to show.

However, this isn't the best we know. We know an even better algorithm, with a disjoint forest. But first, we must digress to amortized runtime, to formalize the idea of "good" average cost.

Definition 4.3 (Amortized Runtime)
Suppose a data structure supports operations $O_1, O_2, \dots, O_k$. Then, we say the amortized cost of each operation t_j if for any sequence of operations with N_i of operation O_i over all i, the total time is

$$\leq \sum_{j=1}^{k} t_j N_j$$

Now, we look at the best way we know of implementing union find.

Algorithm 4.4 (Disjoint Forest Union Find)
Let us represent sets as collections of rooted trees. First, we consider the path compression optimization. What this means is that whenever we traverse a find from some node to a root, then for every node we pass along the way, we make its pointer point directly to the root.
Then, we do an analogous "length" optimization for union, where you make the shallower "list" (now trees) just point its root to the deeper tree's root (again, by storing the depth of the tree e.g. in an array). Then, to update the depth; it doesn't change if the depths of the trees are different, and if they are the same, then the depth of the root increases by 1.
However, doing both of these optimizations creates a problem: we have to update the depth every time we do path compression. We just ignore updating the heights during a path compression (and maybe call this number rank instead of height).
Here is the pseudo-code.

```
$p[1 \dots n], r[1 \dots n]$
  function MakeSet($x$)
      $p[x] \leftarrow x$
      $r[x] \leftarrow 0$
  function Find($x$)
      if $x = p[x]$ then
          return $x$
      $p[x] \leftarrow$ Find($x$) return $p[x]$
  function Union($x, y$)
      $x \leftarrow$ Find($x$)
      $y \leftarrow$ Find($y$)
      if $x = y$ then
          return
      if $r[x] > r[y]$ then
          Union($x, y$)
      $p[x] \leftarrow y$
      if $r[x] = r[y]$ then
          $r[y] \leftarrow r[y] + 1$
```

Runtime Analysis Let $\log^*(n)$ be the amount of times you have to take the $\log(n)$ before you get down to 1 (for all practical purposes, this is no more than 5). We claim any sequence of at most m Finds and n Unions/Makesets takes total time

$$\mathcal{O}((m+n)\log^*(n))$$

This gives us amortized $\log^*(n)$ runtime for all the operations.
Before we do this, we claim some properties:

1. Any root node x has $\geq 2^{r[x]}$ elements in its tree.
2. Ranks strictly increase as you follow parent pointers.
3. The number of nodes with rank exactly k is $\leq \frac{n}{2^k}$.

Proof
Imagine every number from 1 to n either pays cash or charges its credit card (in terms of running time, every time it does an operation). Then, to find the total running time (cost) we add up this "cash" and add up all the credit card dues.
Look at our n items at any point in time. They all have some ranks; the ranks go from 0 to $\log n$. We can place these items into buckets based on rank, in the following way:

$$[0,1), [1,2^1), [2,2^2), [2,2^{2^2}), \dots$$

The largest rank that can exist is $\log_2(n)$ (by claims 1 and 2), so the number of groups is $\log^*(\log_2(n)) = \log^*(n) - 1$.

Now let's do some "accounting." Find is generally what takes time; the total time is:

$$\mathcal{O}(m + n + \# \text{ of parents pointers I follow})$$

Suppose we following a parent pointer from u to v. Then, we have a few cases:

1. v is the root of its tree. Let's pay cash here. In every find/union operation, we do this exactly once, so this is $\mathcal{O}(1)$ per op.
2. u, v are in different groups (as defined above) with neither as the root. We will again "pay cash". how many times do we change groups? Since rank increases as we follow parent pointers, so the maximum amount of times we can change groups while going up is $\mathcal{O}(\log^*(n))$ per op/
3. u, v are in the same groups (as defined above) with neither as the root. We charge these operations to u's credit card; we will account for this at the end.